

# Supplementary Information

MaPIP1-3	.....MIFALVY..CTAGISGGHINFA	20	MaPIP1-3	ITCTGTNPARSLGPAIYINKDHWDDHWIFWVGFFIGAAI	172
MaPIP1-2	.....MIFALVY..CTAGISGGHINFA	20	MaPIP1-2	ITCTGTNPARSLGPAIYINKKHAWDDHWIFWVGFFIGAAI	172
MaPIP1-9	.....MIFILVY..CTAGISGGHINFA	20	MaPIP1-9	ITCTGTNPARSLGPAIYVYDKSHAWDDHWIFWVGFFIGAAI	172
MaPIP1-4	.....MIFALVY..CTAGISGGHINFA	20	MaPIP1-4	ITCTGTNPARSLGPAIYINKDHWDDHWIFWVGFFIGAAI	172
MaPIP1-7	.....MIFALVY..CTAGISGGHINFA	20	MaPIP1-7	ITCTGTNPARSFGPAIYINKDHWDDHWIFWVGFFIGAAI	172
MaPIP1-1	.....MIFALVY..CTAGISGGHINFA	20	MaPIP1-1	ITCTGTNPARSLGPAIYINKDHWDDHWIFWVGFFIGAAI	172
MaPIP1-8	.....MIFALVY..CTAGISGGHINFA	20	MaPIP1-8	ITCTGTNPARSLGPAIYINKHAWDDHWIFWVGFFIGAAI	172
MaPIP1-6	STRKSTVGIQGIAWAFGGMIFALVY..CTAGISGGHINFA	44	MaPIP1-6	ITCTGTNPARSLGPAIYINKGHWDDHWIFWVGFFIGAAI	196
MaPIP1-5	DTKSTVGIQGIAWAFGGMIFALVY..CTAGISGGHINFA	44	MaPIP1-5	ITCTGTNPARSLGPAIYINKDHWDDHWIFWVGFFIGAAI	196
MaPIP2-6	ADQCSGVGLIGIAWAFGGMIFILVY..CTAGISGGHINFA	104	MaPIP2-6	ITCTGTNPARSLGPAIYINQDKAWDDHWIFWVGFFIGALA	256
MaPIP2-9	.....MIFILVY..CTAGISGGHINFA	20	MaPIP2-9	ITCTGTNPARSFGPAIYINKDHWDDHWIFWVGFFIGAAI	172
MaPIP2-7	ADQCSGVGLIGIAWAFGGMIFILVY..CTAGISGGHINFA	103	MaPIP2-7	ITCTGTNPARSLGPAIYINQDKRFDHWIFWVGFFIGALA	255
MaPIP2-5	.....MIFILVY..CTAGISGGHINFA	20	MaPIP2-5	ITCTGTNPARSFGPAIYINKDHWDDHWIFWVGFFIGAAI	172
MaPIP2-10	.....MIFILVY..CTAGISGGHINFA	20	MaPIP2-10	ITCTGTNPARSLGPAIYINQDKRFDHWIFWVGFFIGALA	172
MaPIP2-4	.....MIFILVY..CTAGISGGHINFA	20	MaPIP2-4	ITCTGTNPARSLGPAIYINQDKAWDDHWIFWVGFFIGAAI	172
MaPIP2-13	.....MIFILVY..CTAGISGGHINFA	20	MaPIP2-13	ITCTGTNPARSFGPAIYINRHKRFDHWIFWVGFFIGALA	172
MaPIP2-11	.....MIFILVY..CTAGISGGHINFA	20	MaPIP2-11	ITCTGTNPARSFGPAIYINQKRFHDHWIFWVGFFIGALA	172
MaPIP2-3	.....MIFILVY..CTAGISGGHINFA	20	MaPIP2-3	ITCTGTNPARSFGPAIYINKDHWDDHWIFWVGFFIGAAI	172
MaTIP1-1	DGAATPAGLIAAALAHGFALFVAVS..VGNISGGHINFA	87	MaTIP1-1	FSGASINPARSFGPAIVS...WSWTHQWVWVVGFLIGGGL	228
MaTIP1-4	DGSTTPAGLVASLAAHGFALFVAVS..VGNISGGHINFA	87	MaTIP1-4	FDGASINPARSFGPAIVS...WTWNNHWVWVVGFLIGGGL	229
MaTIP1-6	GAATTPAGLIAAALAHGFALFVAVS..VGNISGGHINFA	87	MaTIP1-6	FDGASINPARSFGPAIVS...WSWDDHWVWVVGFLIGGGL	228
MaTIP4-1	GEDRIMVVVAFAAQAAMLVAMITA..VGLDVSAGHINFA	85	MaTIP4-1	FSGASINPARSFGPAIVS...WDWNNHWVWVVGFLIGGGL	228
MaTIP3-2	D.TSTAGGLVVVAIAHALALFVAVS..VSLNISGGHINFA	86	MaTIP3-2	FDGAAINPARAFGPAIVG...WRWKSHWVWVVGFLIGGGL	228
MaTIP5-1	DVTSDASSLVATALAQGFALFAAVY..IAADISGGHINFA	89	MaTIP5-1	ITGGSINPARSFGPAIVS...GNFKNHVWVWVVGFLIGGGL	240
MaTIP3-1	D.TSTAGGLVVVAIAHALALFVAVS..IAFNISGGHINFA	86	MaTIP3-1	FDGAAINPARAFGPAIVG...WRWKNHWVWVVGFFIGAAI	228
MaTIP1-5	GGAAFTPTGLIMAALAHGFALFVAVS..VGNISGGHINFA	87	MaTIP1-5	FDGASINPARSFGPAIVS...WSWTHQWVWVVGFLIGGGL	229
MaTIP2-1	GAALDPAGLVAAALAHGLALFVGVS..MAANISGGHINFA	85	MaTIP2-1	FSGGSINPARSFGPAIVS...GDFAGNHWVWVVGFLIGGGL	227
MaTIP2-4	SAALDPAGLVAAIVCHGFALFVAVS..VGFNISGGHINFA	85	MaTIP2-4	FSGGSINPARSFGPAIVS...GDFSDLVWVWVVGFLIGGGL	226
MaTIP4-2	GQDSIMGLTAV.AVAQAMLVAVMVA..VGLDVSAGHINFA	84	MaTIP4-2	FSGASINPARSFGPAIVS...WDWNNHWVWVVGFFIGGGL	226
MaTIP4-3	G.DSIMGLTAV.AVAHALVVAVMIS..AGLHISGGHINFA	83	MaTIP4-3	FSGASINPARSFGPAIVS...WNWTDHWVWVVGFLAGGGL	225
MaTIP2-2	SAALDPAGLVAAIVCHGFALFVAVS..VGNISGGHINFA	85	MaTIP2-2	FSGGSINPARSFGPAIVS...GNFSDLVWVWVVGFLIGGGL	226
MaTIP1-2	DGSTTPAGLVAAALAHGFALFVAVS..VGNISGGHINFA	87	MaTIP1-2	FDGASINPARSFGPAIVS...WTWNNHWVWVVGFLIGGGL	229
MaTIP2-5	GAALDAAGLVAAALCHGFALFVAVS..IAANISGGHINFA	85	MaTIP2-5	FSGGSINPARSFGPAIVS...GDFADLVWVWVVGFLIGGGL	224
MaTIP1-3	DGAATPEGLIAAALAHGFALFVAVS..VGNISGGHINFA	87	MaTIP1-3	FDGASINPARSFGPAIVS...WSWTHQWVWVVGFLIGGGL	228
MaTIP2-3	GAALDPAGLVAAALAHGLALFVGVS..MAANISGGHINFA	85	MaTIP2-3	FSGGSINPARSFGPAIVS...GDFSGNHWVWVVGFLIGGGL	227
MaNIP1-1	MITFFG....ICVWGLAVVMVY..SVGHISGAHINFA	98	MaNIP1-1	ISGASINPARTLGPAIVAN...RWEGFWVWVVGFCIGTVV	238
MaNIP1-2	IVIFFG....ICLAWGLVVMVY..SLGHVSGAHINFA	116	MaNIP1-2	ISGASINPARTLGPAIVAN...RWEGFWVWVVGFCIGTVV	256
MaNIP2-1	VVSQLG....QSVAGGLIVTVMY..AVGHISGAHINFA	113	MaNIP2-1	ISGGSINPARTLGPAIVAS...KFDLSLVWVWVVGFLIGGGL	252
MaNIP2-2	LVSQLG....ASVAGGLIVTVMY..AVGHISGAHINFA	107	MaNIP2-2	ISGGSINPARTLGPAIVAS...NYDSLWVWVVGFLIGGGL	246
MaNIP2-3	AVSQLG....ASVAGGLIVTVMY..AVGHISGAHINFA	107	MaNIP2-3	ISGGSINPARTLGPAIVAS...NYDALWVWVVGFLIGGGL	246
MaNIP2-5	VVSQLG....ASVAGGLIVTVMY..AVGHISGAHINFA	107	MaNIP2-5	ISGGSINPARTLGPAIVAS...KYDALWVWVVGFLIGGGL	245
MaNIP3-2	AETLIG....NAACAGLAVMIVIL..STGHISGAHINFA	152	MaNIP3-2	SSGGSINPARTLGPAIVAS...NYERINWVWVVGFLIGGGL	291
MaNIP2-4	VVSQLG....ASVAGGLIVTVMY..AVGHISGAHINFA	137	MaNIP2-4	VSGGSINPARTLGPAIVAS...NYQSLWVWVVGFLIGGGL	276
MaNIP4-1	.....MVY..SVGHISGAHINFA	16	MaNIP4-1	ISGASINPARTLGPAIVM...NYKAINWVWVVGFLIGGGL	156
MaSIP1-1	ALQIQGVAFSLFVITLILAFVVEGLITAAIGGASINFT	73	MaSIP1-1	YTGPAINPARAFGPAIVNNRHNTEQFVWVWVVGFLIGGGL	219
MaSIP2-1	TGMDPISVLLKGYLIV.YLYYFSQ..LRKVINGGTINBL	94	MaSIP2-1	ITGGMVNFASAFGPAIVYQGHKLTREHLCVWVWVVGFLIGGGL	234
MaSIP2-2	LGHRRFGGEALKMALVVG.YMFLFAW..LGHVIRGGAYNBL	70	MaSIP2-2	ITGGINNFASAFGPAIVYARGDHTITDQLIVWVWVVGFLIGGGL	212

**Figure S1.** Alignment of amino acid sequences of MaAQPs. The two conserved NPA motifs are shown in blue box. Amino acids with high identities were shown in black background.

