```
AT4G10380.1-AtNIP5;1            MAPPEAEVGAV----------MVMAPPT-PGTPGTPGGPLIT--GMRVDSMSFD---HRKP---TPRC-KCLP-VMGSTWG-QHDTCFTD 68
AT1G80760.1-AtNIP6;1            -----MDHE--------EIPSTPSTPATTPGTPG---APLFG--GFEGKRNGHNGRYTPKS--LLKSCKCFSVDNEWALEDGRLPPVTCS 70
Bradi3g30540.1.p-OsNIP3;1       -----MEGAAT--------PNM-SAPAT-PGTP----APLFP--GARVDSMSY----ERKSSMSVPRC-RCLP---VEAWMSSQHACVLE 61
Brara.B02894.1.p-AtNIP5;1       MAPTEAEMGAV----------AVTAPPT-PGTP---GGPLIT--GMRVDSMSFD---HRKP---MPPC-KCLP-VMGHIWG-QPDTCFTD 65
Brara.B02396.1.p-AtNIP6;1       -----MDHE--------EIPSMPSTPATTPGTPG---APLFG--GFDGKRSGHNGRYTPKS--LLKSCKCFSVDNEWALEDGRLPPVSCA 70
Brara.C02640.1.p-AtNIP5;1       MSPPEAEMGAV----------AVTAPPT-PGTP---GGPLIT--GMRVDSMSFD---HRKP---IPPC-KCLP-VMGNRWG-QHDTCFAD 65
Cre12.g549300.t1.2-ZmPIP1;5     -----MSLEVQ---------SKYDRGYQDEGQGLVELGTAHDAVPKTTAQPKYG---DDDD--LLPVVLERYLEKAGVMQKLRPYLDPSG 71
Cucsa.193180.1-AtNIP5;1         -MP-ESESGTP----------VASAPAT-PGTPG---GPLFS--GLRVDSLSY----DRKS---MPRC-KCLP-VNAPTWG-QPHTCFTD 62
Eucgr.D02548.1-AtNIP5;1         ----MAESPT-----------AASAPPT-PGTP----APLFP--GMRVDSLSY----DRKS---MPRC-KCLP-VTAPTWG-EPHSCFTD 58
Eucgr.J03103.1-AtNIP6;1         -----MENE--------EVPSAPSTPVT-PGTPG---APLFG--GGQRAERS----HGRKS--LLRNCSGCFTVEAWSMEGGLPRSLSSS 65
Glyma.08G217400.1.p-AtNIP6;1    -----MNNE--------EVPSLPSTSAT-PGTPG---APLFG--GLRFEKPNG-SVVRKSS--FLKSCK-CFSVAEWTLEDGAMPRVSCS 67
Glyma.10G221100.1.p-AtNIP5;1    --MPESEIGTP---------TAASVPAT-PDTPG---GPLFT--SLRVDSLSHE---RESFS--MAGC-KCLP--------TKGHSCFTD 59
Glyma.15G003900.1.p-AtNIP6;1    -----MD----------NNEEIPSTPAT-PGTPG---APLFG--GFSNGRN----NNSKKS--LLKSCR-CFSVEEWSLEDGGLPAVSCS 62
Gorai.004G126900.1-AtNIP5;1     -MP-DEETATP----------TASAPAT-PGTPG---GPLFN--SMRVDSLSY----DRKS---MPRC-KCFP-VTAPTWG-QPHTCFTD 62
Gorai.009G124500.1-AtNIP6;1     -----MENE--------DVPSAPSTPVT-PGTPG---APLFG--GFKGDHRG---GFNKKS--LLKSCK-CFSVED-SMEEGRLPPVSCS 64
Medtr2g104940.1-AtNIP6;1        -----MEHI--------NNEEIPSTPAT-PGTPG---VPLFG--GFKSERSGNGSNKYKKS--LLKNCK-CFGVQEWNLEDGALPTVTCS 68
Medtr4g006730.1-AtNIP6;1        -----MDNE--------EIPSVPSTPAT-PGTPG---APLFG--GFRSERTG---NGRKNS--LLKNLK-CFSVEDWTLEDGALPKVTCS 65
Medtr1g097840.1-AtNIP5;1        --MPESESGTP---------TAASVPAT-PDTPG---GPLFS--SIRIDSLDQ----RESFA--MGRCNMCMPG-------GKSNSCIAN 60
LOC_Os10g36924.1-OsNIP3;1       --MEMAAPNGGGAAGMSSPVNGASAPAT-PGTP----APLFA--GPRVDSLSY----ERKS---MPRC-KCLPAAVAEAWAPSAHGCVVE 73
