Supplementary file 2. Multiple alignment of the predicated amino acid sequences of *B. napus* PIPs in our study with five *Arabidopsis* PIP proteins. Amino acid sequences are aligned by the *ClustalW* software. Amino acid numbers are shown on the right. Common amino acid residues are indicated with asterisks. Similar amino acid residues are indicated with colons or periods. The accession numbers for known proteins in GenBank are as follows: AtPIP1;1 (NP_001078323.1), AtPIP1;2 (NP_001078067.1), AtPIP1;3 (NP_171668.1), AtPIP1;4 (NP_974489.1), AtPIP2;1 (NP_190910.1), AtPIP2;2 (NP_181254.1), AtPIP2;5 (NP_191042.1), AtPIP2;7 (NP_001190920.1), BnPIP1 (AAD39373.1), BnPIP2 (AAD39374.1).

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AtPIP1_1        MEGKEEDVRVGANKFPERQPIGTSAQS-DKDYKEPPPAPFFEPGELSSWSFWRAGIAEFI 59

BnPIP1_1        ----------KFPERQPIGTSAQS-DKDYNEPPPAPLFEPGELSSWSFWRAGIAEFI 46

AtPIP1_2        MEGKEEDVRVGANKFPERQPIGTSAQS-DKDYKEPPPAPLFEPGELASWSFWRAGIAEFI 59

BnPIP1_2        ----------KFPERQPIGTSAQS-DKDYKEPPPAPLFEPGELASWSFWRAGIAEFI 46

AtPIP1_4        MEGKEEDVRVGANKFPERQPIGTSAQSTDKDYKEPPPAPLFEPGELSSWSFYRAGIAEFI 60

BnPIP1_4        ----------KFPERQPIGTSAQS-DKDYKEPPPAPLFEPGELSSWSFWRAGIAEFI 46

AtPIP1_3        MEGKEEDVRVGANKFPERQPIGTSAQT-DKDYKEPPPAPFFEPGELSSWSFYRAGIAEFI 59

BnPIP1_3        ----------------------------------------------------ALIAEFI 7

AtPIP2_1        ----------MAKDVEAVPGEGFQTRDYQDPPPAPFIDGAELKKWSFYRAVIAEFV 46

AtPIP2_2        ----------MAKDVEGP--EGFQTRDYEDPPPTPFFDADELTKWSLYRAVIAEFV 44

BnPIP2_2        ----------------------------------------------------AVIAEFV 7
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AtPIP2_5          ----------MTKEVVGDK-RSFSGKDYQDPPPEPLFDATELGKWSFYRALIAEFI 45
BnPIP2_5          ----------------------------------------------------AVIAEFI 7
AtPIP2_7          ----------MSKEVSEEG-KTHHGKDYVDPPPAPLLDMGELKSWSFYRALIAEFI 45
BnPIP2_7          ----------------------------------------------------AVIAEFI 7
                                                                        * ****:

AtPIP1_1          ATFLFLYITVLTVMGVKRSPNM------CASVGIQGIAWAFGGMIFALVYCTAGISGGHI 113
BnPIP1_1          ATFLFLYITVLTVMGVKRSPNM------CSSVGIQGIAWAFGGMIFALVYCTAGISGGHI 100
AtPIP1_2          ATFLFLYITVLTVMGVKRSPNM------CASVGIQGIAWAFGGMIFALVYCTAGISGGHI 113
BnPIP1_2          ATFLFLYITVLTVMGVKRAPNM------CASVGIQGIAWAFGGMIFALVYCTAGISGGHI 100
AtPIP1_4          ATFLFLYITVLTVMGVKRAPNM------CASVGIQGIAWAFGGMIFALVYCTAGISGGHI 114
BnPIP1_4          ATFLFLYITVLTVMGVKRAPNM------CASVGIQGIAWAFGGMIFALVYCTAGISGGHI 100
AtPIP1_3          ATFLFLYITVLTVMGVKRAPNM------CASVGIQGIAWAFGGMIFALVYCTAGISGGHI 113
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BnPIP1_3          ATFLFLYITVLTVMGVERAPNM------CASVGIQGIAWAFGGMIFALVYCTAGISGGHI 61
AtPIP2_1          ATLLFLYITVLTVIGYKIQSDTDAGGVDCGGVGILGIAWAFGGMIFILVYCTAGISGGHI 106
AtPIP2_2          ATLLFLYITVLTVIGYKIQSDTKAGGVDCGGVGILGIAWAFGGMIFILVYCTAGISGGHI 104
BnPIP2_2          ATLLFLYVTVLTVIGYKISSDTKAGGDECGGVGILGISWAFGGMIFILVYCTAGISGGHI 67
AtPIP2_5          ATLLFLYVTIMTVIGYKSQTDPALNPDQCTGVGVLGIAWAFGGMIFILVYCTAGISGGHI 105
BnPIP2_5          ATLLFLYVTVMTVIGYKSQTDPTLYPDQCAGVGVLGIAWAFGGMIFILVYCTAGISGGHI 67
AtPIP2_7          ATLLFLYVTVATVIGHKKQTGP------CDGVGLLGIAWAFGGMIFVLVYCTAGISGGHI 99
BnPIP2_7          ATLLFLYVTVATVIGHKKQTGP------CDGVGLLGIAWAFGGMIFVLVYCTAGVSGGHI 61
                  **:****.*: **:* :  ..        * .**: **:******** *******:*****