SlPIP1-1	MAENKEEDVNLGANKFREPCPLGTSAQTDKDYKEPPAPL	40
MaPIP1-3	.....	0
MaPIP1-2	.....	0
MaPIP1-9	.....	0
MaPIP1-4	.....	0
MaPIP1-7	.....	0
MaPIP1-1	.....	0
MaPIP1-8	.....	0
MaPIP1-6	.....	0
MaPIP1-5	.....	0
MaPIP2-6	.....MSKEVSVEVEQPPAKDYSDFPPAPL	25
MaPIP2-9	.....	0
MaPIP2-7	.....MSKEVS.EAEQAPAKDYRDFPPAPL	24
MaPIP2-5	.....	0
MaPIP2-10	.....	0
MaPIP2-4	.....	0
MaPIP2-13	.....	0
MaPIP2-11	.....	0
MaPIP2-3	.....	0
Consensus		
SlPIP1-1	YEPGELSSWSFYRAGIAEFMATFLFLYITILTVMG..LKR	78
MaPIP1-3	.....	0
MaPIP1-2	.....	0
MaPIP1-9	.....	0
MaPIP1-4	.....	0
MaPIP1-7	.....	0
MaPIP1-1	.....	0
MaPIP1-8	.....	0
MaPIP1-6	.....MG..VVK	5
MaPIP1-5	.....MG..VVK	5
MaPIP2-6	LDFGEVRLWSFYRALIAEFVATLLFLYVSIATVIGHKEQN	65
MaPIP2-9	.....	0
MaPIP2-7	LDFGELRLWSFYRALIAEFVATLLFLYVTIATVIGHKEQN	64
MaPIP2-5	.....	0
MaPIP2-10	.....	0
MaPIP2-4	.....	0
MaPIP2-13	.....	0
MaPIP2-11	.....	0
MaPIP2-3	.....	0
H2		
SlPIP1-1	SDSLCSSVGIQGVAWAFGGMIEFLVYCTAGISGGHINPAV	118
MaPIP1-3	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP1-2	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP1-9	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP1-4	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP1-7	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP1-1	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP1-8	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP1-6	SSTKCSVGIQGIAWAFGGMIEFLVYCTAGISGGHINPAV	45
MaPIP1-5	SDTKCSVGIQGIAWAFGGMIEFLVYCTAGISGGHINPAV	45
MaPIP2-6	AADQCSGVGLLGIAWAFGGMIEFLVYCTAGISGGHINPAV	105
MaPIP2-9	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP2-7	AADQCSGVGILGIAWAFGGMIEFLVYCTAGISGGHINPAV	104
MaPIP2-5	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP2-10	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP2-4	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP2-13	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP2-11	.....MIEFLVYCTAGISGGHINPAV	21
MaPIP2-3	.....MIEFLVYCTAGISGGHINPAV	21

Figure S2. Cont.

SlPIP1-1	TEGIFLARKLSITRAVFYVMVQCCLGAICGAGVVKGFQKGP	158
MaPIP1-3	TEGIFLARKLSITRAIFYVMVQCCLGAICGAGVVKGFQKGV	61
MaPIP1-2	TEGIFLARKLSITRALFYVMVQCCLGAICGAGVVKGFQKGL	61
MaPIP1-9	TEGIFLARKLSITRALFYVMVQCCLGAICGAGVVKGFQKGL	61
MaPIP1-4	TEGIFLARKLSITRAIFYVMVQCCLGAICGAGVVKGFQKGV	61
MaPIP1-7	TEGIFLARKLSITRALFYVMVQCCLGAICGAGVVKGFQKGL	61
MaPIP1-1	TEGIFLARKLSITRAVFYVMVQCCLGAVCGAGVVKGFQKGV	61
MaPIP1-8	TEGIFLARKLSITRAIFYVMVQCCLGAICGAGVVKGFQKGV	61
MaPIP1-6	TEGIFLARKLSITRALFYVMVQCCLGAICGAGVVKGFQKGL	85
MaPIP1-5	TEGIFLARKLSITRALFYVMVQCCLGAICGAGVVKGFQKGL	85
MaPIP2-6	TEGIFLARKVSIIRAVLYIVVQCCLGGIVGVGIVKGIKMHQ	145
MaPIP2-9	TEGIFLARKVSIVRALLYMIAQCCLGAICGAGVVKGFQKAY	61
MaPIP2-7	TEGIFLARKVSIIRALLYIVAQCCLGAIVGVGIVKGIKMHQ	144
MaPIP2-5	TEGIFLARKVSIIRALLYMIGQCCLGAICGAGVVKGFQKAF	61
MaPIP2-10	TEGIFLARKVSIIRALLYMVAQCCLGAIVGVGIVKGIKMHQ	61
MaPIP2-4	TEGIFLARKVSIVRALLYMVAQCCLGAICGAGVVKGFQKAY	61
MaPIP2-13	TEGIFLARKVSIIRAVFYVMVQCCLGAICGAGVVKGIKMHQ	61
MaPIP2-11	TEGIFLARKVSIIRAVFYVMVQCCLGAICGAGVVKGIKMHQ	61
MaPIP2-3	TEGIFLARKVSIIRAVFYVMVQCCLGAICGAGVVKGFQKAY	61
SlPIP1-1	YQRIGGGANVVAQGYTKGDGLGAEIIGTFVLVYTVFSATD	198
MaPIP1-3	YENNGGGANVVAAGYSKGDGLGAEIVGTIFILVYTVFSATD	101
MaPIP1-2	YESNGGGANVVAQGYTKGDGLGAEIVGTIFILVYTVFSATD	101
MaPIP1-9	YENNGGGANVVAQGYTKGGGLGAEIVGTIFILVYTVFSATD	101
MaPIP1-4	YQSNNGGGANVVAAGYSKGDGLGAEIVGTIFILVYTVFSATD	101
MaPIP1-7	YQSNNGGGANVVAAGYTKGDGLGAEIVGTIFILVYTVFSATD	101
MaPIP1-1	YESNGGGANVVAAGYSKGDGLGAEIVGTIFILVYTVFSATD	101
MaPIP1-8	YESNGGGANVVAAGYTKGDGLGAEIVGTIFILVYTVFSATD	101
MaPIP1-6	YENNGGGANVVAQGYTKGDGLGAEIVGTIFILVYTVFSATD	125
MaPIP1-5	YESNGGGANVVAAGYTKGDGLGAEIVGTIFILVYTVFSATD	125
MaPIP2-6	YNSIGGGANVVAIGYSKGTALGAEIIGTFVLVYTVFSATD	185
MaPIP2-9	YVRYGGGANELSDGYSKGTGLAEIIGTFVLVYTVFSATD	101
MaPIP2-7	YNSIGGGANVVAAGYSKGTALGAEIIGTFVLVYTVFSATD	184
MaPIP2-5	FVRYGGGANELSDGYSKGTGLAEIIGTFVLVYTVFSATD	101
MaPIP2-10	YNSIGGGANVVAAGYSKGTALGAEIIGTFVLVYTVFSATD	101
MaPIP2-4	FVRYGGGANELSDGYSKGTGLAEIIGTFVLVYTVFSATD	101
MaPIP2-13	FNREGGGANVVAQGYTKGTALGAEIIGTFILVYTVFSATD	101
MaPIP2-11	FNREGGGANVVAAGYSKGTALGAEIIGTFVLVYTVFSATD	101
MaPIP2-3	FVRYGGGANELSDGYSKGTGLAEIIGTFVLVYTVFSATD	101
	H5 LE1	
SlPIP1-1	PKRNARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	238
MaPIP1-3	PKRNARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP1-2	PKRNARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP1-9	PKRSARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP1-4	PKRNARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP1-7	PKRNARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP1-1	PKRNARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP1-8	PKRSARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP1-6	PKRSARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	165
MaPIP1-5	PKRNARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	165
MaPIP2-6	PKRSARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	225
MaPIP2-9	PKRNARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP2-7	PKRSARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	224
MaPIP2-5	PKRSARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP2-10	PKRSARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP2-4	PKRNARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP2-13	PKRSARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP2-11	PKRSARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141
MaPIP2-3	PKRSARDSHVEFLAPLPIGFAVFLVHLATIFITGTGINPA	141

Figure S2. Cont.



	LE2	
SlPIP1-1	R3NGEAIIFNQDQAWDDHWIFWFGNFI GAALAAIYECIII	278
MaPIP1-3	R3LGEAI IYNKDHPWDDHWIFWVGPF IGAALAAFYECIVI	181
MaPIP1-2	R3LGEAI IYNKKHAWDDHWIFWVGPF IGAALAAIYECIVI	181
MaPIP1-9	R3LGEAI VYDKSHAWNDDHWIFWVGPF IGAALAAAMYQCIVI	181
MaPIP1-4	R3LGEAI IYNKDHPWDDHWIFWVGPF IGAALAAIYECVVI	181
MaPIP1-7	R3FGEAI IYNKDHPWDDHWIFWVGPF IGAALAAIYECVVI	181
MaPIP1-1	R3LGEAI IYNKDHPWDDHWIFWVGPF IGAALAAIYECVVI	181
MaPIP1-8	R3LGEAI IYNKEHAWNDDHWIFWVGPF IGAALAAIYECVVI	181
MaPIP1-6	R3LGEAI IYNKGHAWDDHWIFWVGPF IGAALAAIYECVVI	205
MaPIP1-5	R3LGEAI IYNKDHPWDDHWIFWVGPF IGAALAAAMYECVVI	205
MaPIP2-6	R3LGEAI IYNQDKAWDDHWIFWVGPF IGAALAAAYECYIL	265
MaPIP2-9	R3FGEAI IYNKDKAWDDQWIFWVGPF IGAALAAAYECYIL	181
MaPIP2-7	R3LGEAI IYNQDKAWDDHWIFWVGPF IGAALAAAYECYIL	264
MaPIP2-5	R3FGEAI IYNKDKAWDDQWIFWVGPF IGAALAAAYECYIL	181
MaPIP2-10	R3LGEAI IYNQDKAWDDHWIFWVGPF IGAALAAAYECYIL	181
MaPIP2-4	R3LGEAI IYNQDKAWDDQWIFWVGPF IGAALAAAYECYVL	181
MaPIP2-13	R3FGEAI IYNRHKEFWDDHWIFWVGPF IGAALAEVYECYVL	181
MaPIP2-11	R3FGEAI IYNQHKFWDDHWIFWVGPF IGAALAAVYECYVL	181
MaPIP2-3	R3FGEAI IYNKDKAWDDQWIFWVGPF IGAALAAAYECYVL	181
SlPIP1-1	RAIPFKSRA.....	287
MaPIP1-3	RAIPFKSRS.....	190
MaPIP1-2	RAIPFKSRP.....	190
MaPIP1-9	RAIPFKSRP.....	190
MaPIP1-4	RAIPFKSRS.....	190
MaPIP1-7	RAIPFKNRT.....	190
MaPIP1-1	RAIPFKNRS.....	190
MaPIP1-8	RAIPFKSKR.....	190
MaPIP1-6	RAIPFKSRS.....	214
MaPIP1-5	RAIPFKSRP.....	214
MaPIP2-6	RAAAIKALGSFRSNPSN	282
MaPIP2-9	RASGAKALGSSSSI...	195
MaPIP2-7	RAAAIKALGSFRSNPTN	281
MaPIP2-5	RAGAVKALGSFRSNA..	196
MaPIP2-10	RAAAIKALGSFRSNPTN	198
MaPIP2-4	RASGAKAMGSFGSNA..	196
MaPIP2-13	RAANVKTLGSFRSSRSN	198
MaPIP2-11	RAAAIKALGSFRSSRSN	198
MaPIP2-3	RASGVKALGSFRSSA..	196

**Figure S2.** Alignment of amino acid sequences of MaPIPs. Residues comprising the ar/R filter are marked in red box and labeled as H2, H5, LE1 and LE2. Amino acids with high identities were shown in black background.

