

Full Length Research Paper

In-silico identification and phylogenetic analysis of auxin efflux carrier gene family in *Setaria italica* L.

Tapan Kumar Mohanta^{1*}, Mickael Malnoy², Nibedita Mohanta³ and Chidananda Nagamangala Kanchiswamy^{4*}

¹National Institute of Plant Genome Research, Aruna Asaf Ali Marg, 110067 New Delhi, India.

²Istituto Agrario San Michele all'Adige, Research and Innovation Centre, Foundation Edmund Mach, Trento, Italy.

³Departent di Biologia Vegetale, Viale Mattioli, 10125, University of Turin, Italy.

⁴Istituto Agrario San Michele all'Adige, Research and Innovation Centre, Foundation Edmund Mach, Trento, Italy.

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The phytohormone auxin is crucial for plant growth and development. Transportation and distribution of auxin throughout the plant is very important to maintain the auxin homeostasis. Auxin efflux carrier genes play significant roles in auxin transport. In this study, we identified 12 auxin efflux carrier genes from the *Setaria italica* genome, which are similar in number with that of monocotyledonous plant *Oryza sativa*. Twelve (12) *SiPIN* genes are distributed in eight scaffolds. All the identified genes possess the transmembrane auxin efflux carrier domain. Phylogenetic analysis shows that *SiPIN* genes are much closer to *Sorghum bicolor* and *O. sativa PIN* genes of the grass family.

Key words: Auxin efflux carrier, auxin efflux carrier domain, phosphorylation, transmembrane domain.

INTRODUCTION

In the model plant *Arabidopsis thaliana*, auxin plays a crucial role in regulating and coordinating plant growth and is involved in many developmental processes, including embryogenesis, meristem maintenance, organogenesis, lateral root initiation, vascular tissue differentiation and tropisms. Specific auxin influx carriers (*AUX/LAX* proteins) and efflux carriers (*PIN* and *PGP/MDR* proteins) mediate a directional, active, cell-to-cell auxin transport, creating auxin concentration maxima in specific tissues or cells. *PIN* auxin efflux carriers play a major role in mediating and regulating polar auxin transport (PAT), creating the auxin gradients that provide positional information for cells and tissues development (Benkova et al., 2003; Michniewicz et al., 2007; Reinhardt et al., 2000).

In *A. thaliana*, there are eight *PIN* genes (*AtPIN1–AtPIN8*) coding for proteins that differ in the length of the hydrophilic loop in the middle of their polypeptide chain (Krecek et al., 2009a; Zazimalova et al., 2007). The long *PIN* proteins of *Arabidopsis* viz., *PIN1/PIN4* and *PIN7* show plasma membrane localization and their polar localization determines direction of auxin flux(Friml 2010). The three *PIN* proteins *PIN5*, *PIN6*, and *PIN8*, have a shorter central hydrophilic domain and both *PIN5* and *PIN8*, have been shown to localize in the endoplasmic reticulum, suggesting a possible role in regulating intracellular auxin homeostasis(Wabnik et al., 2010; Wabnik et al., 2011). The classification of *AtPIN6* is more controversial since it has a partially reduced hydrophilic loop with high sequence similarities at trans-membrane

*Corresponding author. E-mail:nostoc.tapan@gmail.com. and chidananda.nagamangala@fmach.it.

Abbreviations: **AtPIN**, *Arabidopsis thaliana* auxin efflux carrier; **OsPIN**, *Oryza sativa* auxin efflux carrier; **PpPIN**, *Physcomitrella patens* auxin efflux carrier; **PtPIN**, *Populus trichocarpa* auxin efflux carrier; **SbPIN**, *Sorghum bicolor* auxin efflux carrier; **SiPIN**, *Setaria italica* auxin efflux carrier.

regions (Krecek et al., 2009a; Mravec et al., 2009). In addition to the eight *AtPIN* proteins, *Arabidopsis* encodes seven *PIN* like genes and they form a different clusters and the role of these is yet to find out (Paponov et al., 2005).

Many homologous *PIN* genes were well characterized in monocot species like rice (*Oryza sativa*) and maize (*Zea mays*). Both specific features and homologies between monocots and *Arabidopsis* (eudicot) *PIN* families have been shown. Monocot-specific features comprise both sequence clustering in phylogenetic analyses and expression pattern at transcript and protein level. In rice, the sequence analysis of the 12 *PIN* genes present in the genome showed that rice has four *PIN1* genes and one *OsPIN2*, while no *OsPIN* protein was grouped into the *AtPIN3*, *AtPIN4* and *AtPIN7* cluster. Four *OsPIN* genes encode for rice *PIN* proteins with a short central hydrophilic domain: three *OsPIN5* and one *OsPIN8*. Furthermore, three *OsPIN* proteins appear monocot-specific: *OsPIN9*, *OsPIN10a*, and *OsPIN10b*. *OsPIN9* has a central hydrophilic domain intermediate in length between long and short *PINs* of *Arabidopsis* and its expression analysis at transcription level suggests a possible function in adventitious root differentiation. *OsPIN10a* and *OsPIN10b* have a long central hydrophilic domain (Carraro et al., 2006; Forestan et al., 2012; Forestan and Varotto 2010; 2012; Xu and Scheres 2005). So far, three *PIN1* genes were described in maize using an antibody raised against *AtPIN1* protein (Forestan and Varotto, 2010). Recent studies of *PIN* genes on *Sorghum bicolor* revealed the presence of 11 *PIN* genes; at least there members were grouped in the *AtPIN1* cluster and another three in the *AtPIN5* cluster (Shen et al., 2010; Wang et al., 2010).

S. italica [(L.) P. Beauv.] commonly known as foxtail millet is one of the most cultivated millet species grown worldwide including India, China, Japan, Australia North and South America (Devos et al., 1998). Foxtail millet is a diploid grass with small genome (\approx 515 Mb) and its draft sequences has been published recently (Bennetzen et al., 2012). The major phytohormone auxin is central to plant growth and development. Availability of publicly accessible genome sequences of *S. italica* lead us to find the auxin efflux carrier genes (*PIN*) using an in-silico approach. Here, we used bioinformatics and comparative genomics approaches to find auxin efflux carrier genes in *S. italica*.

MATERIALS AND METHODS

Auxin efflux carrier (*PIN*) genes of *S. italica* were identified from plant genome database (<http://www.plantgdb.org>) and phytozome (www.phytozome.net) database (Dong et al., 2004; Duvick et al., 2008; Goodstein et al., 2012). To identify *PIN* genes, orthologous auxin efflux carrier genes from *A. thaliana* were used as search query. *Arabidopsis* *PIN* genes were downloaded from "The Arabidopsis Information Resources" (<http://www.arabidopsis.org/>). Hidden markov model approach was carried out to find the auxin

efflux carrier genes of *S. italica* (Altschul et al., 1997). Identified *StPIN* genes were again confirmed by running BLASTP searches in "The Arabidopsis Information Resources" and presence of auxin efflux carrier domains were confirmed by SWISS MODEL Workspace (www.swissmodel.expasy.org/workspace/). Nomenclature of identified *StPIN* genes were carried out according to BLASTP similarity found with *A. thaliana* *AtPIN* genes. TMMOD (The Hidden Markov Model for Transmembrane Protein Topology Prediction) (<http://www.cbs.dtu.dk/services/TMHMM/>) analyses were carried out to confirm the presence of transmembrane domains in *SiPIN* proteins (Kahsay et al., 2005; Kahsay et al., 2004). Orthologous *PIN* genes from *A. thaliana* (*AtPIN*), *O. sativa* (*OsPIN*), *Physcomitrella patens* (*PpPIN*), *Populus trichocarpa* (*PtPIN*), and *S. bicolor* (*SbPIN*) were used to analyze protein sequence similarity and construction of phylogenetic trees. *OsPIN* genes were downloaded from The TIGR Rice Genome Annotation Resources (Ouyang et al., 2007) whereas, *PpPIN*, *PtPIN*, *SbPIN* genes were downloaded from plant genome database and phytozome database. Multiple alignments of *PIN* genes from the above mentioned species were carried out by using the online available software Multalin (<http://multalin.toulouse.inra.fr/multalin/>). Phylogenetic tree was constructed by using MEGA5.2 software.

RESULTS AND DISCUSSION

Genome wide analysis of the *S. italica* genome led to the identification of 12 auxin efflux carrier (*SiPIN*) genes (Table 1). This result shows, *Setaria* has the same number of *SiPIN* genes as of rice and has four more *SiPIN* genes than *A. thaliana*. The major genome assembly of *S. italica* is arranged in 336 scaffolds. The first nine scaffolds are pseudomolecules and 98.9% of sequence data is presented in the nine pseudomolecule. Besides, the *Setaria* genome has 35,471 loci containing 40,599 protein coding transcripts (Bennetzen et al., 2012). The 12 identified *S. italica* auxin efflux carrier genes are distributed in eight scaffolds. Scaffold five contains four auxin efflux carrier genes (*SiPIN4a*, *SiPIN5a*, *SiPIN5b* and *SiPIN8*). The biggest *SiPIN* gene was *SiPIN2* with an ORF (open reading frame) length of 1890 nucleotides present in scaffold 4, whereas the smallest one was *SiPIN5c* which was present in scaffold 6. Among the 12 *SiPIN* genes, seven *SiPIN* genes (*SiPIN1a*, *SiPIN1b*, *SiPIN4a*, *SiPIN4b*, *SiPIN4c*, *SiPIN4d* and *SiPIN8*) contained five introns each and *SiPIN2* and *SiPIN5d* contained six introns each (Figure 1). *SiPIN1* transcript organization matched with that of *OsPIN1* and *AtPIN1* indicating their close homology (Wang et al., 2009).

Auxin efflux carrier genes are characterized by the presence of a transmembrane auxin efflux carrier domain (Carraro et al., 2006; Forestan et al., 2012). All *SiPIN* genes contain transmembrane auxin efflux carrier domains (Figure 2). Among the 12 *SiPINs*, seven *SiPIN* genes (*SiPIN1a*, *SiPIN1b*, *SiPIN2*, *SiPIN4a*, *SiPIN4b*, *SiPIN4c* and *SiPIN4d*) contain a long transmembrane domain. The other *SiPIN* genes (*SiPIN5a*, *SiPIN5b*, *SiPIN5c*, *SiPIN5d* and *SiPIN8*) contained a short transmembrane domain. In *Arabidopsis*, *AtPIN4* has a short transmembrane domain which is different from that

Table 1. Phytozome locus ID and transcript information of SiPIN. Naming of SiPIN were done as found by BLASTP against the Arabidopsis Information Resources database.