AtPIP1_1          NPAVTFGLFLARKLSLTRALYYIVMQCLGAICGAGVVKGFQPKQYQALGGGANTVAHGYT 173
BnPIP1_1          NPAVTFGLFLARKLSLTRALYYIVMQCLGAICGAGVVKGFQPNQYQALGGGANTVAPGYT 160
AtPIP1_2          NPAVTFGLFLARKLSLTRAVYYIVMQCLGAICGAGVVKGFQPKQYQALGGGANTIAHGYT 173
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BnPIP1_2          NPAVTFGLFLARKLSLTRAVYYIVMQCLGAICGAGVVKGFQPKQYQALGGGANTVAPGYT 160
AtPIP1_4          NPAVTFGLFLARKLSLTRAVFYMIMQCLGAICGAGVVKGFQPTPYQTLGGGANTVAHGYT 174
BnPIP1_4          NPAVTFGLFLARKLSLTRAVFYMITQCLGAVCGAGVVKGFQPTPYQTLGGGANTVAPGYS 160
AtPIP1_3          NPAVTFGLFLARKLSLTRAVFYIVMQCLGAICGAGVVKGFQPNPYQTLGGGANTVAHGYT 173
BnPIP1_3          NPAVTFGLFLARKLSLTRAVFYIVMQCLGAICGAGVVKGFQPSPYQTLGGGANTVAPGYT 121
AtPIP2_1          NPAVTFGLFLARKVSLPRALLYIIAQCLGAICGVGFVKAFQSSYYTRYGGGANSLADGYS 166
AtPIP2_2          NPAVTFGLFLARKVSLIRAVLYMVAQCLGAICGVGFVKAFQSSYYDRYGGGANSLADGYN 164
BnPIP2_2          NPAVTFGLFLARKVSLVRAVLYMVAQCLGAICGVGFVKAFQSAYYVRYGGGANPLADGYS 127
AtPIP2_5          NPAVTFGLLLARKVTLVRAVMYMVAQCLGAICGVALVKAFQSAYFTRYGGGANGLSDGYS 165
BnPIP2_5          NPAVTFGLFLARKVTLVRAVMYMVAQCLGAICGVALVKSFQSSYYTRYGGGANGLTHGYS 127
AtPIP2_7          NPAVTFGLFLARKVSLVRALGYMIAQCLGAICGVGFVKAFMKTPYNTLGGGANTVADGYS 159
BnPIP2_7          NPAVTFGLFLARKVSLVRAVGYMIAQCLGAICGVGFVKAFMKTPYNTLGGGANTVAPGYS 121
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AtPIP1_1 KGSGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAPLPIGFAVFLVHLATIPITGTG 233

BnPIP1_1 KGSGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAPLPIGFAVFLVHLATTPITGTG 220

AtPIP1_2 KGSGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAPLPIGFAVFLVHLATIPITGTG 233

BnPIP1_2 KGSGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAPLPIGFAVFLVHLATIPITGTG 220