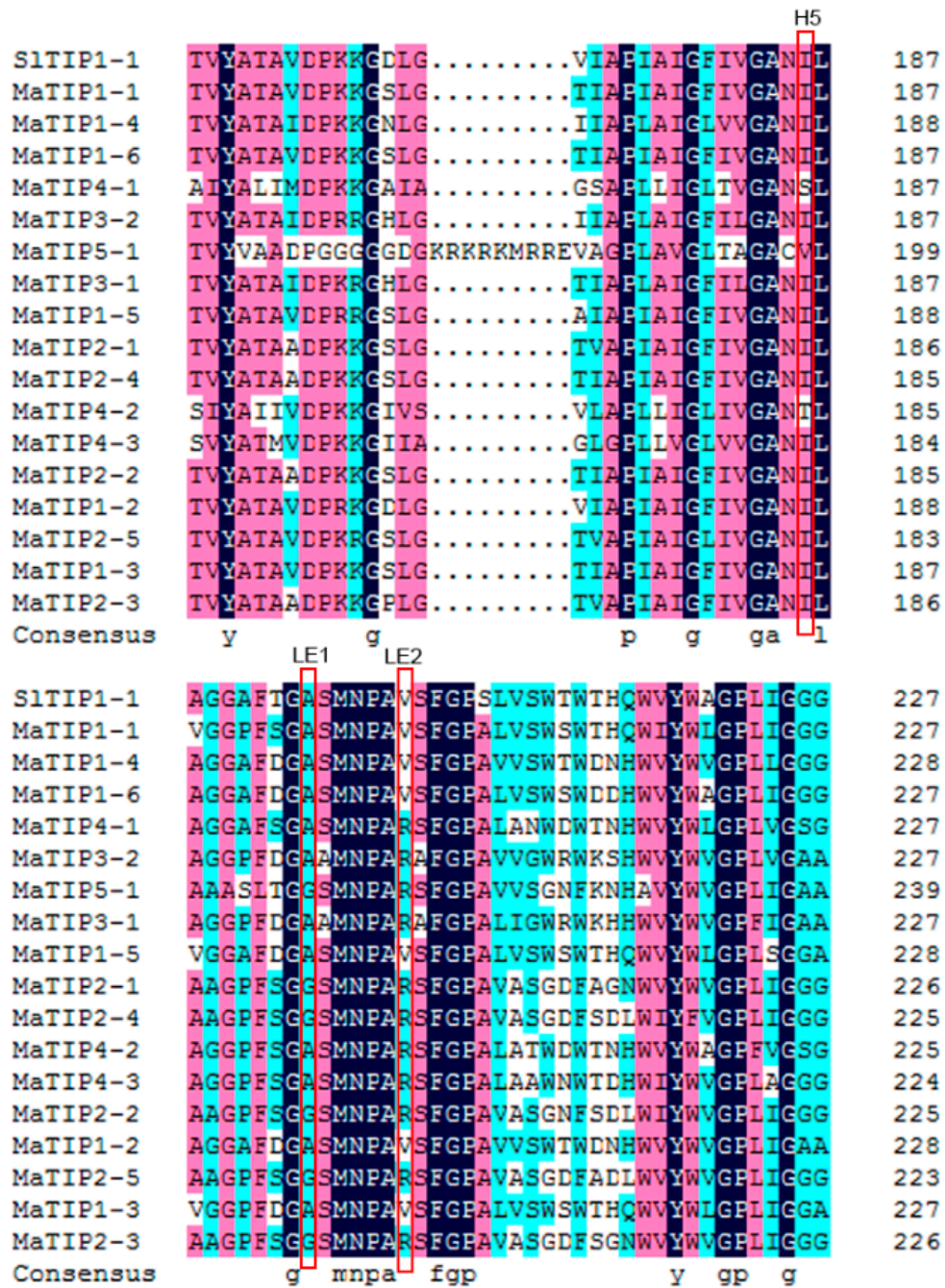
SlTIP1-1	..MFINQITIGSHEELRHPGALKAAALAEFISTLIFVFEAGQ	38
MaTIP1-1	..MPFSQIAIGRPFEATHPSALKAAALAEFICTLIFVFEAGQ	38
MaTIP1-4	..MPILRITIGTPFEARHPTALKAAALAEFISVLIFVFEAGQ	38
MaTIP1-6	..MPFPIRIAVGTQEEATHPGTLKAAALAEFISTLIFVFEAGQ	38
MaTIP4-1	...MRKITLGSRNEAVEPFDVRSVFTBLLLTFLFVFEAGV	36
MaTIP3-1	..MPRRFAFGRAEDAVHFDTMRAALSBEFIATLIFVEAAE	38
MaTIP5-1	MSSKLLCFFTSGVNFWLSAASLSYLAEFISTFFVFEAAV	40
MaTIP3-1	..MPRRFAFGRTDDAVHFDTMRAALSBEFIATLIFVEAAE	38
MaTIP1-5	..MPISRIAIGTTEEATHPSALKAAALAEFICTFIFVFEAGQ	38
MaTIP2-1	...MVKLALGSLGDSFSVSVSLKSYLAEFIATLIFVFEAGV	36
MaTIP2-4	...MAGIAFGRFDDSFVSGSLKAYLAEFISTLIFVFEAGV	36
MaTIP4-2	...MARIKLGSRKEMTDFEFARSVLTBLLLTFLFVFEAGV	36
MaTIP4-3	...MAKIALGNHHEAAEPGCIRAVLAEVVLTFLFVFEAGV	36
MaTIP2-2	...MAGIAFGQFDDSFVSGTLKAYLAEFISTLIFVFEAGV	36
MaTIP1-2	..MPISGIAIGAPGEASHFDTIKASLAEFISTLIFVEAGE	38
MaTIP2-5	...MACIAFGRCDDSFSATSLKAYLAEFISTLIFVFEAGV	36
MaTIP1-3	..MPITQIAIGTTAEATHPTALKAAALAEFICTFIFVFEAGQ	38
MaTIP2-3	...MVKITLGLGDSFSAGSLKAYLAEFIATLIFVFEAGV	36
Consensus	e fvf	
	H2	
SlTIP1-1	GSGMAFNKLT.DGVATPAGLISASIAHAFGLFVAVSVGAN	77
MaTIP1-1	GSGMAYNKLTSDGAATPAGLIAAALAHGFALFVAVSVGAN	78
MaTIP1-4	GSGMAFNKLTDDGSTTPAGLVSASLAHGFGLYVAVAVGAN	78
MaTIP1-6	GSGMAFSKLTGGAAATTPAGLIAAALAHAFALFVAVSVGAN	78
MaTIP4-1	GAVMTAEFVAGGEDRIMWVVAAPAAACQMLVAMITAVGLD	76
MaTIP3-2	GSVLSLGKLY.KDTSTAGGLVVVAIAHALALSVAVSVSIN	77
MaTIP5-1	GSAISARMLTPDVTSASSIVATALAQGFALFAAVYIAAD	80
MaTIP3-1	GSILSLGKLY.KDTSTAGGLVVVAIAHALALAVAVAIAFN	77
MaTIP1-5	GSGMAYSKMTSGGAATFTGLIMAALAHAFALFVAVSVGAN	78
MaTIP2-1	GSAIAYGKLTGGAAALDPAGLVAVALAHGLALFVGVSMAN	76
MaTIP2-4	GSAIAYNKLTSSAALDPAGLVAIAVCHGHALFVAVSVGFN	76
MaTIP4-2	AASMTAGKMAGGQDSIMGLTAV.AVAQCMVAVMVAVGLD	75
MaTIP4-3	GAAMAAEKMVGG.DSIMGLTAV.AVAHALVVAVMISAGLH	74
MaTIP2-2	GSAIAYNKLTSSAALDPAGLVAIAVCHGLALFVAVSVGAN	76
MaTIP1-2	GSGMAFNKLTNDGSTTPAGLVAASLAHGFALFVAVSVGAN	78
MaTIP2-5	GSAIAYGKLTSGAALDAAGLVAVALCHGLALFVAVAIAN	76
MaTIP1-3	GSGMAYNKLTSDGAATPEGLIAAALAHGFALFVAVSVGAN	78
MaTIP2-3	GSAIAYGKLTSGAALDPAGLVAVALAHGLALFVGVSMAN	76
Consensus		

Figure S3. Cont.