Locus ID	Gene name	ORF Length	Number Of a.a	Number of Introns	5'-3' Coordinates
Si016714m	SiPIN1a	1785	594	5	scaffold_1: 37807344 - 37810727
Si006110m	SiPIN1b	1794	597	5	scaffold_4: 8906772 - 8909697
Si006060m	SiPIN2	1890	629	6	scaffold_4: 30687696 - 30691064
Si000693m	SiPIN4a	1863	620	5	scaffold_5: 30444777 - 30448448
Si009737m	SiPIN4b	1677	558	5	scaffold_7: 34823548 - 34826535
Si025109m	SiPIN4c	1773	590	5	scaffold_3: 9460738 - 9463047
Si026177m	SiPIN4d	1683	560	5	scaffold_8: 1266812 - 1269757
Si001955m	SiPIN5a	1095	364	4	scaffold_5: 44864303 - 44869298
Si003879m	SiPIN5b	1272	423	4	scaffold_5: 39347962 - 39350295
Si015697m	SiPIN5c	1029	342	2	scaffold_6: 33597186 - 33599056
Si033365m	SiPIN5d	1134	377	6	scaffold_2: 36679971 - 36681750
Si003769m	SiPIN8	1081	361	5	scaffold_5: 35148382 - 35150803

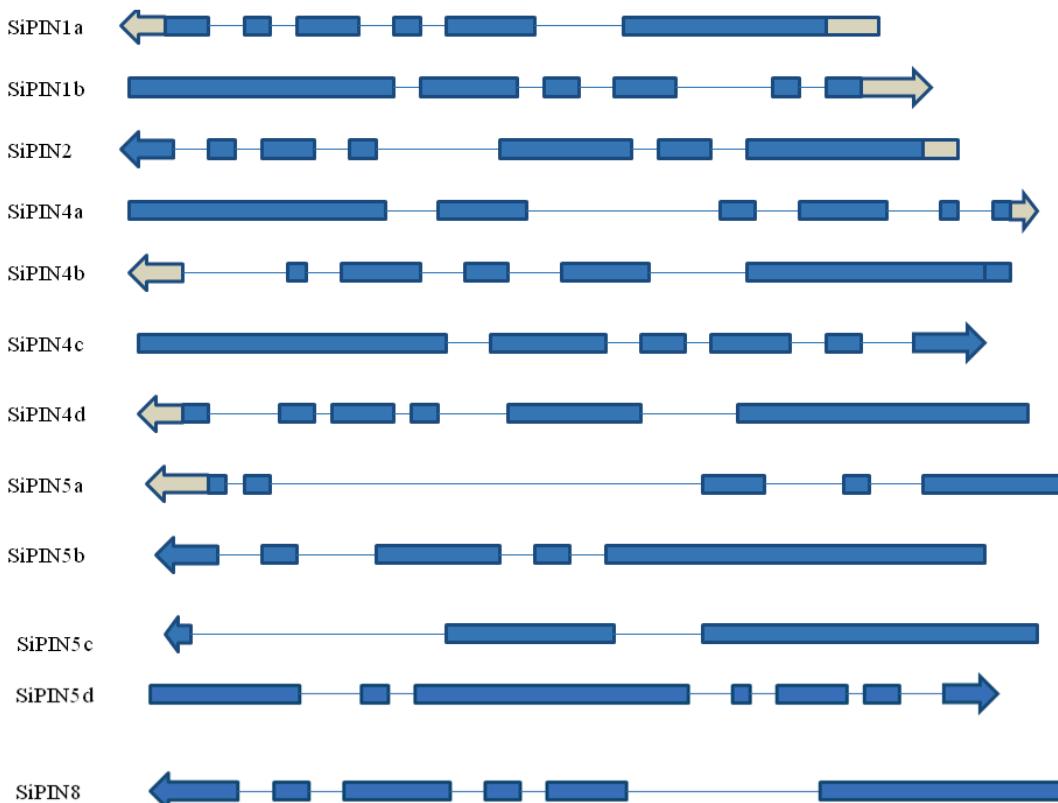


Figure 1. Transcript organization of SiPIN genes. Blue color boxes indicate the exons and lines indicate the introns of respective SiPIN genes. The arrow mark indicate the direction of expression of transcript.

of SiPIN genes showing diversification of PIN genes among species. *Arabidopsis AtPIN1*, rice *OsPIN1* and *OsPIN2* were grouped under long transmembrane auxin efflux carrier domain (Wang et al., 2009). *SiPIN1* and *SiPIN2* genes contain a long transmembrane domain, showing close relationship with that of *AtPIN1*, *OsPIN1*

and *OsPIN2*.

Phylogenetic analysis with orthologous PIN genes from *A. thaliana* (*AtPIN*), *O. sativa* (*OsPIN*), *Physcomitrella patens* (*PpPIN*), *Populus trichocarpa* (*PtPIN*), *S. bicolor* (*SbPIN*) resulted in clustering into three major groups (group I, II and III) (Figure 3). In group I, *SiPIN1a* and

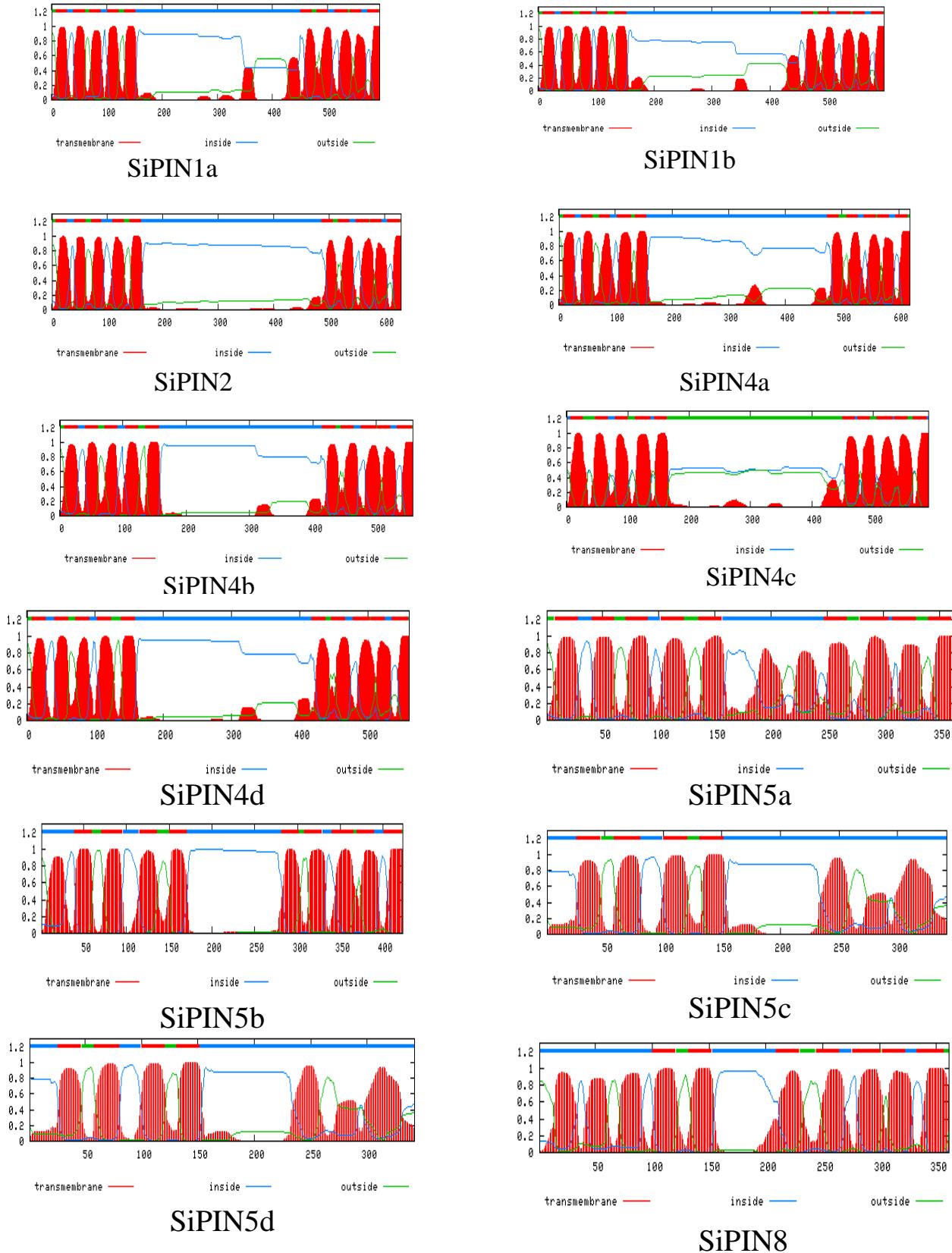


Figure 2. Transmenbrane domain prediction of *SiPIN* genes by TMMPD (Hidden Markov Model for transmembrane protein topology prediction). *SiPIN1a*, *SiPIN1b*, *SiPIN2*, *SiPIN4a*, *SiPIN4b*, *SiPIN4c* and *SiPIN4d* contains long transmembrane domain where as *SiPIN5a*, *SiPIN5b*, *SiPIN5c*, *SiPIN5d* and *SiPIN8* contains short transmembrane domain.

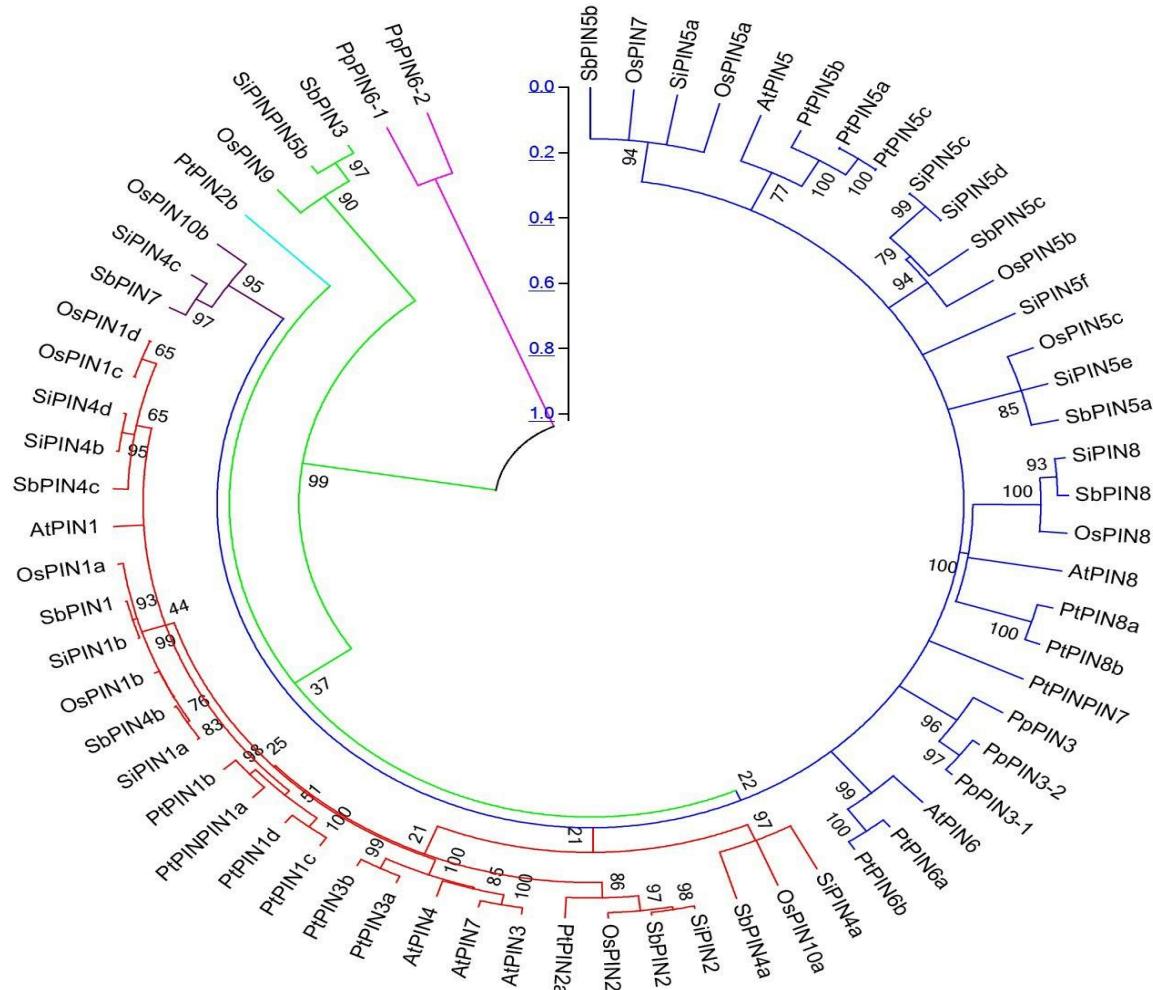


Figure 3. Phylogenetic tree of *SiPIN* genes with orthologous PIN genes of *Arabidopsis thaliana* (*AtPIN*), *Oryza sativa* (*OsPIN*), *Sorghum bicolor* (*SbPIN*), *Populus trichocarpa* (*PtPIN*) and *Physcomitrella patens* (*PpPIN*). Statistical method used to construct the phylogenetic tree was neighbor joining method; test phylogeny-boot strap method; no. of boot strap replication -500; substitution type-amino acids and model used was Jones-Taylor-Thornton (JTT).

