

Figure S5 ABCDE. Amino acid sequence alignments per subfamily of the *Oeu*AQPs members from *Olea europaea* var. *sylvestris*. 5A, PIP; 5B, TIP; 5C, XIP; 5D, NIP; 5E, SIP. Legends are detailed at the end of each subfamily alignment.

		10	20	30	40	50	60	70	80	90	100	110	
				*									
AtPIP1;1		-----	MEGKEEDVRVGANKFPERQPIG	----	TSAQS-DKDYK	KEPPAPFF	EPGELSSWSFWRAGI	AEFIATFLFLYITVLTVMGVK	RSPN-----	MCASVGIQGI			
SlPIP1;1		-----	MAENKEEDVNLGANKFREPQPIG	----	TSAQT-DKDYK	KEPPAPPLY	EPGELSSWSFYRAGI	AEFMATFLFLYITILTVMGLK	RSDS-----	LCSSVGIQGV			
OeuPIP1;1a	Oeu0388001	-----	MESKEEDVRVGANKFAERQPIG	----	TAAQSQDKDYK	KEPPAPLFE	EPGELSSWSFYRAGI	AEFIATFLFLYITVLTVMGVSK	SDS-----	KCKTVGIQGI			
OeuPIP1;1b	Oeu0388011	-----	MESKEEDVRVGANKFAERQPIG	----	TAAQSQDKDYK	KEPPAPLFE	EPGELSSWSFYRAGI	AEFIATFLFLYITVLTVMGVSK	SDS-----	KCKTVGIQGI			
OeuPIP1;1c	Oeu0388022	-----	MESKEEDVRVGANKFAERQPIG	----	TAAQSQDKDYK	KEPPAPLFE	EPGELSSWSFYRAGI	AEFIATFLFLYITVLTVMGVSK	SDS-----	KCKTVGIQGI			
OeuPIP1;2	Oeu0181331	-----	MESKEEDVRVGANKFNERQPIG	----	TAAQSQDKDYK	KEPPAPLFE	EPGELSSWSFYRAGI	AEFIATFLFLYITILTVMGVSK	SDS-----	KCSTVGIQGI			
OeuPIP1;4	Oeu0529541	-----	MESKEEDVRLGANKFTERQPIG	----	TSAQS--	KDYK	KEPPAPLFE	EPGELSSWSFYRAGI	AEFIATFLFLYITILTVMGVSR	SGS-----	KCASVGIQGI		
OeuPIP1;6	Oeu0463501	-----	MEGKEEDVRLGANKFTERQPIG	----	TSAQS--	KDYK	KEPPAPLFE	EPGELQSWFWRAGI	AEFMATFLFLYITILTVMGVSR	SNS-----	KCTSVGIQGI		
OeuPIP1;3	Oeu0423291	-----	MAESKEEDVKLGANKFTEKQPIG	----	TAAQT-DKDYK	KEPPAPLFE	EPGELTSSWSFYRAGI	AEFIATFLFLYISILTVMGVF	SAKN-----	KCASVGVQGI			
OeuPIP1;5	Oeu0613842	-----	MAENREEDVRLGANKFTEKQPIG	----	TAAQT-DKDYK	KEPPAPLFE	EPGEIKSWSFYRAGI	AEFVATFLFLYITILTVMGVGR	SNS-----	KCASVGIQGI			
AtPIP2;1		-----	MAKDV	---	AVPGE	EGFTKDYQ	DDPPAPFDG	AELTKWSFYRAVIAEF	VATLLFLYITVLTVIGYKIQ	SDTDAG--	GVD	CGGVILGI	
SlPIP2;1		MVRHEWLK	ESTRAKKQRQPKKKTETQ	KWAKI	WRLVLNMQKTYQ	DDPPAPLID	PEELGKWSFYRAI	IAEFVATLLFLYITVLTVIGYK	QSST----	DQ	CGGVILGI		
OeuPIP2;1	Oeu0012711	-----	MTKDV	---	SHVEPA	EEYS	AKDYH	DDPPAPLID	FEELSSWSFYRALIAEF	VATLLFLYITVLTVIGYK	QIDPAHG--	GDD	CGGVILGI
OeuPIP2;2	Oeu0301831	-----	MTKDV	---	SHGEP	AE-FA	KDYH	DDPPAPLID	FEELSSWSFYRALIAEF	VATLLFLYITVLTVIGYK	QIDPAHG--	GDD	CGGVILGI
OeuPIP2;3	Oeu0338421	-----	MVKDGG	---	VAEHGS	FTVKDYH	DDPPAPLID	AAELTKWSFYRAI	IAEFVATLLFLYITVLTVIGYK	QTD	TNAGHGGDQ	CGGVILGI	
OeuPIP2;4	Oeu0304391	-----	MAKDAG	---	VAEHGS	FAAKDYQ	DDPPAPLID	AAELTKWSFYRAVIAEF	VATLLFLYITVLTVIGYK	QID	TTVGHGGDQ	CGGVILGI	
OeuPIP2;6	Oeu0172571	-----	MTKDAG	---	VAEHGS	FTTKDYH	DDPPAPLID	AAELTKWSFYRAI	IAEFVATLLFLYITVLTVIGYK	QTD	PDLK--	GDD	CGGVILGI
OeuPIP2;11	Oeu017254	-----	MKDVG	---	VANHS	FMAKDYH	DDPPAPLID	TEELTKWSFYRALIAEF	VATLLFLYITVLTVIGYK	SHL	DTLK--	GDD	CGGVILGI
OeuPIP2;5	Oeu0279871	-----	MDIE	---	VGA-EY	TTKDYQ	DDPPAPLID	PEELTKWSFYRALIAEF	VATLLFLYITVLTVIGYK	SESAA--	DK	CGGVILGI	
OeuPIP2;7	Oeu0181111	-----	MVDV	---	VGGP	EFITKDYQ	DDPPAPLID	PEELTKWSFYRAI	IAEFVATLLFLYITVLTVIGYK	QSAT--	DE	CGGVILGI	
OeuPIP2;8	Oeu0232321	-----	MSKEVT	---	EEGQV	HPHGKDY	EDPPAPLLD	MGELMLWSFYRAI	IAEFVATLLFLYITVATVIGH	KKLNAA--	DQ	CGGVILGI	
OeuPIP2;9	Oeu0201061	-----	MTKEVS	---	EEGQV	HHHGKDY	VDDPPAPLLD	MGELKLWSFYRALIAEF	VATLLFLYITVATVIGH	KKLNAA--	DQ	CGGVILGI	
OeuPIP2;10	Oeu022438	-----	MENHV	GVA	KDYR	DPLPAPLID	GLMELTKWSFYRAVIAEF	VATLLFLYITVLTVIGYK	QNDTH--	CG	GGVILGI		
						*							