SlTIP1-1	ISGGHVNPAVTFGAFVGGNITLFRGILYIIPQLIGSTAAC	117
MaTIP1-1	ISGGHVNPAVTFGAFVGGNITLLRGILYWIPQLIGSTVAC	118
MaTIP1-4	ISGGHVNPAVTFGAFVGGNITLLRGILYWIPQLIGSVVAC	118
MaTIP1-6	ISGGHVNPAVTFGVFIGGNITLLRSIYWIPQLIGSTVAC	118
MaTIP4-1	VSAGHLNPAVTIGFAAGGYVTVVRVLYVIAQLIGSSMAC	116
MaTIP3-2	ISGGHVNPAVTLGALVGGRIISLILAVFYWVPAQLIGAVVAA	117
MaTIP5-1	ISGGHVNPAVTFGLAVAGHIGVPTAIFYWISQLIGGSILAC	120
MaTIP3-1	ISGGHVNPAVTLGALVGGRIISLVRVIFYWVPAQLIGAVVAA	117
MaTIP1-5	ISGGHVNPAVTFGAFVGGNITLLRGVLYWVPAQLIGSTAAC	118
MaTIP2-1	ISGGHLNPAVTFGLAVGGHITILTGFIFYWVPAQLIGSTVAC	116
MaTIP2-4	ISGGHVNPAVTFGLALGGQITILTGIIFYWISQLIGAVVGA	116
MaTIP4-2	VSAGHLNPAVTIGFAAGGYVTVFRVLYVIVQLIGSSMAC	115
MaTIP4-3	ISGGHLNPAVTLGLAVGGHVTVVRSLLYVPAQLIGSTLAC	114
MaTIP2-2	ISGGHVNPAVTFGLALGGQITILTGIIFYWVPAQLIGAVVGA	116
MaTIP1-2	ISGGHVNPAVTFGAFVGGNISLIRGILYWIPQLIGSVVAC	118
MaTIP2-5	ISGGHVNPAVTFGLALGGQITILTGLLYWVPAQLIGAVVGA	116
MaTIP1-3	ISGGHVNPAVTFGAFVGGNITLLRGILYWIPQLIGSTVAC	118
MaTIP2-3	ISGGHLNPAVTFGLAVGGHITLLTGVIFYWIPQLIGSTVAC	116
Consensus	s gh npavt g g y ql g	
SlTIP1-1	ALLEFATGG.MSTGSFALSAGVSVWNAFVFPIVMTFGLVY	156
MaTIP1-1	LLLRFFSTGG.LETGTFFGLS.GVSAWEALVLEPIVMTFGLVY	156
MaTIP1-4	LLLKFFATGG.LETTFPSLSSSVTVWNALVFPIVMTFGLVY	157
MaTIP1-6	LLLRYSTGG.LSTGSFALS.GVSVWEALVLEPIVMTFGLVY	156
MaTIP4-1	LLLKYYAAGLDVLFVHALAAGMDPLQGVIMPVAVTFESMVF	156
MaTIP3-2	LLLRLATGG.MRPLGFGVASGVSEGHAVLLEPIVMTFGLVY	156
MaTIP5-1	LLLRVASAG.QAIPFTTGIGTEMGTGFGGAVVPSAIFILVY	159
MaTIP3-1	LLLRLATGG.MRPVGFVSASGVSDWHAVLLEPIVMTFGLVY	156
MaTIP1-5	LLLHFATGG.LETGTFFGLSSGVGVWEALVLEPAVMTFGLVY	157
MaTIP2-1	LLLKFTVGG.LAVPTHGVAAGMSELEGVVMPIVITFALVY	155
MaTIP2-4	FLLKFFSTG.LDTPFTHGLGAGVGAGEGVVMBIITFALVY	154
MaTIP4-2	LLLQYIAGG.QAVFVHALGVGIGPLQGAIMPVMTFESMVF	154
MaTIP4-3	LLLKYLTTGG.LDTPFVHTLAAGMGAVQGVIMPVMTFESLLE	153
MaTIP2-2	FLVKFATG.LDTPFTHGLGDGVGAGEAVVMBIITFALVY	154
MaTIP1-2	LLKLATGG.LETSAFSLSSDVSVWNAVVFPIVMTFGLVY	157
MaTIP2-5	FLLKFFATG.LDTPFTHSLG.VGAVEGVVMBIITFALVY	152
MaTIP1-3	LLLRFFSTGG.LETGTFFGLT.GVSVWEALVLEPIVMTFGLVY	156
MaTIP2-3	LLLKFTVGG.MAVPTHGVAAGMSELEGVVMPIVITFALVY	155
Consensus	l e tf	

Figure S3. *Cont.*



**Figure S3. Cont.**

SlTIP1-1	LAGFIYEFIFISH....THEQIPSGDF.....	250
MaTIP1-1	LAGIVYEFFFISH....SHEQLPTTDY.....	250
MaTIP1-4	IAALVYDGVFIGFG...THEQLPTTDY.....	252
MaTIP1-6	LAGLVYEFFFISH....THEQLSSADY.....	250
MaTIP4-1	LAGFAHHHLYVAG....THGVLLPKDDEVGF..	254
MaTIP3-2	LAGLIYEFLVIPDETPTHQPLAPEDY.....	254
MaTIP5-1	IAALVHQYLVFPS....ASSDAYPNSTV.....	263
MaTIP3-1	LAGVMYEFLMIPAEAPRTHQPLAPEDY.....	254
MaTIP1-5	LAGLVYEIFFICS....THEQLASADY.....	251
MaTIP2-1	LAGLIYGDIFIGS....YQPVAAQDYP.....	249
MaTIP2-4	LAGLVYTYAYLLH....DHQPLPQ.....	245
MaTIP4-2	LAGFVYDHLVLMR....PRDDLPGDEESITKPL	254
MaTIP4-3	LAGLVYEHLFMVS....THVPLPREDEGF....	249
MaTIP2-2	LAGLVYTYAYMCS....DHQPLPQ.....	245
MaTIP1-2	IAALVYDGVFIGQA...THEQLPPSDY.....	252
MaTIP2-5	LAGLVYTYAYMCT....DHTPLPQ.....	243
MaTIP1-3	LAGIVYEIFFISH....SHEQLPTADY.....	250
MaTIP2-3	LAGLIYGDIFIGS....YEAVAAQDYP.....	249
Consensus	a	

**Figure S3.** Alignment of amino acid sequences of MaTIPs. Residues comprising the ar/R filter are marked in red box and labeled as H2, H5, LE1 and LE2. Amino acids with high identities were shown in black background.



SlNIP1-1	.....	0
MaNIP1-1	.....	0
MaNIP1-2	.....MSRAG	5
MaNIP2-1	.....MASS	4
MaNIP2-2	.....MASS	4
MaNIP2-3	.....MASH	4
MaNIP2-5	.....MASF	4
MaNIP3-2	MHQYLIQQILTKNILKPKPLAMPEPETPNVSAPATPGTPG	40
MaNIP2-4	.....MKCLKRSEIFSQPGRTQEDHTLRRSSSWRLEMASQ	35
MaNIP4-1	.....	0
Consensus		
SlNIP1-1	.....MADHQINVNGNINHGVSINIKEDHDLNNHKESSS	34
MaNIP1-1	.....MEEGAAGDGREEGVNPDHG.YASSADKG	27
MaNIP1-2	EACCSDGSEERFVEERSAADRGEERVTLDHAGGGSCSAEA	45
MaNIP2-1	HVRPNNS..NEIHDIDVVTIAQTLTTP.SFFDPPRVHRRRN	41
MaNIP2-2	.TRPNSS..NEIHDIDVVTIAQNSY.....ISPTLLHQKS	35
MaNIP2-3	GTRPTTTACNEIH..DAVTHTS.....ISPSLLHRKS	35
MaNIP2-5	.....NEIHDIDVVTIVQTLAAEDDFVPAARLRRRK	35
MaNIP3-2	APLFNSLRVDSLSYDRKSMFRCNRCPLSWASSPHTCFI	80
MaNIP2-4	.TRPNIS..NEIHDIDVVTIAQSS.....VSPRLLHHES	65
MaNIP4-1	.....	0
Consensus		
SlNIP1-1	TSSFLTVPFIQKVIAEMIGTYFLIFAGCGSVVNVNADK.GM	73
MaNIP1-1	CGLSLSIFFLQKILAEIFGTYFLIFAGCASVTVNLSK.GM	66
MaNIP1-2	CVFTFSFCFFQKIIAEILGTYFMIFAGCGSVAVNLST.GI	84
MaNIP2-1	LKELFPPFLPRKVVSEMIATFLLVFEVTCGAGALNKNNPGV	81
MaNIP2-2	LKEVFPPFLARKVVAETIATFLLVFEATCGSAALSKSNPGL	75
MaNIP2-3	LEELFPPFLAEKVVAETIATFLLVFEVTCGSAALSKSEAGA	75
MaNIP2-5	FQEIFFPPFLLRKVIAEVIATFLLVFEVTCGAGALNKNNPRV	75
MaNIP3-2	ELPKPDVSLTRKLGAEFVGTFILIFGATAAPIVNQKYNGA	120
MaNIP2-4	LRELFPFPLARKVVAEMISTFLLVFEVTCGAGALNKNSNGV	105
MaNIP4-1	.....	0
Consensus		

Figure S4. *Cont.*

		H2	
SlNIP1-1	ITFPGVAITWGLVVMVMVYSVGHISGAHFNEAVTIAFASV	113	
MaNIP1-1	ITFPGICVWGLAVMVMVYSVGHISGAHFNEAVTIAFATC	106	
MaNIP1-2	VTFFPGICLAWGLVVMAMVYSIGHVSGAHFNEAVTIAFATC	124	
MaNIP2-1	VSQLGQSVAGGLIVTVMIYAVGHISGAHMNEAVILAFAVA	121	
MaNIP2-2	VSQLGASVAGGLIVTVMIYAVGHISGAHMNEAVILAFAVA	115	
MaNIP2-3	VSQLGASVAGGLIVTVMIYAVGHISGAHMNEAVILAFAVS	115	
MaNIP2-5	VSQLGASVAGGLIVTVMIYAVGHISGAHMNEAVILAFAVS	115	
MaNIP3-2	ETLIGNAACAGLAVMIVILSTGHISGAHINESTIAFAML	160	
MaNIP2-4	VSQLGASVAGGLIVTVMIYAVGHISGAHMNEAVTFAFAVS	145	
MaNIP4-1	.....MVYSVGHISGAHFNEAVTTTETIL	24	
Consensus	gh sgah np t f		
SlNIP1-1	KRFPWKQVEPYVPAQVLGATLASGTLRLIFNGKHDHFAG.	152	
MaNIP1-1	GRFPWKQVEPYVFAQLLGATLASGTLRLMFGGKHEHFPG.	145	
MaNIP1-2	GRFPWRQVEPYVSAQVLGSTISIGTLRLLLFGGKHGQFLG.	163	
MaNIP2-1	RHFPWIQVEFYMLAQIAGSTTASYILRELLDF..IHDLG.	158	
MaNIP2-2	RHFPWIQVEFYMPAQISGAMIASFVLRELLHF..ITDLG.	152	
MaNIP2-3	RHFPWIQVEFYISAQISGAMVSSFVLRELLHF..ITDLG.	152	
MaNIP2-5	RHFPWIQVEFYWSAQFSGAMIASFILRELLHF..ITDLG.	152	
MaNIP3-2	RHFPWAHVEPYILAQVSASICASFALKAVF...HPFLSGG	197	
MaNIP2-4	RHFPWIQVEFYMCAQISGAMVASFVLRELLHF..ITNLG.	182	
MaNIP4-1	KQFPLKQLELYMVAQLVGAILASGAVYLLDFPKAEHFG.	63	
Consensus	fp p y aq g		
SlNIP1-1	.TLPSGTDQSFVIEFIITEFYLMFVISGVATDNRANGELA	191	
MaNIP1-1	.TIPAGSDVQSLVLEFIISEFYLMFVISGVATDNRANGELA	184	
MaNIP1-2	.TVEAGSDLQSLVLEFIISKILMFVISGVATDSRANGELA	202	
MaNIP2-1	TTTFSHTAAKALVAEIVVTFNMMFVTAAVATDTRANGELA	198	
MaNIP2-2	TTTFSDTAVKALVMEIVVTFCEMFVTSAVATDTRANGELA	192	
MaNIP2-3	TTTFSDTALKALVMEIVVTFCEMFVTSAVATDSKANGELA	192	
MaNIP2-5	TTTFSSTFARSLIMEVVVTFSEMFVTSAVATDTRANGELA	192	
MaNIP3-2	VTVPSSSPQAFFIEFLITENLIFVVTAVATDTRANGELA	237	
MaNIP2-4	TTTFSDTAAKALVMEIVVTFCEMFVTSAVATDTRANGELA	222	
MaNIP4-1	.TTEVGSADVQSFVLEIIISFLLMFVISGVATDTRANGELA	102	
Consensus	t p e fv vatd a gela		