SiPIN1b clustered with *OsPIN1*; *SiPIN4b* and *SiPIN4d* clustered with *SbPIN4c*; *SiPIN4a* clustered with *SbPIN4a*; *SiPIN4c* clustered with *SbPIN7* and *OsPIN10b*; *SiPIN2* clustered with *ObPIN2* and *OsPIN2*; *SiPIN8* clustered with *SbPIN8* and *OsPIN8*. In group II, *SiPIN5a* clustered with *SbPIN5b* and *OsPIN5b*; *SiPIN5c* clustered with *SbPIN5c* and *OsPIN5c*; *SiPIN5d* clustered with *SbPIN5a* and *OsPIN5c*: *SiPIN5b* clustered with *SbPIN3* and *OsPIN9*. In group III, *AtPIN6* clustered with *PtPIN6*. There is no gene of *Setaria* or any other grass in this cluster, showing diversification of *PIN* genes. Cluster analysis reflects, *S. italica* *PIN* genes are much closer to *PIN* genes of grasses *Sorghum bicolor* and *Oryza sativa*. Multiple alignment of amino acid sequences shows conserved N and C-terminal domains (Supplementary Figure 1). The N-terminal region shows a conserved S-P/T-P motif, a potential target phosphorylation site for

mitogen activated protein kinases (MAPK) (Sinha et al., 2011). The central hydrophilic loop is dynamic in nature and differs from each other in terms of sequence homology, but some *PIN* genes are conserved in this dynamic region with a T-P-R motif (Supplementary Figure 1). The T-P-R motif is a target phosphorylation site of mitogen activated protein kinase 3 and mitogen activated protein kinase 6 (Sorensson et al., 2012). The T-P-R motif is conserved only in the case of long transmembrane auxin efflux carrier domains. This shows that, although the central hydrophilic loop is diverse in nature, its phosphorylation events are conserved to carry out specific function suggesting that evolution of protein phosphorylation is conserved.

The *PIN*-Formed (*PIN*) proteins are a plant-specific family of transmembrane proteins that transport the phytohormone auxin as substrate molecule. There is very

limited data available which suggests auxin is a signaling molecule of ancient origin. The *PIN* gene family is found only in genomes of land plants. They act as regulator and play key roles in developmental process including embryogenesis, morphogenesis and organogenesis (Krecek et al., 2009b). The number of *PIN* genes present in *S. italica* (12) is equal to that of rice (12) and more than that of *Arabidopsis* (8) suggesting that the presence of more *PIN* genes may have some extra role in development and morphogenesis. The predicted structure of a *PIN* protein is similar to the structure of membrane transport proteins that use the electrochemical gradient across the membrane to transport molecules. All the identified *PIN* proteins have two hydrophobic domains with cytoplasmic orientation. The transmembrane helices of hydrophobic domains are highly conserved in their amino acid sequence. But substantial differences are present between the long and short *PINs*. The hydrophobic domains of all long *PIN* proteins contain the amino acids at invariant position, but these positions are not invariants in short *PINs*. The presence of invariant amino acid sequences in long *PINs* may play major roles, which has not been retained in short *PIN*. The loop between the transmembrane helices being present within the hydrophobic domain exhibits dynamic variability in size and sequence.

Conclusion

S. italica popularly known as foxtail millet is one of the best studied millet species in the world. The genome sequencing project of this plant is going to be completed in the near future. This will open the door for progressing research of this plant at the molecular level. Auxin efflux carrier genes identified in this report will help to understand the role of auxin signaling and its role in growth, development as well as response to different biotic and abiotic stresses. Phylogenetic analysis shows that auxin efflux carrier genes in species of grass family are conserved.

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	1	10	20	30	40	50	60	70	80	90	100	110	120	130
OsPIN1a	M	I	T	G	R	D	F	Y	H	V	M	T	A	M
SbPIN1	M	I	T	G	D	F	Y	H	V	M	T	A	M	L
SiPIN1b	M	I	T	G	D	F	Y	H	V	M	T	A	M	L
OsPIN1b	M	I	T	A	D	F	Y	H	V	M	T	A	M	L
SiPIN1a	M	I	T	G	D	F	Y	H	V	M	T	A	M	L
SbPIN4b	M	I	T	A	D	F	Y	H	V	M	T	A	M	L
AtPIN1	M	I	T	A	D	F	Y	H	V	M	T	A	M	L
PtPIN1c	M	I	S	L	D	F	Y	H	V	M	T	A	M	L
PtPIN1d	M	I	S	L	D	F	Y	H	V	M	T	A	M	L
PtPIN1a	M	I	S	L	D	F	Y	H	V	M	T	A	M	L
PtPIN1b	M	I	S	I	G	F	Y	H	V	M	T	A	M	L
AtPIN3	M	I	S	H	D	L	T	V	A	V	P	L	Y	M
AtPIN7	M	I	S	H	D	L	T	V	A	V	P	L	Y	M
PtPIN3a	M	I	S	H	D	L	T	V	A	V	P	L	Y	M
PtPIN3b	M	I	S	H	D	L	T	V	A	V	P	L	Y	M
AtPIN4	M	I	S	H	D	L	T	V	A	V	P	L	Y	M
PpPIN3-2	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
PpPIN3-1	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
PpPIN3	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
OsPIN2	M	I	T	G	D	I	O	Y	V	P	L	Y	M	L
SbPIN2	M	I	T	G	D	I	O	Y	V	P	L	Y	M	L
SiPIN2	M	I	T	G	D	I	O	Y	V	P	L	Y	M	L
AtPIN2	M	I	T	G	D	I	O	Y	V	P	L	Y	M	L
PtPIN2a	M	I	T	G	D	I	O	Y	V	P	L	Y	M	L
OsPIN1c	M	I	T	V	D	L	Y	H	V	M	T	A	M	L
SbPIN4c	M	I	T	V	D	L	Y	H	V	M	T	A	M	L
SiPIN4b	M	I	T	V	D	L	Y	H	V	M	T	A	M	L
PtPIN4d	M	I	T	V	D	L	Y	H	V	M	T	A	M	L
PtPIN2b	M	I	S	G	K	D	I	Y	V	P	L	Y	M	L
OsPIN10a	M	I	S	G	K	D	I	Y	V	P	L	Y	M	L
SbPIN4a	M	I	S	G	K	D	I	Y	V	P	L	Y	M	L
SiPIN4a	M	I	S	G	K	D	I	Y	V	P	L	Y	M	L
OsPIN10b	M	I	S	G	K	D	I	Y	V	P	L	Y	M	L
SbPIN7	M	I	S	G	K	D	I	Y	V	P	L	Y	M	L
SiPIN4c	M	I	S	G	K	D	I	Y	V	P	L	Y	M	L
AtPIN6	M	I	S	G	K	D	I	Y	V	P	L	Y	M	L
PtPIN6a	M	I	T	A	D	F	Y	H	V	M	T	A	M	L
PtPIN6b	M	I	T	A	D	F	Y	H	V	M	T	A	M	L
PtPIN17	M	I	S	E	D	L	Y	H	V	M	T	A	M	L
OsPIN1d	M	I	T	G	D	I	Y	H	V	M	T	A	M	L
OsPIN9	M	I	T	G	D	I	Y	H	V	M	T	A	M	L
SbPIN3	M	I	T	G	D	I	Y	H	V	M	T	A	M	L
SiPIN5b	M	I	T	G	D	I	Y	H	V	M	T	A	M	L
PpPIN6-1	M	I	T	G	D	I	Y	H	V	M	T	A	M	L
OsPIN5a	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
SiPIN5a	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
SbPIN5b	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
AtPIN5	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
PtPIN5a	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
PtPIN5c	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
PtPIN5b	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
OsPIN5b	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
SbPIN5c	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
OsPIN5c	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
SbPIN5a	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
SiPIN5d	M	I	N	G	H	I	D	Y	H	V	M	T	A	M
AtPIN8	M	I	S	M	D	I	Y	H	V	M	T	A	M	L
PtPIN8a	M	I	S	M	D	I	Y	H	V	M	T	A	M	L
PtPIN8b	M	I	S	M	D	I	Y	H	V	M	T	A	M	L
SbPIN8	M	I	S	M	D	I	Y	H	V	M	T	A	M	L
SiPIN8	M	I	S	M	D	I	Y	H	V	M	T	A	M	L
SiPIN5c	M	I	S	M	D	I	Y	H	V	M	T	A	M	L
OsPIN7	M	A	E	I	P	G	L	G	H	M	I	D	G	H
OsPIN8	M	V	W	K	D	I	L	V	E	A	T	P	V	L
PpPING-2	M	T	Q	G	E	H	D	F	I	G	P	S	V	A

Supplementary Figure 1. Multiple sequence alignment of amino acid shows presence of N and C-terminal conserved region. N-terminal region shows presence of conserved S-P/T-P motif, target phosphorylation site of mitogen activated protein kinase. The central hydrophilic region is very dynamic in nature and differ from each other, but still contains conserved S-P-R/T-P-R motif, target phosphorylation site of mitogen activated protein kinase 3 and mitogen activated protein kinase 6. S-P-R/T-P-R motifs are conserved only in long transmembrane domain containing PIN gene.