Phpat.015G050300.1.p-AtNIP5;1   ----MVKVETA---------AAAQAPLT--TVPTLFALPPER--QLSIQSAGMERQLSTTS----ATSAKCFP-VECMIESSYFTTPVVS 68
ppa009083m-AtNIP6;1             -----MDNNNE------EVPSAPSTPVT-PGTPG---APLFG--GFKADHRSS--GIGRKS--LLKSCSRCFTVEDWALEEGTLPKVSCA 69
Potri.003G180900.1-AtNIP6;1     -----MDNA--------EVPSVPSTPAT-PGTPG---APLFG--GFKGE-RG---VHGRKS--LLRSCK-CFSVEEWAMEEGRLPPVSCS 64
Potri.001G455000.1-AtNIP5;1     -MP-ESEAGTP----------AVSAPNT-PGTPG---GPLFT--GLRVDSLSYS---DRKI---MPKC-KCLP-VTAPTWG-QPHTCFLD 63
Potri.001G046800.1-AtNIP6;1     -----MDTE--------EVPSAPSTPAT-PGTPG---APLFG--GFKGE-RG---VHGRKS--LLRSCK-CFGVEEWAMEEGRLPPVSCS 64
Potri.011G146900.1-AtNIP5;1     -MPGPEEAGTP----------TVTAPNT-PGTPG---GPLFT--GLRVDSLSYS---DRKI---MPKC-KCLP-VTAPNWG-QPHTCFLD 64
Phvul.007G084000.1-AtNIP5;1     --MPESETGTP---------TAASVPAT-PDTPG---GPLFT--SLRVDSLSHE---RNSFT--MNRC-KCFP--------TKDQSCFTD 59
Phvul.005G182400.1-AtNIP6;1     -----MD----------NNEEIPSTPAT-PSTPG---APLFG--GFNNGRNRT-NNTNKNS--LLKSCR-CFSVEDWSIEDGALPAVSCS 65
Phvul.010G160200.1-AtNIP6;1     -----MDSE--------EVPSAPSTPAT-PGTPG---LPLFG--GLRFEKPN---IVRKSS--FLRSCK-CFSVEEWTLEDGAMPRASCS 65
Sobic.001G195800.1.p-OsNIP3;1   ----MAEPGST------TPPNG-SAPAT-PGTP----APLFS-GGPRVDSLSY----ERKS---MPRC-KCLP--AVEGWGIATHTCVVE 63
Solyc03g117050.2.1-AtNIP6;1     -----MDPE--------EGVSAPSTPAT-PGTPG---APLFG--GLIKHERRNG-GNGKKS--LLKSCK-CFGVEPWASEEGTLPAVTCM 67
Solyc08g013730.2.1-AtNIP5;1     ----MAELEN-----------GISAPAT-PGTP----TPLFP--SLRVDSMGSY---DRKS---MPRC-KCLP-LDAPTWG-APHTCLAD 59
GSVIVT01019729001-AtNIP5;1      -MA-EAETGTP----------TASAPAT-PGTPG---GPLFS--SLRVDSLSY----DRKS---MPRC-KCLP-VGAASWA-PSPTCFTD 62
GSVIVT01034224001-AtNIP6;1      -----MDTDH-------DVPSAPSTPVT-PSTPG---APLFH--GFKAHGTSS--GNGRRS--FLRSCK-CFSVEQWAMEEGSLPTLSCS 67
GRMZM2G176209_P01-ZmNIP3;1      -----MEPGS-------TPPNG-SAPAT-PGTP----APLFSSGGPRVDSLSY----ERKS---MPRC-KCLPLPAVEGWGVATHTCVVE 64

AT4G10380.1-AtNIP5;1            FPS-----PDVSLTRKLGAEFVGTFILIFTATAGPIVNQKYDGAETLIGNAAGAGLAVMIIILSTGHISGAHLNPSVTIAFAALRHFPWA 153
AT1G80760.1-AtNIP6;1            LPPP-----NVSLYRKLGAEFVGTLILIFAGTATAIVNQKTDGAETLIGCAASAGLAVMIYILSTGHISGAHLNPAVTIAFAALKHFPWK 155
Bradi3g30540.1.p-OsNIP3;1       IPA-----PDVSLTRKLGAEFVGTFILIFFATAAPIVNQKYNNAISPFGNAAGAGLAVTTIILSTGHISGAHLNPSVTIAFAALRHFPWL 146
Brara.B02894.1.p-AtNIP5;1       FPS-----PVVSLTRKLGAEFVGTFILIFTATAGPIVNQKYDGAETLIGNAAGAGLAVMIIILSTGHISGAHLNPSVTIAFAALRHFPWA 150
Brara.B02396.1.p-AtNIP6;1       LPPP-----NVSLYRKLGAEFVGTLILIFAGTATAIVNQKTDGAVTLIGCAASAGLAVMIYILSTGHISGAHLNPAVTISFAALKHFPWK 155