		120	130	140	150	160	170	180	190	200	210	220
AtPIP1;1					AWAFGGMIF	ALVYCTAGISGGHINPAVTFGLFLA	KFL	LT	ALFYIV	MQCLGAICGAGVVKGF	PKQYQALGGGANVVAHGYTKG	SGLGAEIIGTFVLVYTVFSATDAKR
SlPIP1;1					AWAFGGMIF	ALVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYVMV	MQCLGAICGAGVVKGF	MQGPYQRLGGGANVVPQGYTKGD	LGAEIIGTFVLVYTVFSATDAKR
OeuPIP1;1a	Oeu0388001				AWAFGGMIF	ALVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYVMV	MQCLGAICGAGVVKGF	PKTLMTKGGGANVVAHGYTKGD	LGAEIIGTFVLVYTVFSATDAKR
OeuPIP1;1b	Oeu0388011				AWAFGGMIF	ALVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYVMV	MQCLGAICGAGVVKGF	PKTLMTKGGGANVVAHGYTKGD	LGAEIIGTFVLVYTVFSATDAKR
OeuPIP1;1c	Oeu0388022				AWAFGGMIF	ALVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYVMV	MQCLGAICGAGVVKGF	PKTLMTKGGGANVVAHGYTKGD	LGAEIIGTFVLVYTVFSATDAKR
OeuPIP1;2	Oeu0181331				AWAFGGMIF	ALVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYVMV	MQCLGAICGAGVVKGF	PKTLMTKGGGANVVAHGYTKGD	LGAEIIGTFVLVYTVFSATDAKR
OeuPIP1;4	Oeu0529541				AWAFGGMIF	ALVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	PSFYKANGGGANVVAHGYTKGD	LGAEIIGTFVLVYTVFSATDAKR
OeuPIP1;6	Oeu0463501				AWAFGGMIF	ALVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	PSFYKANGGGANVVAHGYTKGD	LGAEIIGTFVLVYTVFSATDAKR
OeuPIP1;3	Oeu0423291				AWAFGGMIF	ALVYCTAGISGGHINPAVTFGLFLA	KFL	LT	ALFYVMV	MQCLGAICGAGVVKGF	FMKGQYERLQGGANIVQHGYTKGD	ALGAEIIGTFVLVYTVFSATDAKR
OeuPIP1;5	Oeu0613842				AWAFGGMIF	ALVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	MEGPYQRLQGGANVVAHGYTKGD	LGAEIIGTFVLVYTVFSATDAKR
AtPIP2;1					AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QSSYTRYGGGANSLADGYSTGT	GLAEIIGTFVLVYTVFSATDAKR
SlPIP2;1					AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKAYYVKYGGGANLNDGYSTGT	GLAEIIGTFVLVYTVFAATDPKR
OeuPIP2;1	Oeu0012711				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKSYHYKYGGANLAPGYNKG	VLGAEIIGTFVLVYTVFSATDPKR
OeuPIP2;2	Oeu0301831				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKSYHYKYGGANLAPGYNKG	VLGAEIIGTFVLVYTVFSATDPKR
OeuPIP2;3	Oeu0338421				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKSYHYKYGGANLADGYSTG	VGLSAEIIGTFVLVYTVFSATDPKR
OeuPIP2;4	Oeu0304391				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKSHYKYGGANLADGYSTG	VGLSAEIIGTFVLVYTVFSATDPKR
OeuPIP2;6	Oeu0172571				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKSYHYKYGGANLADGYSTG	VGLSAEIIGTFVLVYTVFSATDPKR
OeuPIP2;11	Oeu017254				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKSYHYKYGGSNELAEGYSTSV	GLS--IGTFVLVYTVFSATDPKR
OeuPIP2;5	Oeu0279871				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKSYHYKYGGANLADGYSTG	TGLAEIIGTFVLVYTVFSATDPKR
OeuPIP2;7	Oeu0181111				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QRAYYVRYGGGANLADGYSTG	TGLAEIIGTFVLVYTVFSATDPKR
OeuPIP2;8	Oeu0232321				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKSYHYKYGGANLADGYSTG	TGLAEIIGTFVLVYTVFSATDPKR
OeuPIP2;9	Oeu0201061				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKSYHYKYGGANLADGYSTG	TGLAEIIGTFVLVYTVFSATDPKR
OeuPIP2;10	Oeu022438				AWAFGGMIF	ILVYCTAGISGGHINPAVTFGLFLA	KFL	LT	AVFYIV	MQCLGAICGAGVVKGF	QKSHYKYGGSNELSDGYSTG	GLAEIIGTFVLVYTVFSATDAKR

