

**Table S1.** Nomenclatures of *Oeu*APQ sequences from the wild olive specie *Olea europaea* var. *sylvestris*.  
*Oeu*AQP sequences (genomic, CDS and protein) are detailed in Supplemental FigureS1

MIP Subclasses	Phytozom loci ("Pseudogenes" in red)	UniProtKB - <i>Olea europaea</i> * Secchi et al., 2007	Location	Nucleotide location (location corrected in red, if necessary)	Remarks
PIP1	<i>Oeu038800.1</i> <i>Oeu</i> PIP1;1a	A0A385A1M4 / A0A385A1N7 GN=PIP1.1 ABB13429.1*	chr19	7203994..7205679 forward	Exon 1 extended with 63n
	<i>Oeu038801.1</i> <i>Oeu</i> PIP1;1b	A0A385A1M4 / A0A385A1N7 GN=PIP1.1 ABB13429.1*	chr19	7208573..7210258 reverse	Exon 1 extended with 63n
	<i>Oeu038802.2</i> <i>Oeu</i> PIP1;1c	A0A385A1M4 / A0A385A1N7 GN=PIP1.1 ABB13429.1*	chr19	7217774..7219459 forward	Exon 1 extended with 63n
	<i>Oeu018133.1</i> <i>Oeu</i> PIP1;2	A0A1D5AHZ6 GN=PIP1.2	scaffold17619	410..2065 forward	-
	<i>Oeu042329.1</i> <i>Oeu</i> PIP1;3	A0A1D5AHZ7 GN=PIP1.3	chr13	11012950..11015602 forward	-
	<i>Oeu052954.1</i> <i>Oeu</i> PIP1;4	-	chr3	21471493..21473698 reverse	-
	<i>Oeu061384.2</i> <i>Oeu</i> PIP1;5	-	scaffold87	524214..526575 reverse	Third predicted Exon as part of the second intron
	<i>Oeu046350.1</i> <i>Oeu</i> PIP1;6	-	scaffold4751	4496..7173 forward	-
	<i>Oeu022396.1</i> <i>Oeu</i> PIP1-related	-	scaffold1994	48682..48948 forward	Incomplete sequence
	<i>Oeu010785.1</i> <i>Oeu</i> PIP1-related	-	chr3	8511236..8513098 reverse	Incomplete sequence
	<i>Oeu019177.1</i> <i>Oeu</i> PIP1-related	-	chr8	2118675..2120753 reverse	Incomplete sequence
	<i>Oeu018831.2</i> <i>Oeu</i> PIP1-related	-	chr4	15354575..15359491 forward	Incomplete sequence
PIP2	<i>Oeu030183.1</i> <i>Oeu</i> PIP2;1	Q38PG7 / ABB13430.2*	chr4	8070191..8071649 reverse	-
	<i>Oeu001271.1</i> <i>Oeu</i> PIP2;2	-	scaffold1031	177815..179775 reverse	-
	<i>Oeu033842.1</i> <i>Oeu</i> PIP2;3	-	chr12	7848155..7849789 reverse	-
	<i>Oeu030439.1</i> <i>Oeu</i> PIP2;4	-	scaffold2530	66057..67614 forward	-
	<i>Oeu027987.1</i> <i>Oeu</i> PIP2;5	-	scaffold2335	58720..59930 reverse	-
	<i>Oeu017257.1</i> <i>Oeu</i> PIP2;6	-	chr6	11700750..11703098 forward	-
	<i>Oeu018111.1</i> <i>Oeu</i> PIP2;7	-	scaffold176	1251179..1252336 forward	-
	<i>Oeu023232.1</i> <i>Oeu</i> PIP2;8	-	scaffold20321	54..1165 reverse	Exon 1 extended in its 5'end with 84n
	<i>Oeu020106.1</i> /scaffold870 <i>Oeu</i> PIP2;9	-	scaffold18654 scaffold870	1671..2018 forward 312817..313578 forward	linking between 2 scaffolds
	<i>Oeu022438.1</i> /scaffold2530 <i>Oeu</i> PIP2;10	-	scaffold19979 scaffold2530	1..1328 reverse	5' end extended with 66n 3' end extended with the scaffold 2530