Brara.C02640.1.p-AtNIP5;1       FPS-----PGVSLTRKLGAEFVGTFILIFTATAGPIVNQKYDGAETLIGNAAGAGLAVMIIILSTGHISGAHLNPSVTIAFAALRHFPWA 150
Cre12.g549300.t1.2-ZmPIP1;5     QVKN-------EFARCLMAEFFGTLLFQMFGGSAPAKDTTAP---------AANGFALVAYIYAFANISGAHLNPAVTFALICTGHMKWW 145
Cucsa.193180.1-AtNIP5;1         FPA-----PDVSLTRKLGAEFVGTFILIFAATAGPIVNQKYNGVETLIGNAAGAGLAVMIIILSTGHISGAHLNPSVTIAFAALRHFPWV 147
Eucgr.D02548.1-AtNIP5;1         FPA-----PDISLTRKLGAEFVGTFILIFAATAGPIVNQKYTNSETLIGNAAGAGLAVMIIILSTGHISGAHLNPSVTIAFAALRHFPWT 143
Eucgr.J03103.1-AtNIP6;1         LLHP-----PVSLARKVGAEFIGTLILVFAGTATPIVNQKTNGSETLLGLAASSGLAVMIYILAVGHISGAHLNPAVTISFAALKHFPWK 150
Glyma.08G217400.1.p-AtNIP6;1    LP----S-PHIPLAKKIGAEFIGTFILMFAAIGTAIVNQKTHGSETLIGCAAANGLAVMIIIFSTGHISGAHLNPAVTISFAALKHFPWK 152
Glyma.10G221100.1.p-AtNIP5;1    FSVG-VPLPNVSLTQKVGAEFVGTFILIFAATAGPIVNNKYNGVESLMGNAAGAGLTVMFIILSIGHISGAHLNPSVTIAFAAFRHFPWT 148
Glyma.15G003900.1.p-AtNIP6;1    LPLPSPP-PVVPLARKIGAEFIGTFILMFAGTAAAIVNQKTNGSETLIGCAATTGLAVMIYILATGHISGAHLNPAVTISFAALKHFPWK 151
Gorai.004G126900.1-AtNIP5;1     FPA-----PDVSLTRKLGAEFVGTFILIFAATAGPIVNQKYSGAETLLGNAAGAGLAVMIIILSTGHISGAHLNPSVTIAFAACRHFPWT 147
Gorai.009G124500.1-AtNIP6;1     LPPP-----PVSLTRKVGAEFIGTFILIFAGTATAIVNQKTQGSETLIGLAASTGLAVMIYILSTGHISGAHLNPAVTIAFAALKHFPRK 149
Medtr2g104940.1-AtNIP6;1        LMP--PP-PPVPLAKKIGAEFIGTLILMFAGAATAIVNQKTQGSETLIGCATSTGLAVMIIILSTGHISGAHLNPAVTISFAALKHFPWK 155
Medtr4g006730.1-AtNIP6;1        LP----P-PPVPLAKKVGAEFIGTYILMFAGIATAIVNQKIHNSETLIGCAGATGLAVMIIILSTGHISGAHLNPAVTISFAALKHFPWK 150
Medtr1g097840.1-AtNIP5;1        FSAG-VRVPSVSLTQKIGAEFVGTFILIYAATAGPIVNNKYNGVETLMGNAAGAGLTVMFIILSIGHISGAHLNPSVTIAFAAFRHFPWA 149
LOC_Os10g36924.1-OsNIP3;1       IPA-----PDVSLTRKLGAEFVGTFILIFFATAAPIVNQKYGGAISPFGNAAGAGLAVTTIILSTGHISGAHLNPSVTIAFAALRHFPWL 158
Phpat.015G050300.1.p-AtNIP5;1   PPN-------ISLTRKFATELIGTFVLIFAATATPIVNEKTKGSVTLLGNAATAGLAIMIYIFATGHISGAHLNPAITIAFASLRHFPWV 151
ppa009083m-AtNIP6;1             LPHP-----PVSLARKVGAEFLGTFILIFAGTATAIVNQKTQGTETLIGLAASTGLAVMIYILSTGHISGAHLNPSVTIAFAALKHFSWK 154
Potri.003G180900.1-AtNIP6;1     LPPP-----PVSLARKVGAEFIGTLILIFAGTATAIVNQKTQGSETLVGLAASSGLAVMIYILATGHISGAHLNPSITIAFAALKHFPWK 149
Potri.001G455000.1-AtNIP5;1     FPA-----PDVSLTRKLGAEFVGTFILIFAATAGPIVNQKYNNAETLIGNAAGAGLAVMIIILSTGHISGAHLNPSVTIAFAALRHFPWV 148
Potri.001G046800.1-AtNIP6;1     LPPP-----PVSLARKLGAEFMGTLILIFAGTATAIVNQKTQGSEALIGLAASTGLAAMIYILSTGHISGAHLNPSITIAFAALKHFPWK 149