---TM2---
 -NPA;LB-
-----TM3-----
-----TM4-----

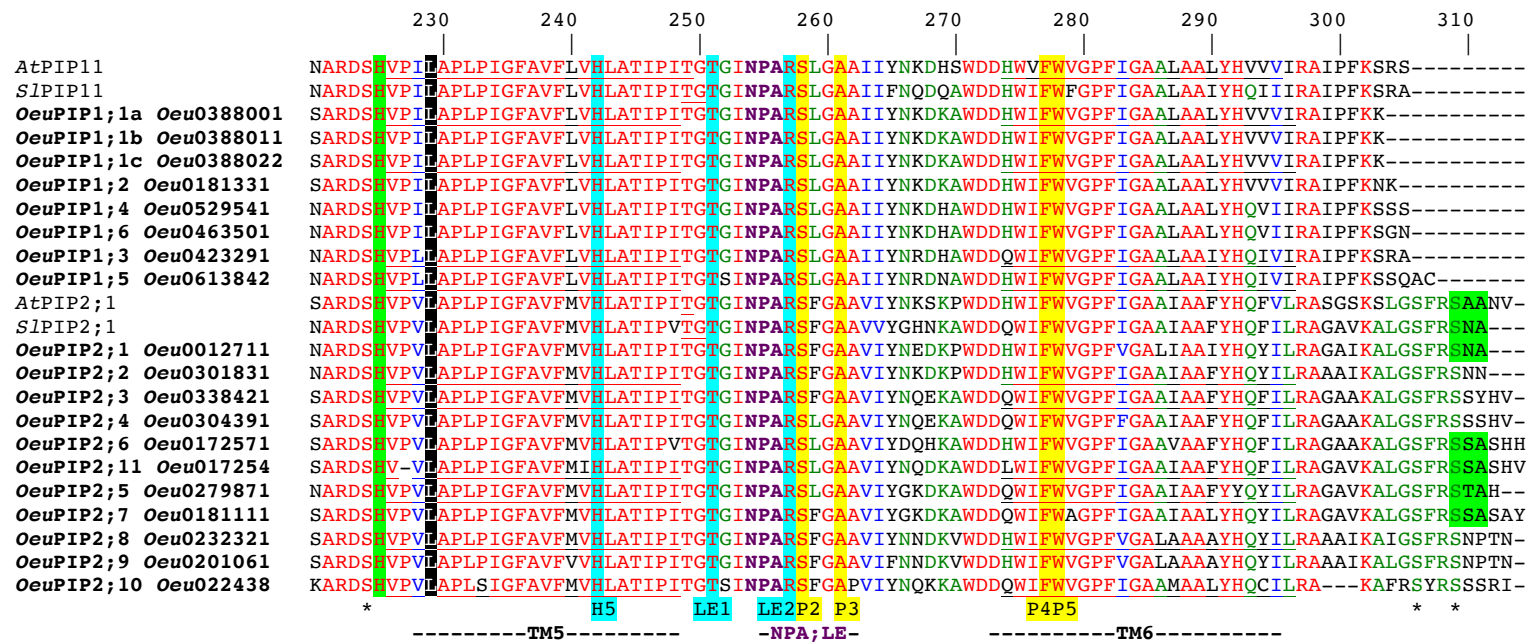


Figure S5A. Amino acid sequence alignment of the *OeuPIPs* subfamily members from *Olea europaea* var. *sylvestris*. *SlPIP1*;1 and *SlPIP2*;1 (Soly10g054840.1; Reuscher et al., 2013) from Tomato and *AtPIP1*;1 (At3g61430) and *AtPIP2*;1 (At3g53420) (Muries et al., 2011) from *Arabidopsis thaliana* were used as references. The highest residue similarities between MIP members are shown in red (100%), and green (>80%). Residues with similar physicochemical behaviors are shown in blue. The six transmembrane domains (TMH1-6) and the two hemi-helicoidal regions that include the «NPA» motives «NPA1» (in Loop B) and «NPA2» (in Loop E) (framed in purple) are underlined. The amino acids residues constituting the ar/R constriction region are shown with blue highlights and labeled H2, H5, LE1 and LE2, and residues constituting the Froger's positions are shown with yellow highlights and labeled P1 to P5. In addition, AEF motif, the His residue involved in gating, the RKxSxxR motif, the SxA motif for putative phosphorylation by PKC are marked in green, the KdvE motif for putative conserved methylation sites are marked in red, and the putative conserved blocking residue (L) is marked in black. Lastly, the Cysteines (C) involved in the tetramerization of PIPs are mentioned in purple. Columns or regions with conserved putative phosphorylation sites are marked with an asterisk.

		10	20	30	40	50	60	70	80	90
AtTIP1;2		-----	MPTRNIAIGGVQE	EVYHPNALRAALAEFISTLI	FVFAGSGSGIAFNKITDNGATT	PSGLVAAALAHAFGLFVAVSVGANISGG				
SlTIP1;1		-----	MPINQITIGS-HEELRHPGALKAAALAEFISTLI	FVFAGQSGMAFNKLT	DGVAT-PAGLISASIAHAFGLFVAVSVGANISGG					
OeuTIP1;3	Oeu0354791		MSSEFFNVPLRRVAFGH-RDEFRQPGA	KAALAEFFSTLI	FVFAGEGSGMAYNKLTGNAPTSP	PSGLVAAAVAHGFALFVAVSVGANISGG				
OeuTIP1;1	Oeu0585311		-----	MPISRVAIGS-PAEFSQLDAIKAAVAEFISMLI	FVFAGQSGMAFAKLT	DNESTTPAGLIAASIAHAFALFVAVSVGANISGG				
OeuTIP1;4	Oeu0402901		-----	MPISRIVAGS-LAEASQPEALKATLAEFISMLI	FVFAGEGSGMAFAKLT	TNNGSTTPTGLIAEAIHAFALFVAVSVGANISGG				
OeuTIP1;5	Oeu0402891		-----	MPISRIVAGS-LAEASQPEALKATLAEFISMLI	FVFAGEGSGMAFAKLT	TNNGSTTPTGLIAEAIHAFALFVAVSVGANISGG				
OeuTIP1;2	Oeu0410141		-----	MPFSRISVGS-PAEASHPDTLKAAALAEFISMLI	FVFAGEGSGMAFAKLT	DGGSSTPAGLIAAAIAHAFALFVAVSVGANISGG				
OeuTIP1;6	Oeu0332441		-----	MPIYRIAIGT-PGEASHPDALKAAALAEFFSMLI	FVFAGQSGMAFNKLSNDGSPNPSGLLAAALAHAFALFVAVSVGANISGG					
OeuTIP1;7	Oeu0452371			MYSNSM-RSGNQIAVGR-LEEATQQDALKAAALAEFISTLI	FVFAGSGSGMAFNKLT	DDGATTAGLIAAAVAHAFALFVAVSVGANISGG				
OeuTIP2;1	Oeu0240741		-----	MPAIAVGR-LDDSF SIGSLKAYVAEFISTLL	FVFAGVGSIAIAYNKLTADAALDPAGLVAVAICHGFALFVAVSIGANISGG					
OeuTIP2;2	Oeu0240761		-----	MPAIAVGR-LDDSF SIGSLKAYVAEFISTLL	FVFAGVGSIAIAYNKLTADAALDPAGLVAVAICHGFALFVAVSIGANISGG					
OeuTIP2;3	Oeu0539881		-----	MPTIAFGR-IDDSLSVGS	LKAYLAEFISTLLFVFAGVGSIAIAYNKLT	YDAALDPAGLVAVAVCHGFALFVAVSIGANISGG				
OeuTIP2;4	Oeu0023291		-----	MVKMTLGS-IGDSFSVPSLKAYLAEFIATLL	FVFAGVGSIAIAYNKLTSDAALDPPGLVAVAVAHAFALFVGVSMANVSGG					
OeuTIP2;5	Oeu0402071		-----	MVKINWGS-IGDSFSVPSLKAYIAEFIATLL	FVFAGVGSIAIAYNKLTSDAALDPPGLVAVAVAHAFALFVGVSMANVSGG					
OeuTIP3;1	Oeu0383871		-----	MPRGYTFGRAEATHPDSARATLAEFLSMLV	FVFAGEGSLVALDKMYKDTALGASSLVVIALAHALS	LFAAVASSMNVSGG				
OeuTIP4;1	Oeu0302291		-----	MAKIALGN-AREAFQSDCIQALIVEFICTFL	FVFAGVGAAMATDKLNGDPLV--GLFFVMAHALVAVMISAGFRVSGG					
AtTIP5;1			-----	MRRMIPTSFSSKFQGVLSMNALRCYVSEFISTFF	FVLAAGVSMSSRKLMAGDVSGPFGLVIPAIALNALALSSSVYISWNVSGG					
SlTIP5;1			-----	MASLASRLQHSVTPNALRSYLAEFISTFF	FVFAAGASMSTRKMVPDATSDPSSLVAIAVANAFALSVAVYISANISGG					
OeuTIP5;1	Oeu0217081		-----	MASLKSRLHETVTPNALRSYLAEFISTFF	FVFASVGATMSTLKMMPDAASNSSGLVAIAVANAFALSVAVYIAYNISGG					
OeuTIP5;2	Oeu0217091		-----	MASLKSRLHETVTPNALRSYLAEFISTFF	FVFASVGATMSTLKMMPDAASNSSGLVAIAVANAFALSVAVYIAYNISGG					
OeuTIP5;3	Oeu0224791		-----	MASLKSRLHESVTAIALRSYLAEFISTFF	FVFAAGATMSSRKMPDAASDSSSLVAIAVANAFALSVTVYISANISGG					