Figure S4. *Cont.*

		H5	LE1	LE2	
SlNIP1-1	GLAVGATILLNVMTGFI	ISG	SMNPP	RSIGPAIVSSHYKG	231
MaNIP1-1	GLAVGATILLNVLIAGFI	ISG	SMNPP	RTILGPAIVANRWEG	224
MaNIP1-2	GLVVGATVVVNVLFAGFI	ISG	SMNPP	RSIGPAIIANRWEG	242
MaNIP2-1	GLAVGSAVCITISILAGFI	ISG	SMNPP	RTILGPALASNKFDS	238
MaNIP2-2	GLAVGSSVCITISILAGFI	ISG	SMNPP	RTILGPAVASSNYDS	232
MaNIP2-3	GLAVGSAVCITISILAGFI	ISG	SMNPP	RTILGPALASRNYDA	232
MaNIP2-5	G.PVGSAVCITISILAGFI	ISG	SMNPP	RTILGPAVASRKYDA	231
MaNIP3-2	GIPVGATVMLNILVAGFS	SG	SMNPP	RTILGPAAAGNYER	277
MaNIP2-4	GLAVGSSVCITISILAGFI	ISG	SMNPP	RTILGPAVASRNYQS	262
MaNIP4-1	GIPVGSTILLNVLVAGFI	ISG	SMNPP	RSIGPAIVMRNYKA	142
Consensus	g vg	gp sg	smnp r	gpa	
SlNIP1-1	LWYIVLSFTILGAIAGAWVYNI	IRFTDK	.....	FLR	261
MaNIP1-1	FWYIVIGPICGTVVGAWAYNI	IRFTNK	.....	FLR	254
MaNIP1-2	LWYIVIGPICGTVLGAWAYNI	IRFTDR	.....	FLR	272
MaNIP2-1	LWYIFVGFVGTIVAGALAYS	FIRLDEHSL	.....	SQK	271
MaNIP2-2	LWYIFLGFVLGTLGACSY	SFIRMTE	TETQP	.....	QAT
MaNIP2-3	LWYIFLGFVVGTLGAFSY	SFIRMTE	KQP	.....	LST
MaNIP2-5	LWYIFVGFVLGTLGTM	SYR	FIRMTEKQPPQSLPSMG	SST	271
MaNIP3-2	IWIYIVAFITAGAVTGA	AVYTAVKLKEEDGEM	.....	FRQ	311
MaNIP2-4	LWYIFVGFVLGTVSGS	SFSY	SFIRMTEKQQ	.....	HTT
MaNIP4-1	IWIYVIGFMIGTLAG	GFTYNI	VRYTDK	.....	FLR
Consensus	w y p g g y				
SlNIP1-1	EITKSG..SFLKSKNS	ST	.....		277
MaNIP1-1	EITKSG..SFLKSFRNN	ST	.....		271
MaNIP1-2	EITNIATASFLKRLTRK	DSA	.....		292
MaNIP2-1	DSQKSP.SLKMRVQSQD	MASPTNDAFESGV	.....		301
MaNIP2-2	AAQKLS.SFKLRLRLQ	SLEMASPTNNAFDNI	.....		293
MaNIP2-3	TTQKLS.SFKLRLRLQ	SQDMPSFLADASGRV	.....		293
MaNIP2-5	APKSPSTSLKLRLRLQ	SQEMASFAHVNP	.....		298
MaNIP3-2	QLLEDYPRHTRYALQ	NDSWIVASYFYLCV	KHIFLLQML		351
MaNIP2-4	AAQKLS.SFKLRLRLQ	SQEMASFTSNAFENV	.....		323
MaNIP4-1	EITKSS..SFLKSVSRNR	.....			188
Consensus					
SlNIP1-1	.....				277
MaNIP1-1	.....				271
MaNIP1-2	.....				292
MaNIP2-1	.....				301
MaNIP2-2	.....				293
MaNIP2-3	.....				293
MaNIP2-5	.....				298
MaNIP3-2	NCEYCKL				358
MaNIP2-4	.....				323
MaNIP4-1	.....				188
Consensus					

**Figure S4.** Alignment of amino acid sequences of MaNIPs. Residues comprising the ar/R filter are marked in red box and labeled as H2, H5, LE1 and LE2. Amino acids with high identities were shown in black background.



S1SIP1-1	.....MGVIAKAAIADGLLITFL	16
MaSIP1-1	.....MGAIRAAAADGLLITFL	16
MaSIP2-1	MLDQKEFVNKKETDVEEEKEHSNQASRVKLIIVSDSFLSFM	40
MaSIP2-2	.....MGRLGLVMDAAMSFM	16
Consensus	d f	
S1SIP1-1	WVFCSSNIGVSTYFIASYFGIVNEIPSLFITTLIVFVIFL	56
MaSIP1-1	WVFCVSTVRAATSLVTAALQIQGVAFSLFVITTLIFALVF	56
MaSIP2-1	WVLSG...SVIRYLIYMIILGTGMDPISVLLKGYLALVYLY	77
MaSIP2-2	WWWAG...ALVKLLVYDALGLGHRFGGEALKMAIVVGVMF	53
Consensus	wv	
	H2	
S1SIP1-1	MEDFLGDVIGGAGFNFTGNAAFYAAGLGDDSTVSAAVRCP	96
MaSIP1-1	VEGLITAAIGGASFNFTATAAFYAAGLGSDNLSMAIRFP	96
MaSIP2-1	YFSQLRKVTNGGTYNPLFVLCHAISDNFVEEFLYAVFGRIP	117
MaSIP2-2	LEAWLGHVTRGGAYNPLTVLSYAFSGGPEGFLFTALGRIP	93
Consensus	f g np l r p	
S1SIP1-1	ACVAGAVAGSLAIVELIFKHYHHMLDGEPIKVDVQTGAIA	136
MaSIP1-1	ACAPGAVAGALAIMEVMEFPQHKRMLGGFSIKVDLHTGALA	136
MaSIP2-1	ACVIGSVIGVWLINATFFAAAN...GFRINVDVSYGALI	153
MaSIP2-2	ACVIGSATGVRFIKQTFESIGH...GFRISIDIHARGAWT	129
Consensus	aq g g p gp l d ga	
	H5	
S1SIP1-1	EGVITFVITFMIFVIVLRGPEVLLKRWLLTMVTLPLVLA	176
MaSIP1-1	EGVITFIIITLAVLWIIIRGFRSPVVKIWMVAVSTVAMVVA	176
MaSIP2-1	EGLITFAIIIVSLGLNKFFRSS...HKTWISSFAKLALHVL	191
MaSIP2-2	EGFITFMIVMASIMLKKKDPGSFFMKTWISSIFKLAINVL	169
Consensus	eg t f i s k w	
	LE1 LE2	
S1SIP1-1	GSNETGFSMPNPAFAFGWAYLSNTHKTLHFYVYWISFFIG	216
MaSIP1-1	GAGYTGFAMNPAFAFGWAYINNRRHTWEQFYVYWIQFFIG	216
MaSIP2-1	ASDITGGVMNPASAFGWAYAQGKHITKEHLCVYWLAFLEA	231
MaSIP2-2	GSDITGGIMNPASAFAWAYARGDHTLDQLIVYWFAPICA	209
Consensus	tg mnpa af way h t vyw p	
S1SIP1-1	AILAAWIFRVLFPPPEVEQKPKQKQKRN...	242
MaSIP1-1	AIVAGWFFRIIFP...QRAEKAKKA...	238
MaSIP2-1	TLIVVWICSLFIKLPKRRKQHEMQRKDKL	260
MaSIP2-2	TLAVWTFGLLITE.PKSKVQKAEENKVK	237
Consensus	w	

**Figure S5.** Alignment of amino acid sequences of MaSIPs. Residues comprising the ar/R filter are marked in red box and labeled as H2, H5, LE1 and LE2. Amino acids with high identities were shown in black background.

**Table S1.** The amino acids of banana AQPs.

>MaPIP1-3

MIFALVYCTAGISGGHINPAVTFGLFLARKLSLTRAIFYMVMQCLGAICGAGVVKGFKGVYENNGGGANVVAAG  
YSKGDGLGAEIVGTFILVYTVFSATDAKRNARDSHVPILAPLPIGFAVFLVHLATIPITGTGINPARSLGAAIHYNKDHA  
WDDHWIFWVGPFIGAALAAFYHQIVIRAIPFKSRS

## &gt;MaPIP1-2

MIFALVYCTAGISGGHINPAVTFGLFLARKLSLTRALFYMVMQCLGAICGAGVVKG YQKGLYESNNGGGANVVAPG  
YTKGDGLGAEIVGTFILVYTVFSATDAKRNARDSHVPILAPLPIGFAVFLVHLATIPITGTGINPARSLGAAIYNKKH  
AWDDHWIFWVGPFIGAALAAIYHQIVIRAIPFKSRP

## &gt;MaPIP1-9

MIFILVYCTAGISGGHINPAVTFGLLLARKLSLTRALFYMVMQCLGAICGAGVVKGFKKGLYENNGGGANVVAPG  
YTKGGGLGAEIVGTFILVYTVFSATDAKRSARDSHVPVLAPLPIGFAVFLVHLATIPITGTGINPARSLGAAIVYDKSH  
AWNDDHWIFWVGPFIGAALAAAMYQQIVIRAIPFKSRP

## &gt;MaPIP2-9

MIFILVYCTAGISGGHINPAVTFGLFLARKISLVRALLYMIAQCLGAICGVGLVKGFQSAYYVRYGGGANELSDGYS  
KGTGLAAEIIGTFVLVYTVFSATDPKRNARDSHVPVLAPLPIGFAVFMVHLATIPITGTGINPARSFGAAVIYNKDKA  
WDDQWMFWVGPFIGAAVAAAYHQYILRASGAKALGSSSSI

## &gt;MaPIP1-4

MIFALVYCTAGISGGHINPAVTFGLFLARKLSLTRAIFYMVMQCLGAICGAGVVKGFKGVYQSNGGGANVVASG  
YSKGDGLGAEIVGTFILVYTVFSATDAKRNARDSHVPILAPLPIGFAVFLVHLATIPITGTGINPARSLGAAVIYNKDH  
AWDDHWIFWVGPFIGAALAAALYHQVVIRAIPFKSRS

## &gt;MaTIP1-6

MPIPRIAVGTQEEATHPGTLKAALAEFISTLIFVFAGQGSGMAFSKLTGGAATTPAGLIAAALAHAFALFVAVSVGAN  
ISGGHVNPVAVTFGVFIGGNITLLRSIIYWIAQLLGSTVACLLLRYSTGGLSTGSFALSGVSVWEALVLEIVMTFGLVY  
TVYATAVDPKKGSLGTIAPIAIGFIVGANILAGGAFDGMNPVAVSFGPALVSWSWDDHWVYWAGPLIGGGLAGLV  
YEFFFISHTHEQLSSADY