Potri.011G146900.1-AtNIP5;1     IPS-----PDVSLTRKLGAEFVGTFILIFMATAGPIVNQKYDHAETLIGNAAGAGLAVMIIILSTGHISGAHLNPSVTIAFAALRHFPWV 149
Phvul.007G084000.1-AtNIP5;1     FSLG-VSLPNVSLTQKVGAEFVGTFILIFAATAGPIVNNKYNGVETLMGNAAGAGLTVMFIILSIGHISGAHLNPSVTIAFAAFRHFPWT 148
Phvul.005G182400.1-AtNIP6;1     LP---PP-PPVPLARKVGAEFIGTFILMFAATAAAIVNQKTNGSETLIGCAATTGLAVMIYILATGHISGAHLNPAVTLSFAALKHFPWK 151
Phvul.010G160200.1-AtNIP6;1     LP----A-PPIPLAKKVGAEFIGTFILMFAAIGTAIVNQKTHGSETLVGCAAANGLAVMIIIFSTGHISGAHLNPAVTISFAALKHFPWK 150
Sobic.001G195800.1.p-OsNIP3;1   IPA-----PDVSLTRKLGAEFVGTFILIFFATAAPIVNQKYGGAISPFGNAAGAGLAVTTIILSTGHISGAHLNPSVTIAFAALRHFPWL 148
Solyc03g117050.2.1-AtNIP6;1     LPPP-----PISLARKVGAEFIGTLILIFAGTATAIVNQKTQGSETLIGLAASTGLAVMIYILSTGHISGAHLNPAVTIGFAALNHFPWK 152
Solyc08g013730.2.1-AtNIP5;1     FPA-----PDVSLTRKLGAEFVGTFILIFAATAGPIVNQKYNGAESLIGNAAGSGLAVMIYILSTGHISGAHLNPSVTIAFAALRHFPWV 144
GSVIVT01019729001-AtNIP5;1      FPA-----PDVSLTRKLGAEFVGTFILIFAATAGPIVNQKYSGVETLIGNAAGAGLAVMIYILSTGHISGAHLNPSVTIAFAALRHFPWV 147
GSVIVT01034224001-AtNIP6;1      WPTP---PLPVSLARKMGAEFIGTFMLIFGGAATGIVNQKTQGSETLLGLAASTGLAVMVIILSTGHISGAHLNPAVTIAFAALRHFPWK 154
GRMZM2G176209_P01-ZmNIP3;1      IPA-----PDVSLTRKLGAEFVGTFILIFFATAAPIVNQKYGGAISPFGNAAGAGLAVATYIILSTGHISGAHLNPSVTIAFAALRHFPWL 149

AT4G10380.1-AtNIP5;1            HVPAYIAAQVSASICASFALKGVFHPFMSG------GVTIP--SVSLGQAFALEFIITFILLFVVTAVATDTRAVGELAGIAVGATVMLN 235
AT1G80760.1-AtNIP6;1            HVPVYIGAQVMASVSAAFALKAVFEPTMSG------GVTVPTV--GLSQAFALEFIISFNLMFVVTAVATDTRAVGELAGIAVGATVMLN 237
Bradi3g30540.1.p-OsNIP3;1       QVPAYVAVQSLASVCAGFALKGVFHPFLSG------GVTVPDAAVSTAQAFFTEFIITFNLLFVVTAVATDTRAVGELAGIAVGAAVTLN 230
Brara.B02894.1.p-AtNIP5;1       HVPAYIAAQVSASICASFALKAVFHPFMSG------GVTVP--SVSVGQAFALEFIITFILLFVVTAVATDTRAVGELAGIAVGATVMLN 232
Brara.B02396.1.p-AtNIP6;1       HVPVYIGAQVLASVCAAFALKAVFEPTMSG------GVTVPTV--ALSQAFALEFIISFNLMFVVTAVATDTRAVGELAGIAVGATVMLN 237
Brara.C02640.1.p-AtNIP5;1       HVPAYIAAQVSASVCASFALKAVFHPFMSG------GVTVP--SVSVGQAFALEFIISFILLFVVTAVATDTRAVGELAGIAVGATVMLN 232
Cre12.g549300.t1.2-ZmPIP1;5     KGLLYMIAQILGAIFGALIYAALIPALHLGAGAGSPGCFSPTAGVKNGDVFGWEVMMTFLLVMTVYAAAVAKPGHGNTAPLAIGLSLYAA 235
Cucsa.193180.1-AtNIP5;1         QVPAYIAAQVSASICASFALKGVFHPFMSG------GVTVP--SVSIGQAFALEFIITFNLLFVVTAVATDTRAVGELAGIAVGATVMLN 229
Eucgr.D02548.1-AtNIP5;1         QVPAYIAAQVSASICASFALKGVFHPYMSG------GVTLP--TVSHGQAFALEFLITFNLLFVVTAVATDTRAVGELAGIAVGATVMLN 225