	<i>Oeu017254.1</i> / <i>Oeu017256.1</i> <i>Oeu</i> PIP2;11	-	chr6	11625929..11647223 forward	PIP sequence cleaved by 21268n including <i>Oeu17255</i> gene
	<i>Oeu059136.1</i> <i>Oeu</i> PIP2-related	-	chr10	15785080..15785518 reverse	Incomplete sequence
TIP	<i>Oeu058531.1</i> <i>Oeu</i> TIP1;1	Q2XVV9 / ABB76813.1* GN=TIP	chr22	3077808..3078742 forward	-
	<i>Oeu041014.1</i> <i>Oeu</i> TIP1;2	A0A1C8V910 GN=TIP1.2	chr20	11814751..11816218 reverse	-
	<i>Oeu035479.1</i> <i>Oeu</i> TIP1;3	A0A1D5AHZ9 GN=TIP1.3	scaffold3011	24603..25462 forward	-
	<i>Oeu040290.1</i> <i>Oeu</i> TIP1;4	-	chr4	16254381..16255311 reverse	-
	<i>Oeu040289.1</i> <i>Oeu</i> TIP1;5	-	chr4	16257013..16257943 reverse	-
	<i>Oeu033244.1</i> <i>Oeu</i> TIP1;6	-	scaffold2789	55535..57322 forward	-
	<i>Oeu045237.1</i> <i>Oeu</i> TIP1;7	-	chr11	5861757..5862731 reverse	2059n were removed at the 5' extremity
	<i>Oeu024074.1</i> <i>Oeu</i> TIP2;1	-	chr2	21805437..21806390 reverse	-
	<i>Oeu024076.1</i> <i>Oeu</i> TIP2;2	-	chr2	21795643..21796596 reverse	-
	<i>Oeu053988.1</i> <i>Oeu</i> TIP2;3	-	chr22	5185229..5186864 forward	-
	<i>Oeu002329.1</i> <i>Oeu</i> TIP2;4	-	chr13	8623502..8625525 reverse	-
	<i>Oeu040207.1</i> <i>Oeu</i> TIP2;5	-	chr19	9881246..9883023 forward	Intron 3 converted in exon
	<i>Oeu038387.1</i> <i>Oeu</i> TIP3;1	-	chr10	29024107..29025120 forward	-
	<i>Oeu030229.1</i> - <i>Oeu036364.1</i> <i>Oeu</i> TIP4;1	-	scaffold25131 scaffold311	282..785 reverse 584778..587098 forward	-
	<i>Oeu021708.1</i> <i>Oeu</i> TIP5;1	-	chr12	21524153..21525389 reverse	-
	<i>Oeu021709.1</i> <i>Oeu</i> TIP5;2	-	chr12	21526411..21527647 reverse	-
	<i>Oeu022479.1</i> <i>Oeu</i> TIP5;3	-	chr1	6772133..6773251 reverse	-
	<i>Oeu041020.1</i> <i>Oeu</i> TIP-related	-	chr20	11792223..11792531 for	Incomplete sequence
	<i>Oeu007734.1</i> <i>Oeu</i> TIP1;3-related	-	chr4	20127443..20127820 reverse	Incomplete sequence
	<i>Oeu000463.1</i> <i>Oeu</i> TIP2;2-related	-	chr17	6142042..6142582 forward	Incomplete sequence
	<i>Oeu050612.1</i> <i>Oeu</i> TIP2;1-related	-	chr18	23502061..23503102 forward	Pseudogene

XIP	<b>Oeu010056.1</b> <i>OeuXIP1;1</i>	-	chr3	335356..336578 forward	Exon 1 extended with 21n
	<b>Oeu020684.1</b> <i>OeuXIP1;1</i>	-	chr5	9245927.. <b>9248997</b> reverse	Extended in 5' with 1455n
	<b>Oeu046122.1</b> <i>OeuXIP1;3</i>	-	chr16	11367503.. <b>11369530</b> reverse	Extended in 5'
NIP	<b>Oeu060187.1</b> <i>OeuNIP1;1</i>	-	chr21	7140088..7142220 forward	-
	<b>Oeu040934.1</b> <i>OeuNIP1;2</i>	-	chr13	<b>1731124</b> ..1733943 forward	5' extended with 2042n, generating 3 exons and 3 introns.