H2

		100	110	120	130	140	150	160	170	180
					-----TM1-----				-----TM2-----	
AtTIP1;2		HVNPAVTFG	VLLGGNITLLRGILY	WIAQLLGSVAACFLLSFAT	GGPEIPAFGLSAGVGS	LNALVFEIVMTFGLVYTVYATAVDPKNGSLG				
SlTIP1;1		HVNPAVTFG	AFVGGNITLFRGILY	IIAQLLGSTAAACLLLEFAT	GGMSTGSFALSAGVSVWNAFVFEIVMTFGLVYTVYATAVDPKKGDLG					
OeuTIP1;3	Oeu0354791	HVNPAVTFG	LFLGGNVSLFRGILY	IIAQLLGSVVACLLLFST	GGLETSAFALTAGVSVWNAFVFEIVMTFGLVYTVYATAVDPKKGEIG					
OeuTIP1;1	Oeu0585311	HVNPAVTLG	AFVGGHITLFRS	IMYWIAQLLGSVIACLLLK	FATGGLETSAFALSSGVTWNAVIFEIVMTFGLVYTVYATAVDPKKGNLG					
OeuTIP1;4	Oeu0402901	HVNPAVTFG	AFVGGHITLIRS	ILYWIAQLLGSVVACLLLR	LATGGLETSAFALSSGVTWNAVFEIVMTFGLVYTVYATAVDPKRGNLG					
OeuTIP1;5	Oeu0402891	HVNPAVTFG	AFVGGHITLIRS	ILYWIAQLLGSVVACLLLR	LATGGLETSAFALSSGVTWNAVFEIVMTFGLVYTVYATAVDPKRGNLG					
OeuTIP1;2	Oeu0410141	HVNPAVTFG	AFVGGHLSL	FKTILYWIAQLLGAIVACLLLK	FSTGGLETSAFALSTGVSSWNAVFEIVMTFGLVYTVYATAVDPKRGDIG					
OeuTIP1;6	Oeu0332441	HVNPAVTFG	AFVGGNITLLRS	ILYWIAQLLGSVVACILLK	FATGGLETSAFALSSGVTWNAVFEIVMTFGLVYTVYATAVDPKKGNLG					
OeuTIP1;7	Oeu0452371	HVNPAVTFG	AFVGGNISLIRG	ILYWIAQLLGSVVACLLLK	FATGGLTAAAFSLSAGVNVWNAFVLEIVMTFGLVYTVYATAVDPKRGSLG					
OeuTIP2;1	Oeu0240741	HVNPAVTFG	LAVGGQITLLTGL	FYWIAQLLGSI	VACYLLVFVTGGGLAIPIHGVGAGVGA	FEIVITFALVYTVYATAADPKKGS				
OeuTIP2;2	Oeu0240761	HVNPAVTFG	LAVGGQITLLTGL	FYWIAQLLGSI	VACYLLVFVTGGGLAIPIHGVGAGVGA	FEIVITFALVYTVYATAADPKKGS				
OeuTIP2;3	Oeu0539881	HVNPAVTFG	LAVGGQITILTGL	FYWIAQLLGSI	VACFLKFTVGGGLAIPHSMAGVGAIEGV	MEIVITFALVYTVYATAVDPKKGS				
OeuTIP2;4	Oeu0023291	HLNPAVTFG	LAI	GGNITITGIFYWIAQLLGSTVACLLLK	FVTNGLAIPHTHAVASGMNAVEGV	MEIVITFALVYTVYATAADPKKGS				
OeuTIP2;5	Oeu0402071	HLNPAVTFG	LAI	GGNITITGIFYWIAQLLGSI	VACLLKFTVGGGLAIPHTHAVASGMNAVEGV	MEIVITFALVYTVYATAADPKKGS				
OeuTIP3;1	Oeu0383871	HVNPAVTFG	ALVGG	RVSVLRAIYYWIAQLLGAVLAAI	LLRLATDGLRPRGFSVADGVGEWNALVMEIVLTFGLVYTVYATAIDPKRGSLG					
OeuTIP4;1	Oeu0302291	HINPAVTLG	LLAGGHITV	VSILYWIDQLLASTAACALLKYL	TGGGLTIPVHTLATGVDFAQGVIMEIVLTFSLFTVYATIVDPKGFLE					
AtTIP5;1		HVNPAVTF	AMAVAGRISVPTAMF	YWTSQMIASVMACLV	LKVTVMQHVPIYKIAGEMTGFGASVLEGV	LAFVLVYTVFT-ASDPRRGLPL				
SlTIP5;1		HVNPAVTF	GMAVGGHISIPMSIF	YWISQMGISVTCACLLKFTN--QQVPTHGIPQEMTGFGAAVLEGV	MTFGLVYTVYA-AADPRRCVHA					
OeuTIP5;1	Oeu0217081	HVNPAVTF	GMAIGGHISIPMAIF	YWISQTLGSI	VACILKVTTVGQHVPTHSIPQEMTGFGAAILEGV	MTFGLVYTVYA-AADPRRGMS				
OeuTIP5;2	Oeu0217091	HVNPAVTF	GMAIGGHISIPMAIF	YWISQTLGSI	VACILKVTTVGQHVPTHSIPQEMTGFGAAILEGV	MTFGLVYTVYA-AADPRRGMS				
OeuTIP5;3	Oeu0224791	HVNPAVTF	GMMVGGHISIPMAIF	YYSISQTFGSVMACLLKAT	TAGQHVPTHAIEHMTGFGGAVLEGV	MTFGLVYTVYA-ASNLRPV				