Eucgr.J03103.1-AtNIP6;1         HVPVYIGAQAVASLCAAFALKGIFYPVMGG------GVTVPSAGVSDGQAFALEFIISFNLMLVVTAVATDTRAVGELAGIAVGATVMLN 234
Glyma.08G217400.1.p-AtNIP6;1    NVPVYIGTQVLASVSAAFALKVVFHPFMSG------GVTVPSV--GYGQAFATEFIVSFILMFVVTAVATDTRAVGELAGIAVGATVMLN 234
Glyma.10G221100.1.p-AtNIP5;1    HVPAYIAAQVSASICACYALKGVYHPFLSG------GVTVP--TVSVAQAFATEFIITFILLFVVTAVATDTRAVGELAGIAVGATVLLN 230
Glyma.15G003900.1.p-AtNIP6;1    HVPMYIGAQVLASICAGFALKGVFHPFMSG------GVTVPSG--GYGQSFALEFIIGFNLMFVVTAVATDTRAVGELAGIAVGATVMLN 233
Gorai.004G126900.1-AtNIP5;1     QVPAYIAAQVSASICASFALKGVFHPFMSG------GVTVP--SVSHGQAFALEFLITFNLLFVVTAVATDTRAVGELAGIAVGATVMLN 229
Gorai.009G124500.1-AtNIP6;1     HVPVYIGAQVMASLCAAFGLKGVFHPMMGG------GVTVPSG--GFGQAFALEFIISFNLMFVVTAVATDTRAVGELAGIAVGATVMLN 231
Medtr2g104940.1-AtNIP6;1        HVPMYIGAQILASICAAFSLKAVFHPFMSG------GVTVPSG--GYGQAFALEFIISFNLMFVVTAVATDTRAVGELAGIAVGATVMLN 237
Medtr4g006730.1-AtNIP6;1        NVPLYIAAQVLASICASFTLKGVFHPFMSG------GVTVPSV--EYGQAFALEFIISFNLMFVVTAVATDTRAVGELAGIAVGATVMLN 232
Medtr1g097840.1-AtNIP5;1        HVPAYIAAQVSASICACYALKGVYHPFLSG------GVTVP--TVSVGQAFATEFIITFILLFVVTAVATDSRAVGELAGIAVGATVLLN 231
LOC_Os10g36924.1-OsNIP3;1       QVPAYVAVQVLGSICAGFALKGVFHPFLSG------GVTVPDPTISTAQAFFTEFIITFNLLFVVTAVATDTRAVGELAGIAVGAAVTLN 242
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Phpat.015G050300.1.p-AtNIP5;1  QVPFYIAAQVLGSIAASFTLKGIFHPYMHG------GVTLPQG--AYWPSFLLEFIISFNLMFVITAVATDTRAVGELAGIAVGACVMMN 233
ppa009083m-AtNIP6;1            HVPVYVGAQVLASICAAFALKVIFHPIMGG------GVTVPSG--SYGQAFALEFIISFNLMFVVTAVATDTRAVGELAGIAVGATVMLN 236
Potri.003G180900.1-AtNIP6;1    HVPVYIGAQVLASLCAAFALKGIFHPVMGG------GVTVPSG--GYGQAFALEFITSFILMFVVTAVATDTRAVGELAGIAVGATVMLN 231
Potri.001G455000.1-AtNIP5;1    QVPAYIAAQVSASICASFALKGVFHPFMSG------GVTVP--SVSTGQAFALEFLITFNLLFVVTAVATDTRAVGELAGIAVGATVMLN 230
Potri.001G046800.1-AtNIP6;1    HVPVYIGAQVLASLCAAFALKVIFHPMMGG------GVTVPSG--GHGQAFALEFIISFILMFVVTAVATDTRAVGELAGIAVGATVMLN 231
Potri.011G146900.1-AtNIP5;1    QVPAYIAAQVSASICASFALKGVFHPFMSG------GVTVP--SVSTGQAFALEFFITFNLLFVVTAVATDTRAVGELAGIAVGATVMLN 231
Phvul.007G084000.1-AtNIP5;1    HVPAYIAAQVSASICACFALKGVYHPFLSG------GVTVP--SVSVGQAFATEFIITFILLFVVTAVATDTRAVGEMAGIAVGATVLLN 230
Phvul.005G182400.1-AtNIP6;1    HVPMYIGAQVLASICAAFALKGVYHPFMSG------GVTVPSG--GYAQAFALEFIIAFNLMFVVTAVATDTRAVGELAGIAVGATVMLN 233
Phvul.010G160200.1-AtNIP6;1    NVPVYIGTQILASVSAAFAVKAVFNPFMSG------GVTVPSV--GYGQAFATEFIVSFILMFVVTAVATDTRAVGELAGIAVGATVMLN 232