AtPIP1_4 KGSGLGAEIIGTFVLVYTVFSATDAKRSARDSHVPILAPLPIGFAVFLVHLATIPITGTG 234

BnPIP1_4 KGSGLGAEIIGTFVLVYTVFSATDAKRSARDSHVPLLAPLPIGFAVFLVHLATIPITGTG 220

AtPIP1_3 KGSGLGAEIIGTFVLVYTVFSATDAKRSARDSHVPILAPLPIGFAVFLVHLATIPITGTG 233

BnPIP1_3 KGSGLGAEIIGTFVLVYTVFSATDAKRSARDSHVPILAPLPIGFAVFLVHLATIPITGTG 181

AtPIP2_1 TGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAPLPIGFAVFMVHLATIPITGTG 226

AtPIP2_2 TGTGLAAEIIGTFVLVYTVFSATDPKRNARDSHVPVLAPLPIGFAVFMVHLATIPITGTG 224

BnPIP2_2 TGTGLAAEIIGTFVLVYTVFSATDPKRNARDSHVPVLAPLPIGFAVFMVHLATIPITGTG 187

AtPIP2_5 IGTGVAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAPLPIGFAVFIVHLATIPITGTG 225

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BnPIP2_5          IGTGVAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAPLPIGFAVFIVHLATIPITGTG 187
AtPIP2_7          KGTALGAEIIGTFVLVYTVFSATDPKRSARDSHIPVLAPLPIGFAVFMVHLATIPITGTG 219
BnPIP2_7          KGTALGAEIIGTFVLVYTVFSATDPKRSARDSHIPVLAPLPIGFAVFMVHLATIPITGTG 181
                  *.:.****************.**.*****.*.**********.****** ******


AtPIP1_1          INPARSLGAAIIYNKDHSWDDHWVFWVGPFIGAALAALYHVVVIRAIPFKSRS------- 286
BnPIP1_1          INPARSLGAAIIYNKDHSWDDHWVFWVGPFIGAALAALYHVIVIRAIP---------- 268
AtPIP1_2          INPARSLGAAIIFNKDNAWDDHWVFWVGPFIGAALAALYHVIVIRAIPFKSRS------- 286
BnPIP1_2          INPARSLGAAIIFNKDNAWDDHWVFWVGPFIGAALAALYHVIVIRAIP---------- 268
AtPIP1_4          INPARSLGAAIIYNKDHSWDDHWIFWVGPFIGAALAALYHQIVIRAIPFKSKS------- 287
BnPIP1_4          INPARSLGAAIIYNKDHSWDDHWIFWVGPFIGAALAALY---------- 259
AtPIP1_3          INPARSLGAAIIYNKDHAWDDHWIFWVGPFIGAALAALYHQLVIRAIPFKSRS------- 286
BnPIP1_3          INPARS---------- 187
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AtPIP2_1        INPARSFGAAVIYNKSKPWDDHWIFWVGPFIGAAIAAFYHQFVLRASGSKSLGSFRSAAN 286
AtPIP2_2        INPARSFGAAVIYNKSKPWDDHWIFWVGPFIGAAIAAFYHQFVLRASGSKSLGSFRSAAN 284
BnPIP2_2         INPARSLGA---------------------------------------------------- 196
AtPIP2_5        INPARSLGAAIIYNKDKAWDHHWIFWVGPFAGAAIAAFYHQFVLRAGAIKALGSFRSQPH 285
BnPIP2_5         INPARSLGAA--------------------------------------------------- 197
AtPIP2_7        INPARSFGAAVIYNNEKAWDDQWIFWVGPFLGALAAAAYHQYILRASAIKALGSFRSNAT 279
BnPIP2_7         INPARS------------------------------------------------------ 187
                 ******


AtPIP1_1         -
BnPIP1_1         -
AtPIP1_2         -
BnPIP1_2         -
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AtPIP1_4	-
BnPIP1_4	-
AtPIP1_3	-
BnPIP1_3	-
AtPIP2_1	V 287
AtPIP2_2	V 285
BnPIP2_2	-
AtPIP2_5	V 286
BnPIP2_5	-
AtPIP2_7	N 280
BnPIP2_7	-