## &gt;MaPIP2-6

MSKEVSVEVEQPPAKDYSDPPPAPLLDFGEVRLWSFYRALIAEFVATLLFLYVSIATVIGHKEQNAADQCSGVGLLG  
IAWAFGGMIFILVYCTAGISGGHINPAVTFGLFLARKVSLIRAVLYIVAQCLGGIVGVGIVKGIMKHQYNSLGGANV  
VATGYSKGTALGAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAPLPIGFAVFMVHLATIPITGTGINPARSLGAAVIY  
NQDKAWDDHWIFWVGPFIGALAAAAYHQYILRAAAIKALGSFRSNPSN

## &gt;MaNIP3-2

MHQYLIQQILTKNTLKPPLAMPEPETPNVSAPATPGTPGAPLFNSLRVDSLSYDRKSMPRCNRCPLSWASSPHT  
CFIELPKPDVSLTRKLGAIEFVGTFILIFGATAAPIVNQKYNGAETLIGNAACAGLAVMIVILSTGHISGAHLNPSLTIAF  
AMLRHFPWAHVPAIYLAQVSASICASFALKAVFHPFLSGGVTVPSVSPQAFFIEFLITFNLLFVVTAATDTRAVGEL  
AGIavgatvmlnIlvAgpSSGSMNPVRTLGPAVAAGNYERIWIYLVAPTAgAVTGAAVYTAVKLKEEDGEMPRQQ  
LLEDYPRHTRYALQNDswIVASyFYLCsvKHIFLLQMLNCEYCKLR

## &gt;MaTIP4-1

MRKITLGSRNEAVEPDFVRSVFTELLLTFLFVFAGVGAVMTAEEVAGGEDRIMWVVAAPAAAQAMLVAMITAVGL  
DVSAGHLNPAVTIGFAAGGYVTVVRCVLYVIAQLLGSSMACLLKLYVAAGLDVLPVHALAAGMDPLQGVIMEAV  
FTFSMVFAIYALIMDPKKGAIGSAPLLIGLTVGANSLAGGAFSGASMNPARSFGPALANWDWTNHVVYWLGPLV  
GSGLAGFAHHHLYVAGTHGVLLPKDDEVGF

>MaPIP1-7

MIFALVYCTAGISGGHINPAVTFGLLLARKLSLNRALFYMVMQCLGAICGAGVVKGFKGLYQSNNGGGANVVAAG  
YTKGDGLGAEIVGTFILVYTVFSATDAKRNARDSHVPILAPLPIGFAVFLVHLATIPITGTGINPARSFGAAVIYNKDH  
AWDDHWIFWVGPFIGAALAALYHQVVIRAIPFKNRT

>MaTIP3-2

MPPRRFAFGRAEDAVHPDTMRAALSEFIATLFFVAAEGSVLSLGKLYKDTSTAGGLVVVAIAHALALSVAVSVSLN  
ISGGHVNPVAVTLGALVGGRISLILAVFYWVAQLLGAVVAALLRLATGGMRPLGFGVASGVSEGHAVLLEIVMTFGL  
VYTVYATAIDPRRGHLGIIAPLAIGFILGANILAGGPFDDGAAMNPARAFGPAVVGWRWKSHVVYWVGPLVGAALA  
GLIYEFLVIPDETPTHQPLAPEDY

>MaPIP2-7

MSKEVSEAEQAPAKDYRDPAPLLDFGELRLWSFYRALIAEFVATLLFLYVTIATVIGHKEQNAADQCSGVGILGIA  
WAFGGMIFILVYCTAGISGGHINPAVTFGLFLARKVSLIRALLYIVAQCLGAIVGVGIVKGIMKHQYNSLGGGANEV  
ASGYSGKTALGAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAAPLPIGFAVFMVHLATIPITGTGINPARSLGAAVIYN  
QDKPWDDHWIFWVGPFVGAALAAAYHQYILRAAAIKALGSFRSNPTN

>MaPIP2-5

MIFILVYCTAGISGGHINPAVTFGLFLARKVSLIRALLYMIGQCLGAICGVGLVKGFQKAFFVRYGGGANELSDGYS  
KGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAAPLPIGFAVFMVHLATIPITGTGINPARSFGAAVIYNKDKA  
WDDQWIFWVGPLIGAAIAAAYHQYILRAGAVKALGSFRSNA

>MaTIP5-1

MSSKLLCFFTSGVNFWSAASLRSYLAEFISTFFFVFAAVGSAISARMLTPDVTSDASSLVATALAQGFALFAAVYIA  
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VYTVYVAADPGGGGGDGKRKRKMREVAGPLAVGLTAGACVLAAASLTGGSMNPARSFGPAVVSGNFKNHAVY  
WVGPLIGAAALALVHQYLVFPSASSDAYPNSTV

>MaTIP3-1

MPPRRFAFGRTDDAVHPDTMRAALSEFIATLFFVAAEGSILSLGKLYKDTSTAGGLVVVAIAHALALAVAVIAFNI  
SGGHVNPVAVTLGALVGGRISLVRVAVFYWVAQLLGAVVAALLRLATGGMRPVGFSVASGVSDWHAVLLEIVMTFG  
LVYTVYATAIDPKRGHLGTIAPLAIGFILGANILAGGPFDDGAAMNPARAFGPALIGWRWKHHVVYWVGPFIGAAL  
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>MaPIP2-10



MIFILVYCTAGISGGHINPAVTLGLFLARKVSLIRALLYMVAQCLGAIVGVGIVKGIMKHQYNSLGGGANMVAAGY  
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WDDHWIFWVGPFVVGALAAAAYHQYILRAAAIKALGSFRSNPTN

>MaPIP1-1

MIFALVYCTAGISGGHINPAVTFGLFLARKLSLTRAVFYMMVMQCLGAVCGAGVVKGFKGVYESNNGGGANVVASG  
YSKGDGLGAEIVGTFILVYTVFSATDAKRNARDSHVPLLAPLPIGFAVFLVHLATIPITGTGINPARSLGAAIYNKDH  
AWDDHWIFWVGPFIGAALAAIYHQVVIRAIPFKNRS

>MaTIP1-5

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NISGGHVNPAVTFGAFVGGNITLLRGVLYWVAQLLGSTAACLLHFATGGLETGTGFLSSGVGVWEALVLEAVMTF  
GLVYTVYATAVDPRRGSGLAIAPIAIGFIVGANILVGGAFDGASMNPAVSFGPALVSWSWTHQWVYWLGPLSGGAL  
AGLVYEIFFICSTHEQLASADY

>MaNIP2-3

MASHGTRPTTTACNEIHDAVTTHTSISPSLLHRKSLEELFPPFLAEKVVAETIATFLLVFVTCGSAALSKSEAGAVSQL  
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DTALKALVMEIVVTFMFMFVTSAVATDSKAVGELAGLAVGSAVCITSILAGPISGGSMNPARTLGPALASRNYDAL  
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>MaSIP1-1

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RAEKAKKA

>MaSIP2-1

MLDQKEFVNKKETDVEEEKEHSNQASRVKLIVSDSFLSFMWVLSGVSIRYLIYMILGTGMDPISVLLKGYLALVYL  
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EGLITFAIIIVSLGLNKFPRSSHKTWISSFAKLALHVLASDITGGVMNPASAFGWAYAQGHILTKEHLCVYWLAPLE  
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>MaSIP2-2

MGRGLGLVMCDAAMSFMWVWAGALVKLLVYDALGLGHRPGGEALKMALVVGYMFLFAWLGHVTRGGAYNPLT  
VLSYAFSGGPEGFLFTALGRIPAQVIGSATGVRFIKQTFPSIGHGPRLSIDIHRGAWTEGFLTFMIVMASLMLKKKDP  
GSFFMKTWISSIFKLALNVLGSDLTGGIMNPASAFAWAYARGDHITLDQLIVYWFAPIQATLLAVWTFGLLTEPKSK  
VQKAEENKVKSE

>MaNIP2-4

MKCLKRSEIFSQPGRTQEDHTLRRSSSWRLEMASQTRPNISNEIHDIDVVTAAQSSVSPRLHHESLRELFPFLARKV  
VAEMISTFLLVFVTCGAGALNKSNSGVVSQLGASVAGGLIVTVMYAVGHISGAHMNPAVTFAFVSRHFPWIQVPF

YMCAQISGAMVASFVLRELLHPITNLGTTTPSDTAAKALVMETVVTFCMMFVTSAVATDTKAVGELAGLAVGSSV  
CITSILAGPVSGGSMNPARTLGPASRNYQSLWVYFVGPVLGTVSGSFSYSFIRMTEKQQHTTAAQKLSSFKLRL  
QSQEMASPTSNAFENV

>MaTIP2-4

MAGIAFGRFDDSFVSGSLKAYLAEFISTLLFVFAGVGSIAIYNKLTSSAALDPAGLVIAIVCHGFALFVAVSVGFNIS  
GGHVNPVAVTFGLALGGQITILTGILYWISQLLGAVVGAFLKFKSTGLDTPHGLGAGVGAGEGVVMEIITFALVYT  
VYATAADPKKGSGLTIPIAIGFIVGANILAAAGPFSGGSMNPARSFGPAVASGDFSDLWIYFVGPLIGGGLAGLVYTY  
AYLLHDHQPLPQ

>MaNIP1-1

MEEGAAGDGREEGVNPDHGYASSADKGCGLSLIPFLQKILAEIFGTYFLIFAGCASVTVNLSKGMITFPGICVWWG  
LAVMVMVYSVGHISGAHFNPAVTIAFATCGRFPWKQVPAYVFAQLLGATLASGTLRLMFGGKHEHFPGTIPAGSDV  
QSLVLEFIISFYLMFVISGVATDNRAIGELAGLAVGATILLNVLIAGPISGASMNPARTLGPVAVANRWEGFWVYIVGP  
ICGTVVGAWAYNLIRFTNKPLREITKSGSFLKSFRNNST

>MaTIP1-4

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ISGGHVNPVAVTFGAFLGGNITLLRGILYWIAQLLGSVVACLLKFKATGGLETPFSLSSSVTVWNALVFEIVMTFGLV  
YTVYATAIDPKKGNLGHAPLAIGLVVGANILAGGAFDGAASMNPAVSFGPAVSVSWTDNHWVYVWVGPLLGGGIAA  
LVYDGVFIGFGTHEQLPTTDY

>MaPIP1-8

MIFALVYCTAGISGGHINPAVTFGLLLARKLSLTRAIFYVVMQCLGAICGAGVVKGFQKGVYESNGGGANVVAAG  
YTKGDGLGAEIVGTFILVYTVFSATDAKRSARDSHVPVLAPLPIGFAVFLVHLATIPITGTGINPARSLGAAIYNKEH  
AWNDDHWIFWVGPLIGAALAAIYHQVVIRAIPFRSKR

>MaTIP1-1

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VYTVYATAVDPKKGSGLTIPIAIGFIVGANILVGGPFSGASMNPAVSFGPALVSWSWTHQWIYWLGPLIGGGLAGI  
VYEFFFISHSHEQLPTTDY