	<b>Oeu039868.1</b> <i>OeuNIP1;3</i>	-	chr16	<b>12429545</b> .. <b>12432818</b> reverse	5' extended with 792n 3' truncated of 246n Intron/exon readjusted
	<b>Oeu053221.1a</b> <i>OeuNIP3;1</i>	-	Scaffold 635	<b>392813</b> .. <b>394288</b> forward	-
	<b>Oeu047418.1</b> <i>OeuNIP4;1</i>	-	chr18	8000311..8001846 forward	-
	<b>Oeu020545.1</b> <i>OeuNIP5;1</i>	-	chr18	6958376..6972407 forward	-
	<b>Oeu046374.1</b> <i>OeuNIP5;2</i>	-	scaffold476	396474..398858 forward	-
	<b>Oeu060126.1</b> <i>OeuNIP6;1</i>	-	scaffold830	250629..252602 forward	-
	<b>Oeu011481.1</b> <i>OeuNIP6-related</i>	-	scaffold14354	165..1696 reverse	Incomplete in 3' end
	<b>Oeu037688.1</b> <i>OeuNIP7;1</i>	-	chr4	<b>6837162</b> ..6838876 forward	1841n removed at the 5' end Intron/exon redesigned by homology with Oleu061Scf4622g04016.1
	<b>Oeu053221.1b</b> <i>OeuNIP3;1-related</i>	-	Scaffold 635	<b>402535</b> .. <b>403011</b> forward	Incomplete sequence End of the Scaffold635
	<b>OeuChr8</b> <i>OeuNIP4;2-related</i>	-	chr8	17852182..17858508 forward	Sequence non-annotated in Phytozome database Incomplete sequence
	<b>Oeu053221.1b</b> <i>OeuNIP1-related</i>	-	scaffold635	402535..403011 forward	Incomplete sequence 3' end stopped by an other gene
	<b>Oeu017634.1</b> <i>OeuNIP5-related</i>	-	scaffold1737	102936..103291 forward	Incomplete sequence
	<b>Oeu005264.1</b> <i>OeuNIP7-related</i>	-	scaffold11917	939..1312 reverse	Incomplete sequence
SIP	<b>Oeu060749.1</b> <i>OeuSIP2;1</i>	B0L1W3 SIP1.1	chr9	9170322.. <b>9172494</b> forward	CDS elongated in 3' (intron + exon) with 261n
	<b>OeuChr11</b> <i>OeuSIP2;2</i>	B5KGP0 SIP1.2	chr11	18362597..18364222 reverse	Sequence non-annotated in Phytozome database
	<b>Oeu050292.1</b> <i>OeuSIP1;1</i>	-	chr4	9340524..9350151 reverse	-
	<b>Oeu014723.2</b> <i>OeuSIP1;2</i>	-	scaffold1584	16236..19503 reverse	-
	<b>Oeu061896.1</b> <i>OeuSIP1-related</i>	-	chr22	4366217..4368873 forward	Pseudogene (Oleu061Scf0342g12031.1 homolog )
	<b>Oeu050293.1</b> <i>OeuSIP-related</i>	-	chr4	9356974..9357960 reverse	Incomplete sequence Intron 2 and Exon 3 truncated