P1

-NPA;LB--

-----TM3-----

-----TM4-----

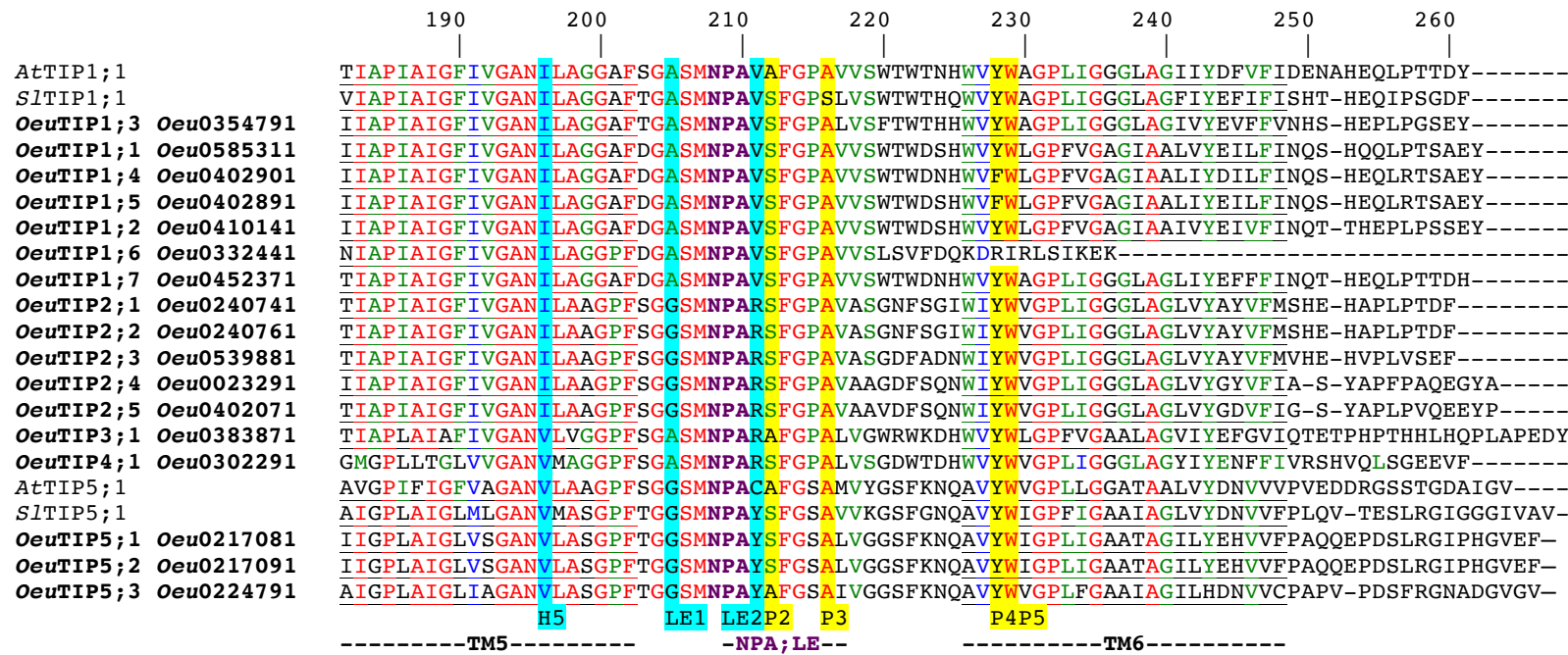


Figure S5B. Amino acid sequence alignment of the *OeuTIPs* subfamily members from *Olea europaea* var. *sylvestris*. *SlTIP1;1* (Solyc06g074820.1) and *SlTIP5;1* (Solyc03g093230.1) (Reuscher et al., 2013) from Tomato and *AtTIP1;1* (At2g36830) and *AtTIP5;1* (At3g47440) from *Arabidopsis thaliana* were used as references. The highest residue similarities between MIP members are shown in red (100%), and green (>80%). Residues with similar physicochemical behaviors are shown in blue. The six transmembrane domains (TMH1-6) and the two hemi-helicoidal regions that include the «NPA» motives «NPA1» (in Loop B) and «NPA2» (in Loop E) (framed in purple) are underlined. The amino acids residues constituting the ar/R constriction region are shown with blue highlights and labeled H2, H5, LE1 and LE2, and residues constituting the Froger's positions are shown with yellow highlights and labeled P1 to P5.