	131	140	150	160	170	180	190	200	210	220	230	240	250	260
OsPIN1a	TITLFSLSLPTNLV	MGIPLLKGHYGEFS		GSLMVQIVVLQCIIWYTLMLF	MFEYRGARILITEQFPDTAG-A	--IASIYDADYVSL-DGRRDMIETEAEVK	--EDGKIHVTYRRSNAS							
SbPIN1	TITLFSLSLPTNLV	MGIPLLKGHYGDFS		GSLMVQIVVLQCIIWYTLMLF	MFEYRGARILITEQFPDTAG-A	--IASIYDPDVYSL-DGRNDRIETEAEVK	--EDGKIHVTYRRSNAS							
SiPIN1b	TITLFSLSLPTNLV	MGIPLLKGHYGDFS		GSLMVQIVVLQCIIWYTLMLF	MFEYRGARILITEQFPDTAG-A	--IASIYDPDVYSL-DGRNDRIETEAEVK	--EDGKIHVTYRRSNAS							
OsPIN1b	TITLFSLSLPTNLV	MGIPLLKGHYGEFS		GSLMVQIVVLQCIIWYTLMLF	MFEYRGARILITEQFPDTAG-A	--IASIYDPDVYSL-DGRRDIETETEVK	--EDGRIHVTYRRSNAS							
SiPIN1a	TITLFSLSLPTNLV	MGIPLLKGHYGDFS		GSLMVQIVVLQCIIWYTLMLF	MFEYRGARMLITEQFPDTAG-A	--IASIYDPDVYSL-DGRRDIETEAEVK	--EDGKIHVTYRRSNAS							
SbPIN4b	TITLFSLSLPTNLV	MGIPLLKGHYGDFS		GSLMVQIVVLQCIIWYTLMLF	MFEYRGARLLITEQFPDNAG-A	--IASIYDPDVYSL-DGRRDIETEAEVK	--EDGKIHVTYRRSNAS							
AtPIN1	TITLFSLSLPTNLV	MGIPLLKGHYGNFS		GDLMVQIVVLQCIIWYTLMLF	MFEYRGAKLLESEQFPDTAG-S	--IVSIHVDSDIMSL-DGRQP-LETERAEIK	--EDGKLHVTYRRSNAS							
PtPIN1c	TITLFSLSLPTNLV	MGIPLLKGHYGDOYS		GSLMVQIVVLQCIIWYTLMLF	MFEYRGAKLLESEQFPDTAG-S	--IVSIHVDSDIMSL-DGRQP-LETERAEIK	--EDGKLHVTYRRSNAS							
PtPIN1d	TITLFSLSLPTNLV	MGIPLLKGHYGDOYS		GSLMVQIVVLQCIIWYTLMLF	MFEYRGAKLLESEQFPDTAG-S	--IVSIHVDSDIMSL-DGRQP-LETERAEIK	--EDGKLHVTYRRSNAS							
tPIN1a	SITLFSLSLPTNLV	MGIPLLKGHYGERS		GSLMVQIVVLQCIIWYTLMLFL	FMEYRGARILIGEQFPDTAG-S	--IISFRYDSDISSL-DGREP-LQTDAEVG	--EDGKLHVTYRKSTSS							
PtPIN1b	SITLFSLSLPTNLV	MGIPLLKGHYGHSS		GSLMVQIVVLQCIIWYTLMLFL	FMEYRGARILIGEQFPDTAG-S	--IISFRYDSDISSL-DGREP-LQTAEVG	--EDGKLHVTYRKSTSS							
AtPIN3	SITLFSLSLPTNLV	MGIPLLIRHYGEYS		GSLMVQIVVLQCIIWYTLFLF	EFRGAKMLIMEQFPETAA-S	--IVSFKVESDVYSL-DGH-DFLETDAEIG	--DDGKLHVTYRKSNAS							
AtPIN7	SITLFSLSLPTNLV	MGIPLLIRHYGEYS		GSLMVQIVVLQCIIWYTLFLF	EYRGAKLIMEQFPETAA-S	--IVSFKVESDVYSL-DGH-DFLETDAQIG	--DDGKLHVTYRKSNAS							
PtPIN3a	MITIFSVSLPTNLV	MGIPLLIRHYGKYS		GSLMVQIVVLQCIIWYTLFLF	EYRGAKMLIMEQFPETAA-S	--IISFRYDSDVYSL-DGR-DFLETDAEIG	--DDGKLHVTYRKSNAS							
PtPIN3b	MITIFSVSLPTNLV	MGIPLLIRHYDDYS		GSLMVQIVVLQCIIWYTLFLF	EYRGAKMLIMEQFPETAA-S	--IISFRYDSDVYSL-DGR-DFLETDAEIG	--DDGKLHVTYRKSNAS							
AtPIN4	MITIFSVSLPTNLV	MGIPLLIRHYGTYA		GSLMVQIVVLQCIIWYTLFLF	EYRGAKLIMEQFPETAA-S	--IVSFKVESDVYSL-DGH-DFLETDAEIG	--NDGKLHVTYRKSNAS							
PpPIN3-2	MITLFVLTIPNTLV	MGTPLLARYGPGP		GDLTIQAVYLQCIIWYTLFLF	MFEYRAAKILIMQQFPENAG-S	--IVSFKVDSOVYSL-DGREPV-L-TEREIG	--DDGKLHVTYRKSSS							
PpPIN3-1	MITLFVLTIPNTLV	MGTPLLARYGRRP		GDLTVQAVYLQCIIWYTLFLF	MFEYRAAKILIMQQFPENAG-S	--IVSFKVDSOVYSL-DGREPV-L-TEREIG	--DDGKLHVTYRKSSS							
PpPIN3	VITLFLMTTIPNTLV	YGTPLLARYGSKP		GQLTVQAVYLQCIIWYTLFLF	MFEYRAARILIMHHRFPENAA-S	--IVSFKVDSOVYSL-DGPDPV-L-TEREFR	--DDGKLHVTYRKSSS							
OsPIN2	TITLFSLSLPTNLV	MGIPLLRHYGDFS		GSLMVQIVVLQSVIHWYTLMLF	EYRGAKALISEQFPDPVAGS	--IISFRYDSDVYSL-NGREA-LQDAEVG	--RDGRHVHVIRRASASA							
SbPIN2	TITLFSLSLPTNLV	MGIPLLRHYGDFS		GNLMVQIVVLQSVIHWYTLMLF	EYRGAKALISEQFPDPVAGS	--IISFRYDSDVYSL-NGREA-LQDAEVG	--SDGRHVHVIRRASASA							
SiPIN2	TITLFSLSLPTNLV	MGIPLLRHYGDFS		GNLMVQIVVLQSVIHWYTLMLF	EYRGAKALISEQFPDPVAGS	--IISFRYDSDVYSL-NGREA-LQDAEVG	--SDGRHVHVIRRASASA							
AtPIN2	TITLFSLSLPTNLV	MGIPLLRHYGDFS		GNLMVQIVVLQSVIHWYTLMLF	EYRGAKLLESEQFPETAG-S	--ITSFRYDSDVYSL-NGREP-LQDAEIG	--DDGKLHVTYRKSSA							
PtPIN2a	TITLFSLSLPTNLV	MGIPLLRHYGDFS		GNLMVQIVVLQSVIHWYTLMLF	EYRGAKLLESEQFPETAG-S	--ITSFRYDSDVYSL-NGREP-LQDAEIG	--DDGKLHVTYRKSSA							
OsPIN1c	LITLFSLSLPTNLV	MGIPLLKGHYAARRAD		-YDSGSMLMVQIVVLQCIIWYTLMLF	MFEYRGARLLYMEQFPD-TRAS	--IVSFKVDSOVYSL-RGGGGGARELQAEAEY	--DDGKMRYTVRKSTSS							
SbPIN4c	SITLFSLSLPTNLV	MGIPLLRGHYGGGGGSSSSIDRGTLMV	QVWV	QCIIWYTLMLFL	FYEYRARRALVLDQFPDGAAAS	--IVSFKVDSOVYSLA-RGEIELEADAYPVPGAGGDGGRVYTVRKSTSS								
SiPIN4b	SITLFSLSLPTNLV	MGIPLLRGHYGPOSA		GTLMVQVWVQCIIWYTLMLFL	FYEYRARRALVHDQFPDGAAAS	--IVSFKVDSOVYSLADARKGELEADAHYA	--DDGRHVTYRKSTCS							
SiPIN4d	SITLFSLSLPTNLV	MGIPLLRGHYGPOSA		GTLMVQVWVQCIIWYTLMLFL	FYEYRARRALVHDQFPDGAAAS	--IVSFKVDSOVYSLADARKGELEADAHYA	--DDGRHVTYRKSTSS							
PtPIN2b	TITLFSLSLPTNLV	MGVPLLKSHYGEFT		SPLMIQCVFMQSYLWHTLLL	SMFEYRGAKRLYAGQFPETAA-S	--IVSFKVDSOVYSL-GGHEPLETDAEID	--DDGKLHVTYRKSSAT							
OsPIN10a	SITLFSLSLPTNLV	MGIPLLIHYGPYS		GSLMVQIVVLQCIIWYTLMLFL	FERAARMLIADQFPDTAAS	--IVSLHVDPDVYSLLEGHH	--ADGLHVTYRKSSVS							
SbPIN4a	SITLFSVSLPTNLV	MGIPLLIHYGPYA		GSLMVQIVVLQCIIWYTLFLF	FERAARMLIADQFPDTAAS	--IASLHVDADYVSLLEGGR	--ADGLHVTYRKSSAS							
SiPIN4a	SITLFSVSLPTNLV	MGIPLLIHYGPYA		GSLMVQIVVLQCIIWYTLFLF	FERAARMLIADQFPDSAAA	--IASLRVEPDVYSLLEGGR	--ADGLHVTYRKSSVS							
o_PTM1a_h	CTTLECUCI	DNTI	WCTD	I	UCV	YCV	CVC	CTTLECUCI	DNTI	WCTD	I	UCV	YCV	o_PTM1a_h
SbPIN7	SITLFSLSLPTNLV	MGIPLLVHYGPOYS		GDLVQVWVQCIIWYTLFLF	YFRAARYLIAQGQFPACTAARACIADYRVDPDVYSLAGSQ	--AERQAEVY	--PDGRMRLVYVRRTSA							
SiPIN4c	SITLFSLSLPTNLV	MGIPLLVHYGRRP		GDLVQVWVQCIIWYTLFLF	YFRAARYLIAQGQCPDTAAA	--IADVRVDPDVYSLAGSQ	--AERQAEVY	--PDGRVRLVYVRRTSY						
AlPING	TITLFSIATLPTNLV	MGIPLLQHRYGDT		QTLMVQVWVQCIIWYTLFLF	ELRAARLLIRAEFPQGQAGS	--IAKIQYDODVISL-DGMOP-LRTETETO	--VNGRIRLIRRRTSS							
PtPIN6a	LITLFSIATLPTNLV	MGIPLLKHYGDT		QSLMVQVWVQCIIWYTLFLF	YEYRATLLIKTOFPGPKAAS	--ISKIELDDOVISL-DGRDP-LRTESETD	--GNGLRVRIRRRTSS							
PtPIN6b	LITLFSVATLPTNLV	MGIPLLKHYGDT		QSLMVQVWVQCIIWYTLFLF	YEYRATLLIKAOFPGPART	--ISKIELDDOVISL-DGRDP-LRTESETD	--GNGLRVRIRRRTSS							
PtPIN7	ATLFSLSLPTNLV	MGIPLLKSHYGDOK		EGLMIQVWVQCIIWYTLFLF	YEYRARLMLKNFKGSSSS	--SFSNSERSKGSKFGYGEVGLGSRGSNA	--DEVVNIVSTPTSQ							
OsPIN1d					MEQFPDTAAS	--IVSFKVDSOVYSLAGGGGGARELQAEAEY	--DDGKMRYTVRKSTSS							
OsPIN9	VITCF	SVSLPTNTIMGVPLLNGHYGPVS		KOLMKQIVVNQFCIHWVNVIIFLYEYMAARRRSAPPASS		--EGSAKIS	--PSSPVKAARARADT							
SbPIN3	VITNF	SVSLPTNTIMGVPLLNGHYGSVS		GGLMKQIVVNQFCIHWVNVIIFLYEYMAARRDGAKISPATV		--PPAAAAA	--ENDRORVIIDENGGS							
SiPIN5b	VITNF	SVSLPTNTIMGVPLLNGHYGSVS		GGLMKQIVVNQFCIHWVNVIIFLYEYMAARRDGSKISP-V		--SRAAAPP	--EKDR--IGENGGS							
PpPIN6-1	VITLFLQSLVMPNTIVGIPVLSPLSYVTE			SGIAR	--IFIQGVLWLFPTLFLYELEKVRKMGQPAVGSVA	--QVQDDGP	--RSLHSGETTESA							
OsPIN5a	SITFSLSLTLNSL	VLVGPMARRHYGEWA		QQLVYQLSVFQAIWLTLLFLVLEV	RKARIGM		--YY							
SiPIN5a	SITFSLSLTLNSL	VLVGPMARRHYGEWA		QQLVYQLSVFQAIWLTLLFLVLEV	RKARIGM		--YY							
SbPIN5b	SITFSLSLTLNSL	VLVGPMARRHYGEWA		QQLVYQLSVFQAIWLTLLFLVLEV	RKARIGM		--YY							
AtPIN5	SITFSLSLTLNSL	VVGVLPLAKHYGQQA		VDLVYQSSVYQAIWLTLLFLVLE	FRKAGFS		--SN							
PtPIN5a	SITFSLSLTLNSL	VVGVLPLAKHYGPTA		VDLVYQSSVYQAIWLTLLFLVLE	FRRSGLGV		--SS							
PtPIN5c	SITFSLSLTLNSL	VVGVLPLAKHYGPTA		VDLVYQSSVYQAIWLTLLFLVLE	FRRSGLGV		--SS							
PtPIN5b	SITFSLSLTLNSL	VVGVLPIIKAHYGPAR		VDLVYQSSVYQAIWLTLLFLVLE	FRRTGLGF		--SS							
OsPIN5b	SITGFSLSLTLNSL	VVGVLPIIKAHYGQRA		QDLVYQJAVVQSMWFPPLLHAFELRKAVVY	GGGG		--VG							
SbPIN5c	ATGFSLSLAGFNNTLV	VVGVLPIIKAHYGKRA		QDLVYQJAVVQSLFWFPPLLHGFELRKAVVY	GIPSAQGGGGGSCRNSSNSDDDDSAGGGR		--VG							
OsPIN5c	CITGFSLSATLNNTLV	VVGVLPIIKAHYGKRA		RDLIVQISVYQIIVYFPPLLIAFEV	RATTAA		--AA							
SbPIN5a	CITYFSLSATLNNTLV	VVGVLPIIKAHYGKRA		RDLIVQISVYQIIVYFPPLLIAFEV	RATTAA		--AA							
SiPIN5d	CITGFSLSAALNNTLV	VVGVLPIIKAHYGKRA		RDLIVQISVYQIIVYFPPLLIAFEV	RATTAA		--KR							
AtPIN8	VITGLSISVLPNTLILGMPILSAYIHYGDEA			ASILEQIVVLQSLIWIYTLFLFELNAARALPSSGA		--SLEH	--TG							
PtPIN8a	ITITGLSLSLPTNLILGMPILSAYIHYGDEA			EPLLSQIVGLQSLIWIYTLFLFELNAATKEATVAPS		--S	--ET							
PtPIN8b	ITITGLSLSLPTNLILGMPILSAYIHYGDEA			EPLLSQIVGLQSLIWIYTLFLFELNAATKEATVAPS		--S	--ES							
SbPIN8	LITGFSLSLPTNLIVGIPLLKGHYGDEA			VKLLSQIVVLQSLIWIYTLFLFELRAARGMRTTS		--S	--ET							
SiPIN8	LITGFSLSLPTNLIVGIPLLKGHYGDEA			VKLLSQIVVLQSLIWIYTLFLFELRAARGMRTTS		--S	--GT							
SiPIN5c	CVTF	FSLAARFNNTLVVGYPLLDHYGAWA		RDLVYQLAVVQALIVWVPLLLLGFELRKAVVY	YRNGIASAAGDQAAAGGGRVEPVSSQAK		--KA							
OsPIN7	CISGF	SLASLTLNSL	VVGPMARRHYGWA	GQVYVQLSIFQAIWLTSLWVY	LEVRAKAFVSDAHDDESNRHEEG	--SYIDDOTYVGGGSGTSEMQSLEEGVSDATNQDKLGE	--EAVYGVN							
OsPIN8	LITGFSLSLPTNLIVGIPLLKGHYGDEA			GKLLSQIVVLQSLIWIYTLFLFELRAANGMATTTSSETGLIWA	-LYGFRHHLRPLIYSNSIRHLSGGLGMAFSLGLFTALQTKIACG									
PpPIN6-2	PKSCFYLMQ													