Sobic.001G195800.1.p-OsNIP3;1  QVPAYVSVQVLGSICASFALKGVFHPFLSG------GVTVPDVTISTAQAFFTEFIISFNLLFVVTAVATDTRAVGELAGIAVGAAVTLN 232
Solyc03g117050.2.1-AtNIP6;1    HVPVYIGAQIIASFCAAFTLKVVLHPIMGG------GVTVPSG--SYVQAFALEFIISFNLMFVVTAVATDTRAVGELAGIAVGATVMLN 234
Solyc08g013730.2.1-AtNIP5;1    QVPAYVAAQVSASICASFALKGVFHPFMSG------GVTVP--SVNTGQAFALEFLITFNLLFVVTAVATDTRAVGELAGIAVGATVMLN 226
GSVIVT01019729001-AtNIP5;1     QVPAYIAAQVSASICASFALKAVFHPFMSG------GVTVP--SVSIGQAFALEFLITFNLLFVVTAVATDTRAVGELAGIAVGATVMLN 229
GSVIVT01034224001-AtNIP6;1     HVPVYIGSQLMGSLCASFALKGIFNPVMDG------GVTVPSHSGAYGQAFALEFIISFFLMFVVTAVATDTRAVGSLAGIAVGGTVMLN 238
GRMZM2G176209_P01-ZmNIP3;1     QVPAYVAVQALASVCAAFALKGVFHPFLSG------GVTVPDATVSTAQAFFTEFIISFNLLFVVTAVATDTRAVGELAGIAVGAAVTLN 233

AT4G10380.1-AtNIP5;1           ILVAGPSTGGSNPVRILGPAVASG-NYRSLWVYLVAPTLGAISGAAVYTGVKLNDSVT--DPPRPVRSFRR------------------ 304
AT1G80760.1-AtNIP6;1           ILIAGPATSASNPVRILGPAIAAN-NYRAIWVYLTAPILGALIGAGTYTIVKLPEEDEAPKERRSFRR---------------------- 305
Bradi3g30540.1.p-OsNIP3;1      ILIAGPTTGGSNPVRILGPAVAAG-NYRQLWIYLVAPTLGAVAGAGVYTAVKLRDVDGGGEAPRPQRSFRR------------------ 301
Brara.B02894.1.p-AtNIP5;1      ILVAGPSSGGSNPVRILGPALASG-NYRSLWVYLVAPTLGAISGAAVYTGVKLNDSAT--DPPRQVRSFRR------------------ 301
Brara.B02396.1.p-AtNIP6;1      ILIAGPATSASNPVRILGPAIAAN-NYRAIWVYLTAPILGALIGAGTYTVVKLPEEDEEHKETRSFRR---------------------- 305
Brara.C02640.1.p-AtNIP5;1      ILVAGPSTGASNPVRILGPALASG-NYRLLWVYLVAPTLGAISGAAVYTGVKLNDNVT--DPPRQVRSFRR------------------ 301
Cre12.g549300.t1.2-ZmPIP1;5    AISGGPYTGASNPARIIGPAVVFTCNVGVSFLYIFAEFFGAACAAGLSIFLYGRAPDSVRRPAI------------------------- 300
Cucsa.193180.1-AtNIP5;1        ILVAGPSSGGSNPVRILGPAVAAG-NYKALWVYLVAPTLGAIIGAGTYTAVKLRDDEV--DAPSQVRSFRR------------------ 298
Eucgr.D02548.1-AtNIP5;1        ILVAGPSSGGSNPVRILGPAVAAG-NYRALWIYLVAPTLGALAGAGTYTVVKLRDDET--DPPRPVRSFRR------------------ 294
Eucgr.J03103.1-AtNIP6;1        ILIAGPTTGASNPARILGPAIAAG-NYRAIWIYLTAPILGALCGAGIYTAVKLPDDGGNNQGKP------------------------- 298
Glyma.08G217400.1.p-AtNIP6;1   ILIAGPTTGSSNPARILGPAIAAN-NYKGIWVYLIAPILGTLCGAGAYTVVKLPEEE-ATKTPSSAPNGSFRR---------------- 306
Glyma.10G221100.1.p-AtNIP5;1   ILISGPTSGGSNPVRILGPAVAAG-NYKHIWIYLVAPTLGALAGAGVYTLVKLRDEEA--EPPRQVRSFRR------------------ 299
Glyma.15G003900.1.p-AtNIP6;1   ILIAGPVSGGSNPVRILGPAVAAN-NYKAIWVYLVAPILGALAGAGTYTAVKLPEEDDDAKAKTSISS--FRR---------------- 304
Gorai.004G126900.1-AtNIP5;1    ILVAGPSSGGSNPVRILGPAVAAG-NYRALWIYLIAPTLGAVIGSATYTLVKLREDEV--DAPRQVRSFRR------------------ 298