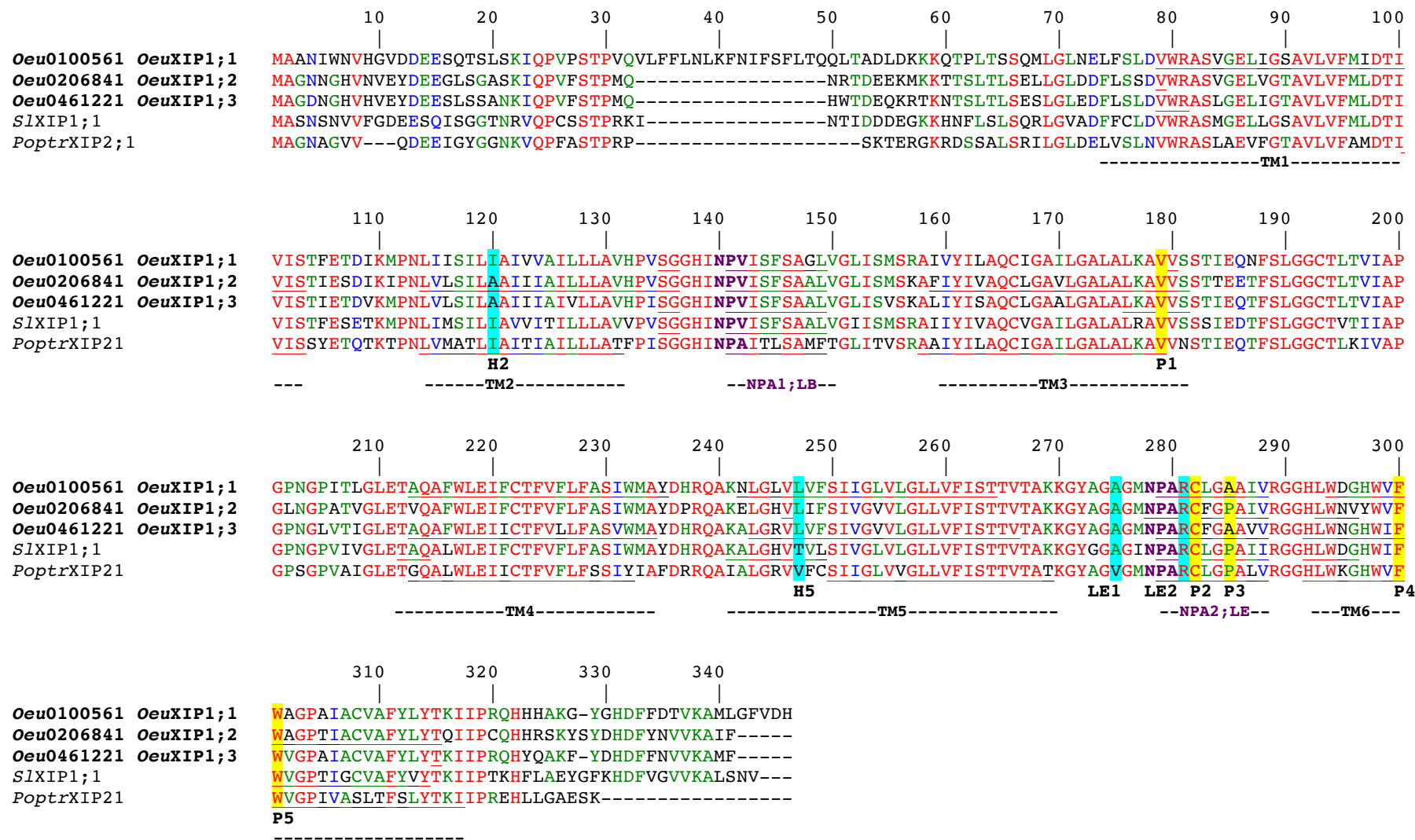


Figure S5C. Amino acid sequence alignment of the *OeuXIPs* subfamily members from *Olea europaea* var. *sylvestris*. *SlXIP1;1* (Solyc10g054840.1; Reuscher et al., 2013) from Tomato and *PoptrXIP2;1* (Potri.009G128500.1; Lopez et al, 2016) from Poplar were used as references. The highest residue similarities between MIP members are shown in red (100%), and green (>80%). Residues with similar physicochemical behaviors are shown in blue. The six transmembrane domains (TMH1-6) and the two hemi-helicoidal regions that include the «NPA» motives «NPA1» (in Loop B) and «NPA2» (in Loop E) (framed in purple) are underlined. The amino acids residues constituting the ar/R constriction region are shown with blue highlights and labeled H2, H5, LE1 and LE2, and residues constituting the Froger's positions are shown with yellow highlights and labeled P1 to P5.

		10	20	30	40	50	60	70	80	90
AtTIP1;2		-----	MPTRNIAIGGVQE	EVYHPNALRAALAEFISTLI	FVFAGSGSGIAFNKITDNGATT	PSGLVAAALAHAFGLFVAVSVGANISGG				
SlTIP1;1		-----	MPINQITIGS-HEELRHPGALKAAALAEFISTLI	FVFAGQSGMAFNKLT	DGVAT-PAGLISASIAHAFGLFVAVSVGANISGG					
OeuTIP1;3	Oeu0354791		MSSEFFNVPLRRVAFGH-RDEFRQPGA	IKAAALAEFFSTLI	FVFAGEGSGMAYNKLTGNAPTSP	PSGLVAAAVAHGFALFVAVSVGANISGG				
OeuTIP1;1	Oeu0585311		-----	MPISRVAIGS-PAEFSQLDAIKAAVAEFISMLI	FVFAGQSGMAFAKLTDNESTTPAGLIAASIAHAFALFVAVSVGANISGG					
OeuTIP1;4	Oeu0402901		-----	MPISRIVAGS-LAEASQPEALKATLAEFISMLI	FVFAGEGSGMAFAKLTTNGSTTPTGLIAEAIHAFALFVAVSVGANISGG					
OeuTIP1;5	Oeu0402891		-----	MPISRIVAGS-LAEASQPEALKATLAEFISMLI	FVFAGEGSGMAFAKLTTNGSTTPTGLIAEAIHAFALFVAVSVGANISGG					
OeuTIP1;2	Oeu0410141		-----	MPFSRISVGS-PAEASHPDTLKAAALAEFISMLI	FVFAGEGSGMAFAKLTDGGSSTPAGLIAAAIAHAFALFVAVSVGANISGG					
OeuTIP1;6	Oeu0332441		-----	MPIYRIAIGT-PGEASHPDALKAAALAEFFSMLI	FVFAGQSGMAFNKLSNDGSPNPSGLLAAALAHAFALFVAVSVGANISGG					
OeuTIP1;7	Oeu0452371			MYSNSM-RSGNQIAVGR-LEEATQQDALKAAALAEFISTLI	FVFAGSGSGMAFNKLTDDGATT	PAGLIAAAVAHAFALFVAVSVGANISGG				
OeuTIP2;1	Oeu0240741		-----	MPAIAVGR-LDDSF SIGSLKAYVAEFISTLL	FVFAGVGSIAIAYNKLTADAALDPAGLVAVAICHGFALFVAVSIGANISGG					
OeuTIP2;2	Oeu0240761		-----	MPAIAVGR-LDDSF SIGSLKAYVAEFISTLL	FVFAGVGSIAIAYNKLTADAALDPAGLVAVAICHGFALFVAVSIGANISGG					
OeuTIP2;3	Oeu0539881		-----	MPTIAFGR-IDDSLSVGS	LKAYLAEFISTLLFVFAGVGSIAIAYNKLYDAALDPAGLVAVAVCHGFALFVAVSIGANISGG					
OeuTIP2;4	Oeu0023291		-----	MVKMTLGS-IGDSFSVPSL	KAYLAEFIATLLFVFAGVGSIAIAYNKLTSDAALDPPGLVAVAVAHAFALFVGVSMANVSGG					
OeuTIP2;5	Oeu0402071		-----	MVKINWGS-IGDSFSVPSL	KAYIAEFIAITLLFVFAGVGSIAIAYNKLTSDAALDPPGLVAVAVAHAFALFVGVSMANVSGG					
OeuTIP3;1	Oeu0383871		-----	MPRGYTFGRAEATHPDSARATLAEFLSMLV	FVFAGEGSVLALDKMYKDTALGASSLVVIALAHALS	LFAAVASSMNVSGG				
OeuTIP4;1	Oeu0302291		-----	MAKIALGN-AREAFQSDCIQALIVEFICTFL	FVFAGVGAAMATDKLNGDPLV--GLFFVMAHALVAVMISAGFRVSGG					
AtTIP5;1			-----	MRRMIPTSFSSKFQGVLSMNALRCYVSEFISTFF	FVLAAGVSMSSRKLMDGVS	GPFGLVIPAIALNALALSSSVYISWNVSGG				
SlTIP5;1			-----	MASLASRLQHSVTPNALRSYLAEFLSTFF	FVFAAGASMSTRKMVPDATSDPSSLVAIAVANAFALSVAVYISANISGG					
OeuTIP5;1	Oeu0217081		-----	MASLKSRLHETVTPNALRSYLAEFISTFF	FVFASVGATMSTLKMMPDAASNSSGLVAIAVANAFALSVAVYIAYNISGG					
OeuTIP5;2	Oeu0217091		-----	MASLKSRLHETVTPNALRSYLAEFISTFF	FVFASVGATMSTLKMMPDAASNSSGLVAIAVANAFALSVAVYIAYNISGG					
OeuTIP5;3	Oeu0224791		-----	MASLKSRLHETVTAIALRSYLAEFISTFF	FVFAAGATMSSSRKMMPDAASDSSSLVAIAVANAFALSVTVYISANISGG					

H2

		100	110	120	130	140	150	160	170	180
AtTIP1;2										
SlTIP1;1										
OeuTIP1;3	Oeu0354791									
OeuTIP1;1	Oeu0585311									
OeuTIP1;4	Oeu0402901									
OeuTIP1;5	Oeu0402891									
OeuTIP1;2	Oeu0410141									
OeuTIP1;6	Oeu0332441									
OeuTIP1;7	Oeu0452371									
OeuTIP2;1	Oeu0240741									
OeuTIP2;2	Oeu0240761									
OeuTIP2;3	Oeu0539881									
OeuTIP2;4	Oeu0023291									
OeuTIP2;5	Oeu0402071									
OeuTIP3;1	Oeu0383871									
OeuTIP4;1	Oeu0302291									
AtTIP5;1										
SlTIP5;1										
OeuTIP5;1	Oeu0217081									
OeuTIP5;2	Oeu0217091									
OeuTIP5;3	Oeu0224791									