Supplementary Figure 1. Contd.

	261	270	280	290	300	310	320	330	340	350	360	370	380	390
OsPIN1a	RSDIVSRRSMGFS-----S-	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSMVG-----R	SNNFAAG-----DAFGV--RTGATPRPSNYEEDAA-----APNKAGS-----											
SbPIN1	RSDIYSRRSMGFS-----S-	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSMVG-----R	SNNFAAG-----DAFGL--RTGATPRPSNYEEEAQ-----GGKAANK-----											
SiPIN1b	RSDIYSRRSMGFS-----S-	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSMVG-----R	SNNFAAG-----DAFGV--RTGATPRPSNYEEDAQ-----G-KANK-----											
OsPIN1b	RSDIYSRRSMGFS-----S-	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSMVG-----R	SNNFGAR-----DAFGV--RTGATPRPSNYEDDAS-----KP-KYPLPASH-----											
SiPIN1a	RSDIYSRRSMGFS-----S-	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSMVG-----R	SNNFGAR-----DAFGI--RTGATPRPSNYEDDAS-----KP-KYPLPVN-----											
SbPIN4b	RSDIYSRRSMGFS-----S-	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSMVG-----R	SNNFGAR-----DAFGI--RTGATPRPSNYEDDAS-----KPAKYPLPVN-----											
AtPIN1	RSDIYSRRSQQLS-----A-	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSMMA-----S	GGRNSNFPG-----EA--VFGSKGPTRPSNYEEDGGPAKPTAAGTAAAGRFRHY-----											
PtPIN1c	RSDIYSRRSQQLS-----A-	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSMMA-----A	RNSNFGAS-----DVYGLSASRGPTPRPSNFEEEHG-----GSNPFRHH-----											
PtPIN1d	RSDIYSRRSQQLS-----S-	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSMMA-----A	RNSNFGAS-----DVYGLSASRGPTPRPSNFEEEHG-----GSNPFRHH-----											
PtPINPIN1a	RSDVFSRSHSGHLN-----SGLS	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSK-N-----	ASNRSPRHNSFLQF-----DEESGLLG-----											
PtPIN1b	RSEVFSHMSHGLN-----SGLS	TPRPSNLTNAEIYSLQSSRNTPRSSS-FNHDFYSMVN-----	GKNASPRHSNFTNLQF-----DEESGLLG-----											
AtPIN3	RRSFCG---PNM-----	TPRPSNLTGAEIYSLST-----	TPRSSN-FNHDFYNMHGFP-----GRLSNFGPA-----DMYSVQSSRGPTPRPSNFEEENCA-----MASSPR-----											
AtPIN7	RRSFYGGGGTM-----	TPRPSNLTGAEIYSLNT-----	TPRSSN-FNHDFYSHMGFP-----GRLSNFGPA-----DMYSVQSSRGPTPRPSNFEEENCA-----MASSPR-----											
PtPIN3a	RRSLPGPSFSGM-----	TPRPSNLTGAEIYSLSSRNTPRSSN-FNPDSFYSHMGVQGFPGRHSNLGPA-----	DLYSVQSSRGPTPRPSNFEEENCA-----PTATLSSPR-----											
PtPIN3b	RRSLPGPSFSGL-----	TPRPSNLTGAEIYSLSSRNTPRSSN-FNPDSFYSHMGVQG-----GRHSNLGPA-----	DLYSVQSSRGPTPRPSNFEEENCA-----PHATITSPR-----											
AtPIN4	RRSLM-----M	TPRPSNLTGAEIYSL-----	TPRSSN-FNHDFYSHMGVQG-----GRLSNFGPA-----DLYSVQSSRGPTPRPSNFEEENNA-----VKGYFVNNT-----											
PpPIN3-2	RSQGMHSRHSMP-----	SSKLTPRPSNLTGAEIYSHSSVNTPRSS-FNQGEFHSMSQRS-PHRQSNFDIS-----	DYVYLSQSSRGPTPRPSNFNEENSKDMHTHHRGLNLTSRFY-----											
PpPIN3-1	RSQGMHSRHSMP-----	SSKLTPRPSNLTGAEIYSHSSVNTPRSS-FNQGEFHSMSQRS-PHRQSNFDTS-----	DYVYLSQSSRGPTPRPSNFNEENSKDIHTHHRGLNMSRFA-----											
PpPIN3	RSQGVHSANHSIP-----	SSKLTPRPSNLSNREIYSHNSSVNTPRSS-FORGEDCSTHAHHD-PNRKSNFDTS-----	DIYSLQSSRGPTPRNSNFNEENSKVEHHNRGALNVNLPRA-----											
OsPIN2	STTGGGGGAARSGVS--RAYGASNA-----	TPRPSNLTGVEIYSLQTRETPRSS-FNQADFYAMFSGSKMASQM-----	ASPMQAQHGGAGGRAQGLDEQVTN-----KFRSGK-----											
SbPIN2	STTGGGGGAARSGVS--RAYGASNA-----	TPRPSNLTGVEIYSLQTRETPRSS-FNQADFYAMFNGSKMASPL-----	AQP-----G-AAPGLDEQVAN-----KFRSGK-----											
SiPIN2	STTG--HGAARSVGVGGYRPyGASSA-----	TPRPSNLTGVEIYSLQTRETPRSS-FNQADFYAMFNGSKMASPL-----	AQP-----GSGARAPGLDEQVAN-----KFRSGK-----											
AtPIN2	SSMISFNKSHGGGL-----	NSSHTTPRPSNLTGVEIYSLQTRETPRSS-FNQADFYAMF-ASKARSPKHKGYTNFQGGI-----	GDYVYLSQSSKGATPTSNFDEEYHKTAKKAGRGRGSRMSGELY-----											
PtPIN2a	SSIYSSFNKSHGLNS-----ITSM-----	TPRPSNLTGVEIYSLQTRETPRSS-FNQADFYAMF-ASKARSPKHKGYTNFQGGI-----	GDYVYLSQSSKGATPTSNFDEEMLKLGKKGR-TNMSGELF-----											
OsPIN1c	RSEAACSHGTQSH-----SQSMQ	TPRPSNLSGVEIYSLQSSRNTPRSS-FNHAEFFNIVG-----	NGKQG-----DEEKG-----											
SbPIN4c	RSEAACSH-SHSH-----SQSMQ	TPRPSNLSGVEIYSLQSSRNTPRSS-FNHDFYSHMGV-----	AGAKGGAAAAAARGDEEKG-----											
SiPIN4b	RSEAACSH-SHSH-----SQSMQ	TPRPSNLSGVEIYSLQSSRNTPRSS-FNHAEFFNIVG-----	AKG-----AGGDEEKG-----											
SiPIN4d	RSEAACSH-SHSH-----SQSMQ	TPRPSNLSGVEIYSLQSSRNTPRSS-FNHAEFFNIVG-----	AKG-----AGGDEEKG-----											
PtPIN2b	SSNFSSRDRFDGHNP-----VLSVH-----	PPRPSNFSSVEVFSVQSS-----PRRSS-YRQTDLPLNLTNSFG-----	DIYSLQSSRNNSVPRISSNLEEMR-----											
OsPIN10a	-RRSLLYT-----	TPRPSNLTGAEIYSLSSRNTPRSS-FNHADFFA-----MVGGGPPPPPTPARV-RGSSFGRSELYSLOSS-RGPTPRQSNFDEHSARP-PKPPATTGALNHDA-----												
SbPIN4a	SRRSLLMVT-----	TPRPSNLTGAEIYSSSSRNTPRSS-FNHADFFA-----MVGGGPPPPPTPARV-RGSSFGRSELYSLOSS-RGPTPRQSNFDEHSARPQNSRPAAGVPSCHDA-----												
SiPIN4a	-RRSMLGVT-----	TPRPSNLTGAEIYSSSSRNTPRSS-FNHADFFA-----MVGGGPPPPPTPARV-RGSSFGRSELYSLOSS-RGPTPRQSNFDEHSARPQNSRPAAGVPSCHDA-----												
OsPIN10b	-RRSAAA-----	TPRPSNLTGVEIYSSSSRNTPRSS-FTFLADI-----PGHQPPN--SALRASSFGRADLFLSHSSRQHTPRPSSFDEHAA-----RARASATVAPTNDL-----												
SbPIN7	PSRRSLAAT-----	TPRPSNLTGVEIYSSSSRNTPRSS-FGIGADIGH-----PAAAPLHGASLRLMSSFGRADLFLSLHP-----TPRPSSFDEQAV-----RARASATVAPSNDP-----												
SiPIN4c	-SRSSLA-----	TPRPSNLTGVEIYSSSSRNTPRSS-FAYGDVSA-----TGAAPPLHGASLRLMSSFGRADLFLSHSS-RQHTPRPSSFDEHAV-----RARASAAVAPSYDP-----												
AtPIN6	VPDVSMSLCL-----	TPRPSNLSNAEIFSVN-----TPRPSNLSNAEIFSVN-----	TPRPSNLSNAEIFSVN-----TPRPSNLSNAEIFSVN-----											
PtPIN6a	APDOSLSSICL-----	TPRPSNLSNAEIFSVN-----TPRPSNLQHEYHGYNGRFS-----	TPRPSNLQHEYHGYNGRFS-----HGPNNIEIMLCNGDL-----											
PtPIN6b	APDOSLSSICL-----	TPRPSNLSNAEIFSVN-----TPVPLHEYHGYNGHFS-----	TPVPLHEYHGYNGHFS-----HGPNNIEIYLNGDL-----											
PtPININ7	EITENVNTKV-----	PPDQOFRSMVAAVADG-----	G-LAY-RSG-----TSPR-LSGYASSO-----											
OsPIN1d	RSEAACSHGTQSH-----SQSMQ	TPRPSNLSGVEIYSLQSSRNTPRSS-FNHAEFFNIVG-----	NGKHGDEEKG-----											
OsPIN9	NGNAYAADR-----	PQEYVNTIEITEMARAST-----												
SbPIN3	SIHEHDHRS-----	HHQVYNTIEITEMARARAVST-----												
SiPIN5b	I---HAERS-----	QNQVYNTIEITEMARARADSP-----												
PpPIN6-1	HGFEGHESG-----	IPALLTQGEHNDFRIGIGDEP-----												
OsPIN5a	DGAEEAAA-----	AGKDYEARAGAAGAAGTYYVAAA-----												
SiPIN5a	-AEEPPVK-----	DYEAASADAAPAAAAYVYVYVYAS-----												
SbPIN5b	DYPDSPVY-----	DYEAADADASATYYYYVYVYAS-----												
AtPIN5	NISDVQVD-----	NINIESGKRET-----VVV-----												
PtPIN5a	SNDPKDLE-----	GNADS-----TVS-----												
PtPIN5c	SNDPKDLE-----	GNADS-----TVS-----												
PtPIN5b	NNSDOKDLE-----	GSVON-----TES-----												
OsPIN5b	PAVMSSSS-----	PPEK-----QSDVEMNGRAYVAAPGGGG-----												
SbPIN5c	PYSSSSASSSSSSPPPPKDKAHEKDVENNAETAAAAAGTT-----													
OsPIN5c	PPPPPPTGT-----	D-DDDVEDGAAARAAATAA-----												
SbPIN5a	RAVEPAGO-----	DVDESGGGGGSGGEITAHH-----												
SiPIN5d	PARAE-----	EEGAGGDOVEESGGET-----												
AtPIN8	NDQEEANI-----	EDEPKEEDEEEVAIVRT-----												
PtPIN8a	TGDQEALQ-----	ES-----QYKEGGEVHSRTT-----												
PtPIN8b	TGDQEALQ-----	EA-----QHKDDEGVQRRT-----												
SbPIN8	TNERESGT-----	TGPMQQRHEEGQEKRYS-----												
SiPIN8	-NEGESGT-----	PGPMEERHEEGRKGYS-----												
SiPIN5c	SSPPPPARE-----	KGDVENVNAAREPDHPPPA-----												
OsPIN7	GARLPLFKSYAR-----	KLACPNLHASVIGISWCISNRSHLTLPPALEGSYQIMSR-----												
OsPIN8	AKRMMLLALAIRFFLGPALMGSSYAIMGRGVLLKIAIVQALPQGIVPFVFAKEYNVQADILSTAIIVGMMVAVPVALAYYFAMIIPAIK-----													
PpPIN6-2														