Gorai.009G124500.1-AtNIP6;1    ILIAGPITGASNPVRILGPAIAAN-NYKAIWVYFTAPILGALCGAGTYTAVKLPEEDG---EKPSTVRSFRR----------------- 300
Medtr2g104940.1-AtNIP6;1       ILIAGPITGASNPVRILGPAIAAN-NYKAIWVYLLAPILGALGGAGTYTAVKLPEEDDNAKTNASSNHPSFRR---------------- 310
Medtr4g006730.1-AtNIP6;1       ILIAGPATGASNPVRILGPAIAAN-NYKGIWLYLIAPILGALGGAGAYTAVKLPDEEFNSEVKASSAPGSFRR---------------- 305
Medtr1g097840.1-AtNIP5;1       ILISGPTSGGSNPVRILGPAVAAG-NYKHLWIYLVAPTLGALAGSGVYTLIKLRDNGA--EPPQPVRSFRR------------------ 300
LOC_Os10g36924.1-OsNIP3;1      ILIAGPTTGGSNPVRILGPAVAAG-NYRQLWIYLIAPTLGAVAGAGVYTAVKLRDENG--ETPRPQRSFRR------------------ 311
Phpat.015G050300.1.p-AtNIP5;1  IMIAGSTSGASNPVRILGPAIAVN-NYKGIWLYMLGPVLGMLAGATAYTAVRLKEEDP---PRLPVRVFHR------------------ 301
ppa009083m-AtNIP6;1            ILIAGETTGASNPVRILGPAIAAN-NYKAIWVYLTAPFLGALFGAGTYTAVKLPEEDGDHIEKPSTRSFRR------------------ 307
Potri.003G180900.1-AtNIP6;1    IFIAGETTGASNPVRILGPAIAVN-NYKAIWIYLTAPILGALCGAGTYSAVKLPEEDGDSNEKTSAARSFRR----------------- 303
Potri.001G455000.1-AtNIP5;1    ILVAGPSSGGSNPVRSLGPAVAAG-TYKDIWIYLVAPTLGALVGAATYTAVKLREEEA--DPPRQVRSFRR------------------ 299
Potri.001G046800.1-AtNIP6;1    ILIAGETTGASNPVRILGPAIAAN-NYKAIWVYLTAPILGALCGAGTYSAVKLPEEDGDTNEKTSATRSFRR----------------- 303
Potri.011G146900.1-AtNIP5;1    ILVAGPSTGGSNPVRILGPAIAAG-NYKKIWIYLVAPTLGAVVGAGAYTLVKLRDDET--DPPRPVRSFRR------------------ 300
Phvul.007G084000.1-AtNIP5;1    ILISGPTSGGSNPVRILGPAVAAG-NYKHIWIYLVAPTLGALAGAGVYTLVKLRDNEA--EPPRQVRSFRR------------------ 299
Phvul.005G182400.1-AtNIP6;1    ILIAGPVSGGSNPVRILGPAIAAN-NYKAIWVYLVAPVLGALAGAGTYTAVKLPEEDDDAKAKASIS---FRR---------------- 303
Phvul.010G160200.1-AtNIP6;1    ILIAGPATGSSNPVRILGPAIAAN-NYKGIWVYLIAPIFGTLCGAGAYTMVKLPQEE-ATKPP---IVESFGR---------------- 301
Sobic.001G195800.1.p-OsNIP3;1  ILVAGPTTGGSNPVRILGPAVAAG-NYRQLWIYLLAPTLGALAGAGVYTAVKLRDENG--ETPRTQRSFRR------------------ 301
Solyc03g117050.2.1-AtNIP6;1    ILIAGETTGASNPVRILGPAVAVG-NYKAIWIYLTAPILGALIGAGVYSAVKLPDEDRDNHPKPSLEHSFRR----------------- 306
Solyc08g013730.2.1-AtNIP5;1    ILVAGPSSGASNPVRILGPAVAAG-NYKSLWIYLVAPTLGALAGAAVYTLVKLRGDTT--ETPRQVRSFRR------------------ 295
GSVIVT01019729001-AtNIP5;1     ILVAGPSSGGSNPVRILGPAVAAG-NYRAIWIYLVAPTLGAVAGAAIYTAVKLRADEG--EQPRQVRSFRR------------------ 298
GSVIVT01034224001-AtNIP6;1     ILIAGETTGASNPVRILGPAIAVN-NFKAIWVYLTAPILGALCGAGVYTAVKLPEEDGNTHSLNKSMTVQSEGDQSMSSVGLQHKFRNF 327
GRMZM2G176209_P01-ZmNIP3;1     ILVAGPTTGGSNPVRILGPAVAAG-NYRQLWIYLLAPTLGALAGASVYKAVKLRDENG--ETPRTQRSFRR------------------ 302