-NPA;LB--

P1

-----TM3-----

-----TM4-----

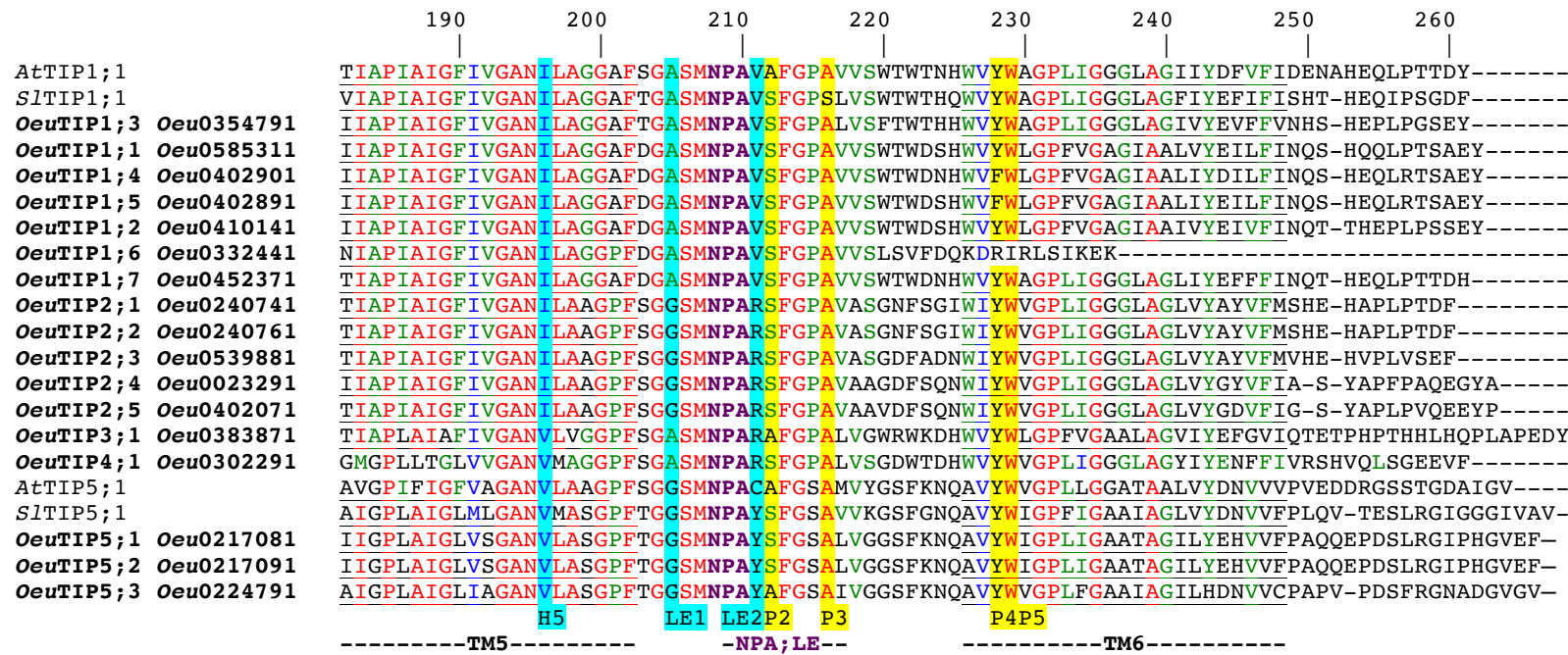


Figure S5B. Amino acid sequence alignment of the *OeuTIPs* subfamily members from *Olea europaea* var. *sylvestris*. *SlTIP1;1* (Solyc06g074820.1) and *SlTIP5;1* (Solyc03g093230.1) (Reuscher et al., 2013) from Tomato and *AtTIP1;1* (At2g36830) and *AtTIP5;1* (At3g47440) from *Arabidopsis thaliana* were used as references. The highest residue similarities between MIP members are shown in red (100%), and green (>80%). Residues with similar physicochemical behaviors are shown in blue. The six transmembrane domains (TMH1-6) and the two hemi-helicoidal regions that include the «NPA» motives «NPA1» (in Loop B) and «NPA2» (in Loop E) (framed in purple) are underlined. The amino acids residues constituting the ar/R constriction region are shown with blue highlights and labeled H2, H5, LE1 and LE2, and residues constituting the Froger's positions are shown with yellow highlights and labeled P1 to P5.