Supplementary Figure 1. Contd.

	391	400	410	420	430	440	450	460	470	480	490	500	510	520
OsPIN1a	-----	KYQYPAP-NPA-----	-----	-----	-----	-----	-----	-----	MRA-----	PPK-----PKKAAN-----	-----	GQAKGEDGKDLMHMFWSSSASPYSO-----	-----	-----
SbPIN1	-----	YGGQYPAP-NPA-----	-----	-----	-----	-----	-----	-----	MRA-----	QAKPMPKTQGLKKAAN-----	-----	GQAKGEDGKDLMHMFWSSSASPYSO-----	-----	-----
SiPIN1b	-----	YG-QYPAP-NPA-----	-----	-----	-----	-----	-----	-----	MRA-----	PAK-GQPKAAN-----	-----	GQAKGEDGKDLMHMFWSSSASPYSO-----	-----	-----
OsPIN1b	RAP-----	MAGHYPAP-NPA-----	-----	-----	-----	-----	-----	-----	VSS-----	APKGAKKAATN-----	-----	GQAKGED---LHMFWSSSASPYSO-----	-----	-----
SiPIN1a	RAP-----	GAGHYPAP-NPA-----	-----	-----	-----	-----	-----	-----	VRA-----	APKGAKKAATN-----	-----	GQAKGED---LHMFWSSSASPYSO-----	-----	-----
SbPIN4b	RAAPYPGAAAGHYPAP-NPA-----	-----	-----	-----	-----	-----	-----	-----	VRA-----	APK-KKAAGTH-----	-----	GQAKGED---LHMFWSSSASPYSO-----	-----	-----
AtPIN1	QSGGSGGGAHYAPAP-NPG-----	-----	-----	-----	-----	-----	-----	-----	MFSPTNTGGGGTAKGN-----	-----	-----	APVYGGKRQDGNGRDLHMFWSSSASPYSO-----	-----	-----
PtPIN1c	YHAP---GGATHYPAP-NPG-----	-----	-----	-----	-----	-----	-----	-----	MFSPTTAASKGVSANANNTAARAKKPNQAAQKNAEDGRDLHMFWSSSASPYSO-----	-----	-----	-----	-----	-----
PtPIN1d	YHAP---GGATHYPAP-NPG-----	-----	-----	-----	-----	-----	-----	-----	MFSPTTA-SKGYAAANN-----	-----	-----	RAAKKPNQAAQKNAEDGRDLHMFWSSSASPYSO-----	-----	-----
PtPIN1a	VFGNVRANGSAYPTPPNAG-----	-----	-----	-----	-----	-----	-----	-----	IFSP-----	GGKKKANG-----	-----	TENGKDHMFVWSSSASPYS-----	-----	-----
PtPIN1b	VFGNVRANGSAYPAPPNAG-----	-----	-----	-----	-----	-----	-----	-----	IFSP-----	GGKKKANG-----	-----	AENGKDHMFVWSSSASPYS-----	-----	-----
AtPIN3	FGYYPGGG-AGSYPPAPNPEF-----	-----	-----	-----	-----	-----	-----	-----	S-----	S-----	-----	S-----	-----	-----
AtPIN7	FGYYPGGA-PGSYPPAPNPEF-----	-----	-----	-----	-----	-----	-----	-----	S-----	TGNKTGSKAPKENHHHV-----	-----	GKSNSNDAKELHMFWNGNSGNSPYSO-----	-----	-----
PtPIN3a	FGFYPQAQTVPTSYPPAPNPEF-----	-----	-----	-----	-----	-----	-----	-----	RSTV-----	TTKTKRNQQQN-----	-----	SKANHDAKELHMFWSSSASPYSSEG-----	-----	-----
PtPIN3b	FGFYPQAQTVPTSYPPAPNPEL-----	-----	-----	-----	-----	-----	-----	-----	RSTI-----	TSKTTKRNQQQNHHQQQLLOPQPQNSKVNHDAKELHMFWSSSASPYSSEG-----	-----	-----	-----	-----
AtPIN4	NSSVPA---RGSYPPAPNPEF-----	-----	-----	-----	-----	-----	-----	-----	STGT-----	GVSTKPNKIPKENQQQLQE-----	-----	KDSKRSHDAKELHMFWSSSASPYSO-----	-----	-----
PpPIN3-2	PPLYRNRYAGGRMFMPTGLGGGLPVHGNPDTGHGSLSTLGTPGMGPDGRTIYPGSQTRAIISLYTPGGTGNI-----	-----	-----	-----	-----	-----	-----	-----	ATPLSSSLNTQIVNPVYSPRSQSIARKVKDKTRTS-----	-----	-----	PKSDEDAKELHMFWSSSASPVS-----	-----	-----
PpPIN3-1	PPLYRNRMGRMFTPRPGLGIGIVPGTOCTGHGTLSTLGAPGMGPDGRTIYPGSQTRAINILTLGGAAANVNTAPSTAVNTQIVNPVYSPRSQSIARKVKDKPKRS-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PpPIN3	PPLYRNMGGRGLFMARSOLGGVGALSFEPARHS-----	-----	-----	-----	-----	-----	-----	-----	MGPDGRTIYPG-----	-----	-----	-----	-----	-----
OsPIN1	-AA-----OPPS-YPAPNPG-----	-----	-----	-----	-----	-----	-----	-----	MMPA-----	PRKKELGGNSN-----	-----	SNKELHMFWSSSASPVS-----	-----	-----
SbPIN2	-GG-----SDATRYPAPNPG-----	-----	-----	-----	-----	-----	-----	-----	MNPP-----	PRKKELGGNSN-----	-----	SNKELHMFWSSSASPVS-----	-----	-----
SiPIN2	-QG-----SDATRYPAPNPG-----	-----	-----	-----	-----	-----	-----	-----	MMPP-----	PRKKELGGNSN-----	-----	SNKELHMFWSSSASPVS-----	-----	-----
AtPIN2	NNN-----S-VPSYPPPNPM-----	-----	-----	-----	-----	-----	-----	-----	FTGSTSGASGVKKKEGGGGSG-----	-----	-----	GGVGVGGONKEHNMFVWSSSASPVS-----	-----	-----
PtPIN2a	NGG-----SLVSSYPPPNPM-----	-----	-----	-----	-----	-----	-----	-----	FSGSTSG-----GPKKKEGGSG-----	-----	-----	PNKELHMFWSSSASPVS-----	-----	-----
OsPIN1c	-----AAGGGGHSPQPVY-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	G-----	-----	-----
SbPIN4c	-----GAGGGHSPQPQAYA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	AVAAKRKDLHMFLVWSSSASPVS-----	-----	-----
SiPIN4b	-----AGGGHSPQPQHAQA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	A-----	-----	-----
SiPIN4d	-----AGGGHSPQPQPHQA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	A-----	-----	-----
PtPIN2b	-----RKNGVAFPGSPSCA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN10a	KELHMFWSSSASPVS-----SEVSG-----	-----	-----	-----	-----	-----	-----	-----	L-----	-----	-----	-----	-----	-----
SbPIN4d	KELHMFWSSSASPVS-----SEVSG-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN4a	KELHMFWSSSASPVS-----SEVSG-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN10b	KOTHMIEWSGGASAASEVTG-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN7	ROVHMIEWSGGASTTSEVRG-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN4e	KDMPTEWSSGASAASEVTG-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN6	-----ARYSLQPTPRASN-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN6a	-----ARYSLQPTPRTSN-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN6b	-----ARYSLQPTPRASN-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN1d	-----AAGGGGHSPQPVY-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN9	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN5b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PpPIN6-1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN5a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN5a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN5b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN5a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN5c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN5b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN5b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN5c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN5c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN5a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN5d	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN8	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN8a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN8b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN8	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN5c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN8	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PpPIN6-2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Supplementary Figure 1. Contd.