>MaPIP2-4

MIFILVYCTAGISGGHINPAVTLGLFLARKVSLVRALLYMVAQCLGAICGVGLVKGFQEAYFVRYGGGANELSAGY  
SKGTGLAAEIIGTFVLVYTVFAATDPKRNARDSHVPVLAPLPIGFAVFMVHLATIPITGTGINPARSLGAAVIYNQDK  
AWDDQWIFWVGPFVGAIAAAAYHQYVLRASGAKAMGSFGSNA

>MaPIP2-13

MIFVLVYCTAGISGGHINPAVTFGLFLARKVSLRAVFYMAQCMGAICGVGIVKGIMKHQFNRFGGGANVVAPG  
YSKGTALGAEIIGTFLLVYTVFAATDPKRRARDSHVPVLAPLPIGFAVFMVHLATIPITGTGINPARSFGPAVIYNRHK  
PWHDDHWIFWVGPFVGAALAEVYHQHVLRAANVKTLGSFRSSRSNC

## &gt;MaPIP2-11

MIFILVYCTAGISGGHINPAVTLGLFLARKVSLLRVVMYMAQCLGAICGVGIVKGIMKHQFNAFGGGANSVAAGY  
 SKGTAFGAESIGTFVLVYTVLSATDPKRSARDSHVPVLAPLPIGFAVFMVHLATIPITGTGINPARSFGA AVIYNQHKP  
 WHDHWIFWVGPFV GALAAVYHQYVLR AAALKALGSFRSSRSN

## &gt;MaNIP4-1

MVYSVGHISGAHFNPAVTTTFTILKQFPLKQLPLYMVAQLVGAILASGAVYLLFDPKAEHFYGTTPVGS AVQS FVLE  
 IISFLLMFVISGVATDTRAIGELAGI AVGSTILLNVLVAGPISGASMNPARSIGPAIVMRNYKAIWAYVLGPMIGTLAG  
 GFTYNLVRYTDKPLREITKSSSFLKS VSRNR

## &gt;MaTIP4-2

MARIKLGSRKEMTDPEFARSVLTELLLTFLFVFVGVAASMTAGKMAGGQDSIMGLTAVAVAQAMLVAVMVA VGLD  
 VSAGHLNPAVTIGFAAGGYVTVFRCVLYVIVQLLGSSMACLLQYIAGGQAVPVHALGVGIGPLQGAIMEVVLTF S  
 MVFSIYAIIVDPKKGIVSVLAPLLIGLIVGANTLAGGPFSGASMNPARSFGPALATWDWTNHVWVWAGPFVGSGLA  
 GFVYDHLVLMRPRDDLPGDEESITKPLC

## &gt;MaTIP2-2

MAGIAFGQFDDSFSGTLKAYLAEFISTLLFVFAGVGSIAIYNKLTSSAALDPAGLVIAIVCHGLALFVAVSVGANIS  
 GGHVNP AVTFGLALGGQITILTGIFYWVAQLLGAVVGAFVLVKFATGLDTPTHGLGDGVGAGEAVVMEIIITFALVYT  
 VYATAADPKKGS LGTIAPIAIGFIVGANILAAGPFSGGSMNPARSFGPAVASGNFSDLWIYWVGPLIGGGIAGLVYTY  
 AYMCS DHQPLPQ

## &gt;MaNIP2-1

MASSHVRPNNSNEIHDIDVVTAQTLTTPSFDPVHRRRNKELFPPFLPRKVVS EMIATFLLVFTCGAGALNKN  
 NPGVVSQLGQSVAGGLIVTVMYAVGHISGAHMNPAVTLAFAVARHFPWIQVPFYMLAQIAGSTTASYILRELLDPI  
 HDLGTTPSHTAAKALVAEIVVTFNMMFVTA AVATDTKAVGELAGLAVGSAVCITSILAGPISGGSMNPARTLGPAL  
 ASNKFD SLWVYFVGPPVGT VAGALAYSFIRLDEHSLSSQKDSQKSPSLKMRRVQSQDMASPTNDAFESGV

## &gt;MaPIP1-6

MGVVKSSTKCSTVGIQGIAWAFGGMIFALVYCTAGISGGHINPAVTFGLFLARKLSLTRALFYMVMQCLGAICGAG  
 VVKGFQKGLYENNGGGANVVAPGYTKGDGLGAEIVGT FILVYTVFSATDAKRSARDSHVPILAPLPIGFAVFLVHL  
 ATIPITGTGINPARSLGAAIYNKGHAWDDHWIFWVGPFIGAALAAALYHQVVIRAIPFKSRS

## &gt;MaTIP1-2

MPIGSIAIGAPGEASHPDTIKASLAEFISTLIFVFAGEGSGMAFNKLTNDGSTTPAGLVAA SLAHGFALFVAVSVGANI  
 SGGHVNP AVTFGAFLGGNISLIRGILYWIAQLLGSSVACLLKLATGGLETSAFSLSSDVSVWNAVVF EIVMTFGLV  
 YTVYATAVDPRKGDLGVIAPIAIGFIVGANILAGGAFDGASMNPAVSFGPAVVS WTWDNHVWVWVGPLIGAAIAAL  
 VYDGVFIGQATHEQLPPSDY

## &gt;MaTIP2-5



MACIAFGRCDSDSATSLSKAYLAEFISTLLFVFAGVGSIAIAYGKLTSGAALDAAGLVAVALCHGLALFVAVAIANIS  
GGHVNPVAVTFGLALGGQITILTGLLYWVAQLLGAVVGAFLKLFATGLDTPHSLGVGAVEGVVMEIITFALVYTVY  
ATAVDPKRGSLGTVAPIAIGLIVGANILAAGPFSGGSMNPARSFPGPAVASGDFADLVVYVWGPLIGGGLAGLVYTYA  
YMCTDHTPLPQ

>MaNIP2-2

MASSTRPNSSNEIHDIDVVTAQNSYISPTLLHQKSLKEVFPPFLARKVVAETIATFLLVFATCGSAALSKSNPGLVSQ  
GASVAGGLIVTVMIYAVGHISGAHMNPVTLAFAVARHFPWIQVPFYMAAQISGAMIASFVRELLHPITDLGTTAP  
SDTAVKALVMEIVVTFMCMFVTSAVATDTKAVGELAGLAVGSSVCITSILAGPISGGSMNPARTLGPAVASSNYDSL  
VVYFLGPVLGTLGACSYSFIRMTETQPQATAAQKLSSFKLRLQSLEMASPTNNAFDNI

>MaTIP4-3

MAKIALGNHHEAAEPGCIRAVLAEVVLTFLFVFAGVGAAMAAEKMVGGD SIMGLTAVAVAHALVVAVMISAGLHI  
SGGHLNPAVTLGLAVGGHVTVVRSLLYVVAQLLGSTLACLLKYLTTGGLDTPVHTLAAGMGAVQGVIMEIVLTFSL  
LFSVYATMVDPPKKGIAGLGPLLVLVVGANILAGGPFSGASMNPARSFPGPALAAWNWDHWIYVWGPLAGGG  
AGLVYEHLFMVSTHVPLPREDEGF

>MaPIP2-3

MIFILVYCTAGISGGHINPAVTFGLFLARKVSLVRAFLYIVAQCLGAICGVGLVKGFQKAYFVRYGGGANELSDGYS  
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WDDQWIFWVGPAIGAAIAAAYHQYVLRASGVKALGSFRSSA

>MaTIP1-3

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ISGGHVNPVAVTFGAFVGGNITLLRGILYWIAQLLGSTVACLLLRFTSTGGLETGTGFLTGVSVWEALVLEIVMTFGLV  
YTVYATAVDPKKGSLGTIPIAIGFIVGANILVGGPFDGASMNPAVSFGPALVSWSWTHQWVYWLGP LIGGALAGIV  
YEIFFISHSHEQLPTADY

>MaTIP2-3

MVKLTGSLGDSFSAGSLKAYLAEFIATLLFVFAGVGSIAIAYGKLTSGAALDPAGLVAVALAHGLALFVGVSM AANI  
SGGHLNPAVTFGLAVGGHITLLTG VFYWIAQLLGSTVACLLLKFTVTGGMAVPTHGVAAGMSELEGVVM EVVITFAL  
VYTVYATAADPPKKGPLGTVAPIAIGFIVGANILAAGPFSGGSMNPARSFPGPAVASGDFSGNWVYVWG PLIGGGLAG  
LIYGDIFIGSYEAVAAQDYP

>MaPIP1-5

MGVVKSDTKCSTVGIQGIAWAFGGMIFALVYCTAGISGGHINPAVTFGLFLARKLSLTRALFYMVMQCLGAICGAG  
VVKGFRKGLYESNGGGANVVAAGYTKGDGLGAEIVGTFILVYTVFSATDAKRNARDSHVPILAPLPIGFAVFLVHL  
ATIPITGTGINPARSLGAAYIYNKD HAWDDHWIFWVGPFIGAALAAMYHQVVIRAIPFKSRP

>MaTIP2-1

MVKLALGSLGDSFSVSLKSYLAEFIATLLFVFAGVGSIAIAYGKLTGGAALDPAGLVAVALAHGLALFVGVSM AAN  
ISGGHLNPAVTFGLAVGGHITILT GIFYWVAQLLGSTVACLLLKFTVTGGLAVPTHGVAAGMSELEGVVM EVVITFAL

VYTVYATAADPKKGS LGTVAPIAIGFIVGANILAAGPFSGGSMNPARSFGPAVASGDFAGNWVYVWGPLIGGGLAG  
LIYGDIFIGSYQPVA AQDYP

>MaNIP1-2

MSRAGEACCS DGSEERFVEERSAADRGEERVTL DHAGGGSCSAEACVFTFSFCFFQKIIAEILGTYFMIFAGCGSVA  
VNLSTGIVTFPGICLAWGLVVMAMVYSLGHVSGAHFNPAVTIAFATCGRFPWRQVPAYVSAQVLGSTISIGTLRLLF  
GGKHGQFLGTV PAGSDLQSLVLEFIISK TLMFVISGVATDSRAIGELAGLVVGATVVVNVLFAGPISGASMNPARS L  
GPAIIANRWEGLWVYIVGPICGTVLGAWAYNLIRFTDRPLLEITNTATASFLKRLTRKDSA

>MaNIP2-5

MASFNEIHDIDVVT VQTLAAEDDFVPAARLRRRKCFQEIFPPFLLRKVIAEVIATFLLVFVTCGAGALNKNNPRVVS  
QLGASVAGGLIVTVM IYAVGHISGAHMNPAVTLAFAVSRHFPWIQVPFYWSAQFSGAMIASFILRELLHPITDLGTTT  
PSSTPARSLIMEVVVTF SMMFVTSAVATDTKAVGELAGAVGSAVCITSILAGPISGGSMNPARTLGPAVASRKYDAL  
WVYFVGPVLGTL SGTMSYRFIRMTEKQPPQSLPSMGSS TAPKSPSTSLKLRRLLQSQEMASPAHVNP