AT4G10380.1-AtNIP5;1           --------------------------- 304
AT1G80760.1-AtNIP6;1           --------------------------- 305
Bradi3g30540.1.p-OsNIP3;1      --------------------------- 301
Brara.B02894.1.p-AtNIP5;1      --------------------------- 301
Brara.B02396.1.p-AtNIP6;1      --------------------------- 305
Brara.C02640.1.p-AtNIP5;1      --------------------------- 301
Cre12.g549300.t1.2-ZmPIP1;5    --------------------------- 300
Cucsa.193180.1-AtNIP5;1        --------------------------- 298
Eucgr.D02548.1-AtNIP5;1        --------------------------- 294
Eucgr.J03103.1-AtNIP6;1        --------------------------- 298
Glyma.08G217400.1.p-AtNIP6;1   --------------------------- 306
Glyma.10G221100.1.p-AtNIP5;1   --------------------------- 299
Glyma.15G003900.1.p-AtNIP6;1   --------------------------- 304
Gorai.004G126900.1-AtNIP5;1    --------------------------- 298
Gorai.009G124500.1-AtNIP6;1    --------------------------- 300
Medtr2g104940.1-AtNIP6;1       --------------------------- 310
Medtr4g006730.1-AtNIP6;1       --------------------------- 305
Medtr1g097840.1-AtNIP5;1       --------------------------- 300
LOC_Os10g36924.1-OsNIP3;1      --------------------------- 311
Phpat.015G050300.1.p-AtNIP5;1  --------------------------- 301
ppa009083m-AtNIP6;1            --------------------------- 307
Potri.003G180900.1-AtNIP6;1    --------------------------- 303
Potri.001G455000.1-AtNIP5;1    --------------------------- 299
Potri.001G046800.1-AtNIP6;1    --------------------------- 303
Potri.011G146900.1-AtNIP5;1    --------------------------- 300
Phvul.007G084000.1-AtNIP5;1    --------------------------- 299
Phvul.005G182400.1-AtNIP6;1    --------------------------- 303
Phvul.010G160200.1-AtNIP6;1    --------------------------- 301
Sobic.001G195800.1.p-OsNIP3;1  --------------------------- 301
Solyc03g117050.2.1-AtNIP6;1    --------------------------- 306
Solyc08g013730.2.1-AtNIP5;1    --------------------------- 295
GSVIVT01019729001-AtNIP5;1     --------------------------- 298
GSVIVT01034224001-AtNIP6;1     TRKVRQFFEEIRNNSPMDRDPASTYNT 354
GRMZM2G176209_P01-ZmNIP3;1     --------------------------- 302
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Figure S2 Alignment of boric acid channel (NIP5;1) homologs in 18 plant species. Two NPA motifs were specified in red frame.

Residues of ar/R region (A, I, G, R) were specified in green frame.