	521	530	540	550	560	570	580	590	600	610	620	630	640	650
OsPIN1a	-----	YFGNG-AEYNDRAAVKERVMAVASPRK--ADG-----	-----	VERDDFSFGNR--GVAERDAEAGDEKSVAARV-SGEHGKPGTLPAFTA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN1	-----	YFGNGA-EYNDRAAVKERVMAVASPRKVAADGRKERGE	-----	DF--TERDDFSFGNK--GAERDAEAGDEK---AAA-LQVGNACGVAAAPAA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN1b	-----	YFGNGNA-EYNDRAAVKERVMAVASPRKVAADGRKERGE	-----	DF--AERDDFSFGNR--GGAERDAEAGDEK---AAV-AQGQNA-GVGA-PAA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN1b	-----	YFGGGAPDYNDAAA-----V-KSPRKMDG--AKDR-E-----	-----	DY--VERDDFSFGNR--GMDRDAEAGDEKARAA--AGDPSKAMRAPTA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN1a	-----	YFGGGAPDYNDAAA-----A-KSPRKMDG--AKER-D-----	-----	DY--VERDEFSGFN--GMDRDAEAGDEKARYA--GGGDPN-AVAAAPTA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN4b	-----	YFGGGAPDYNDAAA-----AVSPRKMDGGAKDR-D-----	-----	DY--VERDEFSGFN--GMDRDAEAGDEKAARAATA-VAGGDPN-AVAAAPTA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN1	-----	YFGGGGGNHHADYSTA-----TNDHQKVOKISYPQGNNSN	-----	-DNYQYEREESFGNK--D-ODSKYLATD-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN1c	-----	YFGGGHDYGRHDLKQVR-----YAVSPGKV-EQORENQE-----	-----	DYN-LERDDFSFGNR--G-LDERSNSHE-----GEK--VGFDFGPKPK-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN1d	-----	YFGGGHDYGRHDKQVR-----LAYSPGKVSEGETHENEQ-----	-----	DYN-LERDGFSFGNR--G-MOREMNNPE-----GEK--VGAAGPKPK-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPINPIN1a	-----	GGLHVFRGGDYG-----NDLGGYANQK-----	-----	DYEEFGRDEFSGNRPVPNGVYDGPVLSKLASSSTAELHPKSANGEPKPTA-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN1b	-----	GGLHVFKGGDYG-----NDLGGYAHHK-----	-----	DYDEFGRDEFSGNRPGPNGVYDGPVLSKLGSGSTAELHPKSANGEKPTV-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN3	-----	AGLNYVFGGP-----DNDQGGRSDQG-AKEIRMLYPDQSHNGETKAYAHPASGDFGQEQQFSFAGKEEEAERPDKAENGLNKLAPNSTAALQSKTGLGGAERSQRKNMPPASVMT-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN7	-----	AGLQYDNGR-----NEQYGKSDQGGAKEIRMLISDHTQNGENKA-----GPMNGDYGE-----	-----	EESERYKEYPNGLHLKRCNSTAELNPKERIETGETYVPHMPPASVMT-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN3a	-----	GGLHVFGGDRDFGRASEQSGRSOOG-AKEIRMLYADHPQNGETKTI-----	-----	DQGDFAGEOFDSFAGRGE-----GEGDDQREKEPTGLNLKLGSSSTAELQPK-----AEAPDGGSRKMP-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN3b	-----	GGLHVFGGTDFGRASEQSGRSOOG-AKEIRMLYADHPQNQDSKTI-----PQA-----GNFAGEOFDSFAGRGE-----GEGDDQREKEPTGLNLKLGSSSTAELHPK-----AVGAPDGGSKQMP-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN4	-----	YFGGGA-GDNVATEQSEQG-AKEIRMVYSDQPRKSNAR-----	-----	GGGDGIGGLDSEGEGERIEKATAGLNKGMSNSAELEARAGGGGGNN-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN3-2	-----	AGLHVFGGNDTSANLHQSFDPKEYRMLVHPQSDLH-----	-----	R-RTDNYQEDSFGNRNDLKLEODKDGPRLDNFKGST-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PpPIN3-1	-----	AGLHVFGGNDTSANLHQSFDPKEYRMLVHPQSDLH-----	-----	R-RTDNYQEDSFGNRNDLKLEODKDGPRLD-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PpPIN3	-----	-----	-----	KFGST-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN2a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN1c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN4c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN4b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN4d	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN2b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN10a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN4a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN4a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN10b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN4c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN6	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN6a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN6b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPINPIN7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN1d	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN9	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN5b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PpPIN6-1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN5a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN5a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN5b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN5a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN5c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN5b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN5b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN5c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN5c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN5a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN5d	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
AtPIN8	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN8a	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PtPIN8b	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SbPIN8	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN8	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
SiPIN5c	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
OsPIN8	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
PpPIN6-2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
ILHICQGIWIACRRPEYSKGGARVYVRLICRHGTAWRGATGHYRERDLMIGWYDIGKLSAITLEYFALALGYCSSRRWWQIFTRDSE	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Supplementary Figure 1. Contd.