**Table S2. The full length cDNAs of banana AQPs.**

>MaNIP1-1

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ATCTTCGCGGGATGTGCTTCGGTCACTGTAAATCTGAGCAAGGGAATGAT  
CACCTTTCCGGGCATCTGCGTCGTGTGGGGGCTCGCCGTCATGGTCATGG  
TGTA CTCCGTCGGCCACATATCCGGTGCCCACTTCAACCCGGCCGTCACG  
ATCGCCTTCGCCACATGCGGGAGGTTCCCATGGAAACAGGTGCCAGCTTA  
CGTTTTTGCTCAGCTTCTGGGCGCGACGCTGGCGAGCGGCACGCTGCGTT  
TGATGTTCCGGGGGAAGCACGAGCACTTCCCGGGGACGATACCGGCCGGC  
TCGGACGTGCAGTCGCTTGTTCTCGAGTTCATTATCTCGTTCTACCTGAT  
GTTTGTGATCTCGGGAGTGGCCACCGACAACAGAGCAATCGGAGAATTGG  
CGGGGTTAGCAGTCGGAGCTACAATCTTATTGAATGTGCTCATCGCCGGG  
CCTATCTCGGGAGCATCGATGAACCCGGCGAGGACGCTGGGGCCGGCGAT  
CGTGGCCAACCGGTGGGAGGGGTTCTGGGTCTACATCGTGGGTCCCATCT  
GTGGGACCGTGGTGGGGGCGTGGGCTTACAACCTCATTCGCTTCACCAAC  
AAGCCCCCTCGTGAGATCACC AAGAGCGGCTCCTTCCTCAAGAGCTTCAG  
GAACA ACTCCACCTGA

>MaPIP1-9

ATGATCTTTATCTTGGTCTACTGCACCGCTGGGATCTCAGGTGGCCACAT  
CAACCCGGCTGTGACCTTTGGGCTGCTCCTGGCCAGGAAGCTGTCCCTGA  
CCAGGGCTCTGTTCTACATGGTGATGCAGTGTCTAGGTGCCATATGCGGT  
GCGGGCGTGGTGAAAGGGTTTAAGAAGGGGCTCTATGAGAACAATGGAGG

TGGAGCGAATGTTGTGGCCCCCTGGTTACACCAAGGGTGGTGGCTTGGGTG  
CTGAGATTGTTGGCACCTTCATCCTGGTTTACACAGTCTTCTCTGCCACT  
GATGCCAAGAGGAGTGCTAGGGACTCTCATGTGCCTGTTCTTGCTCCCTT  
GCCTATTGGATTTGCAGTGTTCCTTGTTACCTGGCCACCATCCCCATCA  
CCGGCACTGGCATCAATCCTGCCAGAAGCCTTGGAGCTGCAATTGTTTAT  
GACAAGAGCCATGCATGGAATGATCATTGGATTTTCTGGGTGGACCATT  
CATTGGAGCTGCTCTTGCTGCTATGTACCAACAGATAGTTATCAGGGCAA  
TCCCATTC AAGAGCAGGCCATGA

>MaTIP2-5

ATGGCTTGCATCGCCTTCGGCCGCTGCGATGACTCCTTCAGCGCCACCTC  
GCTCAAGGCCTACCTCGCCGAGTTCATCTCCACGCTCCTCTTCGTGTTCG  
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CTCGACGCGGCGGGGCTCGTGGCGGTGGCCCTCTGTCACGGGCTCGCCCT  
CTTCGTGCGCGTCGCGATCGCCGCCAATATCTCCGGCGGCCACGTGAACC  
CGGCGGTACCTTCGGATTGGCTCTCGGGGGGCAGATCACCATCCTCACC  
GGACTCCTCTACTGGGTGCGCGAGTTGCTCGGCGCAGTCGTGCGCGGTT  
CCTCCTCAAGTTCGCTACCGGACTCGACACGCCAACCCTAGTTTGGGAG  
TGGGAGCCGTGGAGGGAGTGGTGATGGAGATCATCATCACCTTCGCACTC  
GTGTACACGGTGTACGCCACCGCCGTCGACCCAAAGAGGGGCTCCCTCGG  
CACGGTCGCCCCCATCGCCATCGGCCTTATCGTCGGAGCCAACATCCTCG  
CCGCCGGCCCCCTTCTCCGGCGGCTCCATGAACCCCGCGCGCTCCTTCGGG  
CCGGCAGTGGCGAGCGGCGACTTCGCCGACCTGTGGGTTTACTGGGTGCG  
TCCACTTATTGGTGGTGGGCTGGCTGGGCTTGTCTACACCTATGCCTACA  
TGTGCACCGACCACACTCCGCTCCCCCAGTAA

>MaTIP2-3

ATGGTGAAGCTCACATTGGGAAGCCTGGGCGACTCTTTCAGCGCGGGGTC  
TCTCAAGGCCTATCTTGCTGAGTTCATCGCCACCCTCCTCTTCGTGTTCG  
CTGGCGTTGGCTCCGCCATTGCATATGGTAAGTTGACGTCTGGTGCAGCG  
CTGGATCCGGCGGGCCTGGTTGCGGTGGCCCTCGCTCATGGCTTGGCCCT  
CTTCGTGCGCGTCTCCATGGCGGCCAACATCTCCGGTGGCCACCTTAACC  
CGGCTGTCACTTTCGGGCTCGCCGTGGGCGGCCACATCACCCTCCTCACC  
GGCGTCTTCTACTGGATCGCCCAGCTCCTCGGCTCCACCGTCGCCTGCCT  
CCTCCTCAAGTTCGTACCGGCGGCATGGCTGTACCGACGCACGGCGTGG  
CGGCCGGCATGAGTGAGCTGGAAGGCGTGGTGATGGAGGTGGTCATCACC  
TTCGCGCTCGTGTACACGGTGTACGCCACGGCGGCGGACCCGAAGAAGGG  
GCCGTTGGGGACGGTGGCGCCCATCGCGATCGGGTTCATCGTCGGGGCCA  
ACATCCTGGCAGCCGGGCCCTTCAGCGGCGGCTCCATGAACCCGGCACGG  
TCCTTCGGCCCCGCGGTGGCCAGCGGAGACTTCTCCGGCAACTGGGTCTA  
CTGGGTGGGGCCGCTGATCGGCGGCGGACTGGCCGGGCTCATCTACGGCG  
ACATCTTTATCGGCTCCTACGAGGCGGTGCGGGCGCAGGACTATCCGTAA



## &gt;MaTIP4-3

ATGGCCAAGATCGCGCTCGGGAACCACCACGAGGCGGCCGAGCCCGGCTG  
CATCCGCGCCGTGCTAGCTGAGGTGGTCCTCACCTTTCTCTTCGTCTTCG  
CTGGGGTCGGCGCCGCCATGGCCGCGGAGAAGATGGTGGGCGGGGACTCC  
ATCATGGGGCTGACGGCGGTGGCGGTGGCTCACGCGCTGGTGGTGGCGGT  
GATGATATCGGCGGGACTCCACATCTCCGGCGGCCACCTGAACCCGGCGG  
TGACGCTGGGGCTGGCCGTGGGGGGGCACGTCACCGTCGTCCGGTCGCTG  
CTGTACGTGGTGGCCCAGCTGCTGGGTTCCACCCTGGCCTGCCTTCTCCT  
CAAATACCTCACTGGTGGACTGGATACTCCGGTGCACTCTGGCTGCTG  
GGATGGGTGCCGTACAAGGAGTGATCATGGAGATAGTGCTCACCTTCTCC  
CTGCTCTTCTCCGTCTATGCCACCATGGTGGATCCGAAGAAGGGCATCAT  
CGCGGGGCTTGGGCCGCTACTGGTGGGGCTTGTGGTGGGGGCTAACATCC  
TCGCCGGCGGCCCGTTCTCGGGCGCGTCAATGAATCCGGCGAGGTCGTTC  
GGCCCGGCGTTGGCAGCCTGGAAGTGGACCGACCATTTGGATCTACTGGGT  
CGGACCGCTCGCCGGCGGTGGACTAGCTGGACTCGTCTACGAGCACCTGT  
TCATGGTCAGCACCCATGTTCTCTTCTTAGGGAGGACGAAGGCTTCTGA

## &gt;MaNIP2-3

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TGATGCGGTCACAACCTCACACCTCCATCTCTCCCTCTCTTCTCCACCGGA  
AGAGCCTCGAAGAACTCTTCCCACCCTTCCTTGCCGAGAAGGTCGTGCGG  
GAGACGATCGCCACCTTCCTGCTCGTGTTTCGTACCTGCGGGTCCGCGGC  
GTTGAGCAAGAGCGAGGCTGGCGCGGTGTCGCAGCTGGGGGCGTCGGTCG  
CCGGTGGGTTGATCGTCACGGTGATGATCTATGCCGTGGGCCACATCTCG  
GGGGCGCACATGAACCCCGCCGTACCTTGGCCTTCGCCGTCTCCCGGCA  
TTTCCCATGGATACAGGTTCCATTCTACATCTCTGCTCAGATCTCGGGGG  
CCATGGTCTCCTCCTTCGTCTCCGCGAGCTGCTGCACCCCATCACCGAT  
CTCGGTACCACGACGCCGTCCGACACAGCTCTGAAGGCCTTGGTCATGGA  
GATCGTGGTCACCTTCTGCATGATGTTTCGTACCTCGGCTGTAGCCACTG  
ATTCCAAAGCTGTAGGAGAGTTGGCAGGGTTAGCTGTTGGCTCGGCAGTC  
TGCATAACCTCCATTCTAGCTGGGCCGATCTCAGGAGGGTCGATGAACCC  
AGCGAGGACGTTAGGCCCGGCGTTGGCGAGCAGGAACCTACGATGCTCTAT  
GGGTGTATCTTCTTGGGCCTGTGGTCCGGCACATTGTTAGGGGCGTTCTCC  
TACAGCTTCATAAGGATGACTGAGAAGCAACCGCTGTCGACTACCACCCA  
GAAATTGTCCTCCTTCAAGCTTCGGCGTTTGCAGAGCCAGGACATGCCGA  
GTCCTTTAGCCGATGCTTCCGGGCGTGTTTAG

## &gt;MaTIP2-1

ATGGTGAAGCTCGCATTAGGAAGCTTGGGTGACTCCTTCAGCGTAGTGTC  
TCTCAAGTCCTATTTGGCCGAGTTCATTGCCACTCTCCTGTTCGTGTTTCG  
CTGGCGTCGGCTCCGCCATCGCTTATGGTAAGCTGACGGGTGGTGCAGCG

CTGGACCCGGCGGGCCTGGTCGCCGTGGCCCTCGCGCATGGCTTGGCCCT  
CTTCGTGCGGTGTCTCCATGGCAGCCAACATCTCCGGCGGCCACCTCAACC  
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>MaPIP2-3

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>MaNIP2-4

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>MaTIP2-4

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## &gt;MaSIP2-2

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## &gt;MaPIP2-13

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## &gt;MaTIP5-1

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>MaTIP2-2

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## &gt;MaSIP2-1

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## &gt;MaPIP1-5

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