		10	20	30	40	50	60	70	80	90	
<i>SlSIP1;1</i>		---MGVIKAAIADGLLTFLWVFCSSNIGVSTYFIASYFGIVN-EIPSLFITTLIVFVIFLMFDFLGDVLGGAGFNPTGNAAFYAAAGLG-D									
<i>SlSIP1;2</i>		---MGAVKAAVGDVLTLMWVFCSSTLGIFTYLIATAFGIAQ-GMASLFTITTVLIFMLFFVFGIIGDALGGAAFNPAGTAAFYAAAGVG-K									
<i>AtSIP1;1</i>		---MGVLKSAIGDMLMTFSWVVLSTATFGIQTAAIISAGDFQAITWAPLVILTSLIFVYVSIFTVI---FGSASFNP TGSAAFYVAGVP-G									
<i>AtSIP1;2</i>		---MSAVKSALGDMVITFLWVILSATFGIQTAAIVSAVGFHGITWAPLVISTLVVVFVSISIFTVIGNVLGGASFNPCCGNAAFYTAGVS-S									
<i>OeuSIP1;1</i>	<i>Oeu0502921</i>	---MGAIKAAVADGVLTFMWVFCASLTGALTFVVASALGVSQ-GLPTLLVTTVLVFVLLFVFGIIGDFLGGATFNPTAIAAFYAAAGIGGA									
<i>OeuSIP1;2</i>	<i>Oeu0147232</i>	---MRAIKVAIADAIVTCLWVFCASLTGALTFVVASAFGVSQ-GLPTLLITTFLLFVLLFVFGFIGDALGGATFNPTGPAAFYAAAGVGGT									
<i>AtSIP2;1</i>		---MGRIGLVVTDLVLSFMWVWSSVLIKMFVHKIL---GYGAHDL-----KGGAYNPLTILSGAISG-DLT									
<i>SlSIP2;1</i>		-MGVSRRLVISDFIMSFMWVWSSVLIKMFVHKIL---GYGAHDL-----KGGAYNPLTILSGAISG-DLT									
<i>OeuSIP2;1</i>	<i>Oeu0607491</i>	MAAVGGRLLLVSDFFMSFMWVWSSVLIKMFVYKIL---GYGTHDLKGEILRYGISLVNMFFFAFLAKATKGGAYNPLTILSSAISG-DLS									
<i>OeuSIP2;2</i>	<i>OeuChr11</i>	MAAVRGRRLLVSDFLMSFMWVWSSVLIKMFVYKIL---DYGSHDMKGEILRYGISLVNMFFFAFLAKATKGGAYNPLTVLSSAISG-NFS									
		-----TM1-----H2-----TM2-----NPA;LB-----									
100	110	120	130	140	150	160	170	180			
<i>SlSIP1;1</i>		DSLVSAAVRCPAQVAGAVAGSLALVELIPKHYHHMLDG-PALKVDVQGTGAIAEGVLTFFVITFMIFVIVLVRGPESVLLKNWLLTMVTLPLV									
<i>SlSIP1;2</i>		DSLFTVATRFPAQAAGAVAGAVAILEVIPTQYKHM LGG-PSLKVDLHNGAIAEGILTFFVMTFLVFIIVLKGPKSALLKNWLLAMSTVTMV									
<i>AtSIP1;1</i>		DTLFSLAIRLPAQAI GAAGGALAIMEFIPEKYKHMIGG-PSLQVDVHTGAIAETILSFGITFAVLLIILRGPRRLAKTFLLALATISFV									
<i>AtSIP1;2</i>		DSLFSLAIRSPAQAI GAAGGAIITIMEMIPKEYKTRIGGKPSLQFGAHNGAISEVVLSFSVTFVLVLLIILRGPRKLLAKTFLLALATVSVF									
<i>OeuSIP1;1</i>	<i>Oeu0502921</i>	DSLFSAAALRFPAQAAGAVGGALAIMEVMPMQYKHM LGG-PSLKVDLHTGAIAEGVLTFFITFAVLLIVLVRGPNPLVKNWLLAMATVSAV									
<i>OeuSIP1;2</i>	<i>Oeu0147232</i>	ESLVSAAVRFPAQAAGAVGGALGILEVMPVQYKHM LDC-PSLKVDLNTGAIAEGVLTFFITFAVLYIVLVRGPTNPFVKNWLLAMSTVALV									
<i>AtSIP2;1</i>		SFIFSVFVRIPVEVIGSILAVKHIHVFPE-----IGKGPKLNVAIHGHGALTEGILTFEIVLLSMGLTRKIPGSFFMKTWIGSLAKLTLH									
<i>SlSIP2;1</i>		NFIFTVAAIRIPSQVFGSITGVRFIIAAFP N-----IGRGPVLSIDIHRRGALTEGILTFEIVLSISGLSRRSRASTFMKTWISSSLKLT LH									
<i>OeuSIP2;1</i>	<i>Oeu0607491</i>	NFLFTVGARIPIQVLGSIYGVRFILAAFP E-----IGRGPRLNVDIARGALTEGLLTFGIVIIISQGLSRKIPGSFFMKTWISSSVSKLT LH									
<i>OeuSIP2;2</i>	<i>OeuChr11</i>	NFLFTVGARIPVQVLGSIYGVRLILAAFP E-----IGRGPRLNVDITRGALTEGFLTFGIVIIISQGLSRKLPGSFFMKTWISSSVSKLT LH									
		P1-----TM3-----TM4-----H5-----TM5-----									
		190	200	210	220	230	240	250			
<i>SlSIP1;1</i>		LAGSNFTGPSMNPANAFGWAYLSNTHKTLLEHFYVYWISPFIGAILAAWIFRVLFP PPVEQ-KPQKQKRN-----									
<i>SlSIP1;2</i>		VAGSKYTGPSMNPANAFGWAYINNHNHTWEQFYVYWICPFVGAIMAAWTFRAVFPAPAKKKKPKQKKRN-----									
<i>AtSIP1;1</i>		VAGSKYTGPAMNPAAIAGWAMYSSHNHTWDHIYVYWISSFVGALSAALLFRSIFPPPRPQKKKQKKA-----									
<i>AtSIP1;2</i>		VVGSKFTRPFMNPAAIAGWAIYKSHNHTWDHFYVYWISSYTGAILSAMLFRIFFPAPPLVQKKQKKA-----									
<i>OeuSIP1;1</i>	<i>Oeu0502921</i>	VAGSSYTGPSMNPANAFGWAYVYNKHNHTWEQFYVYWICPFTGAILAAWTFRFLFP PPPTKQDKAKKA-----									
<i>OeuSIP1;2</i>	<i>Oeu0147232</i>	VAGSSYTGPSMNPANAFGWAYVNNHTKHTWEQFYVYWICPFTGAILAAWTFRFLFP PPVPK-KQKKA-----									
<i>AtSIP2;1</i>		ILGSDLTGGCMNPAAVMGWAYARGEHITKEHLIVYWLGPVKATLLAVWFFKVVFKPLTEEQEKPKA-KSE----									
<i>SlSIP2;1</i>		ILGSDLTGGCMNPASVMGWAYARGDHITKEHLIVYWLAPIQATLLAVWTFNLLVSPSKDKEAKKTEKKSE----									
<i>OeuSIP2;1</i>	<i>Oeu0607491</i>	ILGSDLTGGCMNPASVMGWAFAGHEHISKEHLIVYWLAPMEATLAAVWAFRLIVRPKKDETLKAKSVKSDCKNS									
<i>OeuSIP2;2</i>	<i>OeuChr11</i>	MLGSDLTGGCMNPASVMGWAFTRGEHISKEHLIVYWLAPMEATLAAVWAFRVVVRPNDKTPKVKSGKSE----									
		LE1 LE2P2 P3 P4P5 -----NPA;LB-----TM1-----									

Figure S5E. Amino acid sequence alignment of the *OeuSIPs* subfamily members from *Olea europaea* var. *sylvestris*. *SlSIP1;1* (Solyc12g0196.1), *SlSIP1;2* (Solyc10g0784.1) and *SlSIP2;1* (Solyc01g0567.1) (Reuscher et al., 2013) from Tomato, and *AtSIP1;1* (AT3G04090), *AtSIP1;2* (AT5G18290) and *AtSIP2;1* (AT3G56950) (Reuscher et al., 2013) from *Arabidopsis thaliana* were used as references. The highest residue similarities between MIP members are shown in red (100%), and green (>80%). Residues with similar physicochemical behaviors are shown in blue. The six transmembrane domains (TMH1-6) and the two hemi-helicoidal regions that include the «NPA» motives «NPA1» (in Loop B) and «NPA2» (in Loop E) (framed in purple) are underlined. The amino acids residues constituting the ar/R constriction region are shown with blue highlights and labeled H2, H5, LE1 and LE2, and residues constituting the Froger's positions are shown with yellow highlights and labeled P1 to P5.