	651	660	670	680	690	700	710	720	730	740	750	760	770	780
OsPIN1a	SSLIGLIW	--SLVCFRINFEMPAIILKSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNKVA	--TFMAMVRFLTGPAYMRAASIAVGLRGTLHHVAVQ-									
SbPIN1	SSLIGLVW	--SLVCFRINFEMPAIILKSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNKVA	--TFMAMVRFLTGPAYMRAASIAVGLRGTLHHVAVQ-									
SiPIN1b	SSLIGLIW	--SLVCFRINFEMPAIILKSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNKVA	--TFMAMVRFLTGPAYMRAASIAVGLRGTLHHVAVQ-									
OsPIN1b	SSLIGLIW	--SLVCFRINFEMPAIILKSISI	--LSOAGLGMHMFSLGLFMALQ-	PHIIACGNKVA	--TYMAMVRFLGPAYMRAASIAVGLRGTLHHVAVQ-									
SiPIN1a	SSLIGLVW	--SLVCFRINFEMPAIILKSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNKVA	--TFMAMVRFLTGPAYMRAASIAVGLRGTLHHVAVQ-									
SbPIN4b	SSLIGVW	--SLVCFRINFEQMPAIYVLKSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNKVA	--TFMAMVRFLTGPAYMRAASIAVGLRGTLHHVAVQ-									
AtPIN1	SSLFGITW	--SLISFKWNIEMPALIAMSISI	--LSOAGLGMHMFSLGLFMALN-	PRIIACGNRR	--AFAAAHARFVVGPAVMLYASYAVGLRGVLLHHVAVQ-									
PtPIN1c	SSLIGLIW	--SLYSFRWVVKMPLIIAKSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNSIR	--AFSMAMVRFLTGPAYMRAASIAVGIROGTLHHVAVQ-									
PtPIN1d	SSLIGLTW	--SLVSFRWVQMPAIIAKSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNSVA	--AFAMAMVRFLTGPAYMRAASIAVGLRGTLHHVAVQ-									
PtPINPIN1a	SSLIGLTW	--SLVSFKWDELEMPQIAHSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNSIA	--AFAMSVRFLTGPAYMRAASIAVGLRGVLLHHVAVQ-									
PtPIN1b	SSLIGLTW	--SLVSFKWNIIMPALIADSISI	--LSNAGLGMHMFSLGLFMALQ-	PRIIACGNSIA	--SFAMGVRFLLGPAYMRAASIAVGLRGDLRRVAVQ-									
AtPIN3	SSLIGLIW	--RLVAFRHWVHMPKIIQKSISI	--LSOAGLGMHMFSLGLFMALQ-	PKLIACGNSVA	--TFMAMVRFLTGPAYMRAVIAIIGLRGDLLRHVAVQ-									
AtPIN7	SSLIGLIW	--RLVAFRHWVHMPKIIQKSISI	--LSOAGLGMHMFSLGLFMALQ-	PKLIACGNSTA	--TFMAMVRFLFTGPAYMRAVAMAIIGLRGDLLRHVAVQ-									
PtPIN3a	SSLIGLTW	--SLVAFRHWVHEMPKIIQKSISI	--LSOAGLGMHMFSLGLFMALQ-	PKLIACGNSVA	--TFMAMVRFLTGPAYMRAASIAVGLRGTLHHVAVQ-									
PtPIN3b	SSLIGLIW	--SLVAFRHWVHEMPKIIQKSISI	--LSOAGLGMHMFSLGLFMALQ-	PKIIACGNSVA	--TFMAMVRFLTGPAYMRAASIAVGLRGTLHHVAVQ-									
AtPIN4	SSLIGLIW	--RLVAFRHWVHMPKIIQKSISI	--LSOAGLGMHMFSLGLFMALQ-	PKIIACGNSVA	--TFMAMVRFITGPAYMRAVAGIAIIGLRGDLLRHVAVQ-									
PpPIN3-2	SSLLGVW	--SLVANRWHHTPLTLYKSVH	--LSOAGLGMHMFSLGLFMGLG-	DRIIVCGRKMA	--IFGMSLRFLAGPAVFAASYLVGLRGVPLKVSVQ-									
PpPIN3-1	SSLLGVW	--SLVANRWHLSMPLIILYKSYHI	--LSOAGLGMHMFSLGLFMGLG-	DRIIVCGTKMA	--VFGMALRFLAGPAVFAASYLVGLRGVPLKVSVQ-									
PpPIN3	SSLLGVW	--SLISFKCHLDMLPILYKSYHI	--LSOAGIGMAMFSLGLFMGLG-	DRIIVCGTKHA	--LFAMLLRFLVGPAYVFAASYLVGLRGVSLNVSTVQ-									
OsPIN2	SSLIGLVW	--SLVSFRWNIQMPMSIKGSISI	--LSOAGLGMHMFSLGLFMALQ-	PKIISCGKTV	--TFMAMVRFLTGPAYVIAATSIAIIGLRGVLLHHVAVQ-									
SbPIN2	SSLIGLVW	--SLVSFRWNIQMPMSIKGSISI	--LSOAGLGMHMFSLGLFMALQ-	PKIISCGKRVA	--TFMAMVRFLTGPAYVIAATSIAIIGLRGVLLHHVAVQ-									
SiPIN2	SSLGVW	--RLVSFRWNIQMPMSIKGSISI	--LSOAGLGMHMFSLGLFMALQ-	PKIISCGKRVA	--TFMAMVRFLTGPAYVIAATSIAIIGLRGVLLHHVAVQ-									
AtPIN2	SSLFGIAW	--SLVSFKWNIKMPTIMSGSISI	--LSOAGLGMHMFSLGLFMALQ-	PKIACGSKVA	--GFMAMVRFLTGPAYVIAATSIAIIGRGDLHHVAVQ-									
PtPIN2a	SSLLGVW	--SLVSYRWNKMPMSIVSGSISI	--LSOAGLGMHMFSLGLFMALQ-	PKIACGKSVA	--TFMAMVRFLTGPAYVIAATSIAIIGRGVLLHHVAVQ-									
OsPIN1c	SSLLGVW	--SLVSYRWNKMPMSIVSGSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNSLA	--SYAMAVFLYGPAYMRAASIAVGLRGVLLHHVAVQ-									
SbPIN4c	SSLLGVW	--SLVSYRWNKMPMSIVSGSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNSLA	--VIAVFLYGPAYMRAASIAVGLRGVLLHHVAVQ-									
SiPIN4b	SSLLGVW	--SLVSYRWNKMPMSIVSGSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNSLA	--AYAMAVFLYGPAYMRAASIAVGLRGVLLHHVAVQ-									
SiPIN4d	SSLLGVW	--SLVSYRWNKMPMSIVSGSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNSLA	--AYAMAVFLYGPAYMRAASIAVGLRGVLLHHVAVQ-									
PtPIN2b	RSLLGLW	--SLISFRWSIKLPLIVDGSVRI	--LSNAGLGMHMFSLGLFAALQ-	PKVIASGKYLA	--LISMARIKFLIGPAVIAATSLAVGLRGDLLRHVAVQ-									
OsPIN10a	SSLLGLW	--SLVAFRIVHGAAQHHRYHQISRRRLHGRPLPRGCRHGRVVNRHRTPRDAPARRHCGGGSTTRDCAFCFCKR1QCPGPGHEHSGNFWHANSSNNHIAVLP-												
SbPIN4a	SSLIGLW	--SLIARFRWHISMPAVYAKSISI	--LSOAGLGMHMFSLGLFMALQ-	PNIICGHRAT	--GISMGVRFLAGPAVMTAASLAIIGLRGNNLLRVAVQ-									
SiPIN4a	SSLIGLW	--SLIARFRWHISMPAVYAKSISI	--LSOAGLGMHMFSLGLFMALQ-	PNLICGHRAT	--GISMGVRFLAGPAVMTAASLAIIGLRGSSLLQVAVQ-									
OsPIN10b	ASLIGLTW	--SLIARFRFHITMPIVAKSISI	--LSOAGLGMHMFSLGLFMATQ-	PKIIACGYSVA	--ARSMGVRFFFGPAYMRAASAAVGIROGTLHHVAVQ-									
SbPIN7	ASVVGLTW	--SLISFRFHVAMPVVKNSISI	--LSOAGLGMHMFSLGLFMATQ-	PKIIACGKVA	--AITMAMRFLFGPAVMAATSIAIIGLRGDTLLRHVAVQ-									
SiPIN4c	ASVVGLTW	--SLISFRFHVAMPVVKNSISI	--LSOAGLGMHMFSLGLFMATQ-	PKIACGNSVA	--AITMAMRFLLGPAVMAATSIAVGLRGDTLLCTAVQ-									
AtPIN6	SSLLGVW	--SLISFKWNIQMPNIVDFSIKI	--LSOAGLGMHMFSLGLFMALQ-	PKMIPCGKKA	--TMGLHLRFISGPLFMAGASLLVGLRGSRLLHAIHVQ-									
PtPIN6a	SSVLGLW	--SLVSFKWNVGMPSPLVKYSIKI	--LSOAGLGMHMFSLGLFMALQ-	PRIIVCGKKRA	--THMAMAIRFICGPVVMSTTSVAVGMRGVRLRAHVQ-									
PtPIN6b	SSVLGLW	--SLASFKWNVGMPSPLVKYSIKI	--LSOAGLGMHMFSLGLFMALQ-	PRIIVCGKKRA	--THMAMAIRFICGPVIMSTTSVAVGMRGVRLRAHVQ-									
PtPINPIN7	ASLIGLSW	--RLVSCRYGIMKPKQIVDONSVTI	--LSKAGLGMHMFSLGLFMALQ-	PRIIACGNRA	--IYGMLRFLAGPAVAVASIGVGLRGTMKLSIVQ-									
OsPIN1d	SSLLGVW	--SLVSYRWNKMPMSIVSGSISI	--LSOAGLGMHMFSLGLFMALQ-	PRIIACGNSLA	--SYAMAVFLYGPAYMRAASIAVGLRGVLLHHVAVQ-									
OsPIN9	ASFLGLW	--SLIARFKCGFSMPKIVEDSLFT	--IRTTAVGLMSFSSGTFIARQ-	SRVPCGYKIA	--SFVNVIKFLIGPVGMLFASLYVIGHGCTLLHHVAVQ-									
SbPIN3	ASFLGLW	--SLIARFKIGFSMPKIVGDLSFI	--IYTAVGLMSFASGTFIARQ-	SRVPCGYTIA	--SLSMVLFKFLIGPITMLLASLAVGHGCTLLHHVAVQ-									
SiPIN5b	ASFLGLW	--SLIARFKIGFSMPKIVDDSLFT	--IHTTAVGLMSFASGTFIARQ-	SRVPCGYTIA	--SLSMVLFKFLIGPIMLLVSLAIGMHGCTLLHHVAVQ-									
PpPIN6-1	ATVNGIVY	--SLIARFKRGFDPLRILRNSLDI	--MGRITLGLTHYSIGLFGAQ-	KKLV-ASWVY	--FYGAFCRFIVGPCTGMVAVSLLGLRBDLRLFALQ-									
OsPIN5a	ASFVGITW	--ACLANRLHIALPSAFEWSVLI	--MSKSGTGFMHFSMGLFMAMQ-	EKIIACGTSFA	--ALGLVLFKFLGPAMMIGSIAVGLRGDVLRVAVQ-									
SiPIN5a	ASFVGITW	--ACVANRLHIELPSAFEWSVLI	--MSKSGTGFMHFSMGLFMAMQ-	EKVLACGCPFA	--ALGLVLFKFLGPAMMIGSIAVGLRGDVLRVAVQ-									
SbPIN5b	ASFVGITW	--ACVANRLHIELPSAFEWSVLI	--MSKSGTGFMHFSMGLFMAMQ-	EKVLACGPSFA	--ALGLVLFKFLGPAMMIGSIAVGLRGDVLRVAVQ-									
AtPIN5	SCILGIAW	--AFISNRWHLELPGILEGSTI	--MSKAGTGTAMFNMGIFMALQ-	EKLIVCGTSLT	--YGMVYKFLIGPAMMIGSIVLGLHDVLRVAVQ-									
PtPIN5a	ACIIGLW	--AFIARKRWFEMPSIMEGSIL	--MSKTGTGTAMFNSMGIFMALQ-	EKVIACGRSLT	--VIGMVLRFIAGPAMMIGSIAVGLRGDVLRVAVQ-									
PtPIN5c	ACIIGLW	--AFIARKRWFEMPSIMEGSIL	--MSKTGTGTAMFNSMGIFMALQ-	EKVIACGRSLT	--VIGMVLRFIAGPAMMIGSIAVGLRGDVLRVAVQ-									
PtPIN5b	ACIIGLW	--AFISNRWHFEMPMAMMEGSIL	--MSKAGTGTAMFNSMGIFMALQ-	EKVIACGRSLA	--VIGMVLRFIAGPAMMIGSIAVGLRGDVLRVAVQ-									
OsPIN5b	RSVLGVW	--ACIAYRWHLSPLGIVTGSLOV	--HSRTGTGMSHFSMGLFMGQQ-	ERVIACGAGLT	--ALGMALRFVAGPLATLYGAAAGLGLRGDVHLHAIIOQ-									
SbPIN5c	RSVLGVW	--ACIAYRWHLSPLGIVTGSLOV	--HSRTGTGMSHFSMGLFMGQQ-	EKMIACGSSLR	--ALGMALRFVAGPLATLYGAAAGFRLRGDVLRFAIIQ-									
OsPIN5	AGYLGVW	--ACVYNRWHYETPSIIEGSQLI	--MSKTGVGLMSFMSMGLFMALQ-	DKIIYCGAGLT	--VGLMALRFVAGPAATVGAFLGLRGDVLRFAIIQ-									
SbPIN5a	AGILGVW	--ACVYNRWHYETPSIIEGSQLI	--MSKTGVGLMSFMSMGLFMALQ-	EKIIYCGAGPT	--MLGMALRFVAGPAATVGAFLGLRGDVLRVAVMQR-									
SiPIN5d	AGVLGVW	--ACVYNRWHIETPSIIEGSQLI	--MSKTGVGLMSFMSMGLFMALQ-	EKIIYCGAGPT	--FLGMALRFVAGPAATVGAFLGLRGDVLRVAVMQR-									
AtPIN8	ATLIGIWW	--ATLHFRLGWNLPEIDOKSIIH	--LSOGGLGMHMFSLGLFMRSQ-	SSIIACGTKMA	--IITHLLKFVLPALHIAASAYCIRLKSTLKFVAVQ-									
PtPIN8a	ATMVALIW	--ASIHFRWGVLPDIYDKSVI	--LSTGGLGMHMFSLGLFMALR-	PSIISCGIRMA	--VYAMAMKFIVGPALMAYASFAVRLLEGTVLKVAIVQ-									
PtPIN8b	ATLVALIW	--ASIHFRWGVLPDIYDKSVI	--LSTGGLGMHMFSLGLFMASR-	PSIISCGIRMA	--VYAMAMKFIVGPALMAYASFAVRLLEGTVLKVAIVQ-									
SbPIN8	ASLIGLIW	--ALISFRWRIQLPSPVYNNNSIRI	--LSOGGLGMHMFSLGLFTALQ-	TKIIVACGTTKMM	--LLSLGIRFFLGPALMVYSSYAIGMRGTLKKVAVQ-									
SiPIN8	ASLIGLIW	--ALISFRWVQLPSPVYNNNSIRI	--LSOGGLGMHMFSLGLFTALQ-	TKIIVACGTTKMM	--LLSLGIRFFLGPALMVYSSYAIGMRGTLKKVAVQ-									
SiPIN5c	HSVLGW	--ACIARFRWDLRHPGVYSESLQV	--HSRTGTGMSHFSMGLFMHQ-	EKIVACGAGLA	--ALGMALRFVAGPLATLAGAAAFGLRSQYHRFIIQTVLGGV-									
OsPIN7	AINRMVYVFAFPFFTTEFTLHLDPYNYRCSLIADSDIAKLI	--VRAISIGVMLFRK	--EGLCARYTDWCISGFSLASLTSVYVGHPMARAMYGNHAGQIVYQLSIFQAVWLTSL											
OsPIN8														
PpPIN6-2														

Supplementary Figure 1. Contd.

SbPIN5b	-----SLLAF----FFI
AtPIN5	-----ALPQAITSF----VFAKEYGLHADVLSTAVIFGMLVSLPVLVAYYRALEFIH
PtPIN5a	-----AfpQAIISF----VFAQEYGLHAEVLSTAVIFGTIVALPVLIAYYAILDFVH
PtPIN5c	-----AfpQAIISF----VFAQEYGLHAEVLSTAVIFGTIVALPVLIAYYAILDFVH
PtPIN5b	-----ALPQAITSF----VFAKEYGLHAEVLSTAVIFGMLAALPVLITYYYAILEFVP
OsPIN5b	-----ALPQSIASF----VFAKEYGLHADVLSTAVIFGTLSLPVILIAYYAVLGFY
SbPIN5c	-----ALPQSIASF----VFAKEYGLHADVLSTAVIFGTLSLPVLIAYYAVLGIL
OsPIN5c	PEICLNSNGCMHDTSHPDETARDEQAALPQAITTF----VFAKEYGLHAEILSTAVIFGTLSLPVLIIVYYIVLGFI
SbPIN5a	-----ALPQAITTF----VFAREYGLHADVLSTAVIFGTLSLPVLIIVYYIVLGILRC
SiPIN5d	-----ALPQAITTF----VFAKEYSLHADVLSTAVIFGTLSLPVLIIVYYIVLGILRC
AtPIN8	-----ALPQGVVPF----VFAKEYNLHPEIISTGVIFGMLIALPTTLAYYFLLDL
PtPIN8a	-----ALPQGIVPF----VFAKEYNVHPDTLSTGVIFGMLIAMPIALAYYSLLAL
PtPIN8b	-----ALPQGIVPF----VFAKEYNVHPDTLSTGVIFGMLISMPIALAYYSLLAL
SbPIN8	-----ALPQGIVPF----VFAKEYNVHADILSTAIILGMIVAVPVALGYYFYMDHPRL
SiPIN8	-----ALPQGIVPF----VFAKEYNVHADIVSTAIIVGMMIVAVPVALGYYFYIDHPRF
SiPIN5c	
OsPIN7	-----VVVLEYRKAFYSDAHDESNSYEEGSFIDDDTYVGSSGTSEDMQSLEEGYSDATNQDLRGEEARSVAVVNGARLPLFKSVARRTSLCHQLWRGR
OsPIN8	
PpPIN6-2	

Supplementary Figure 1. Contd.