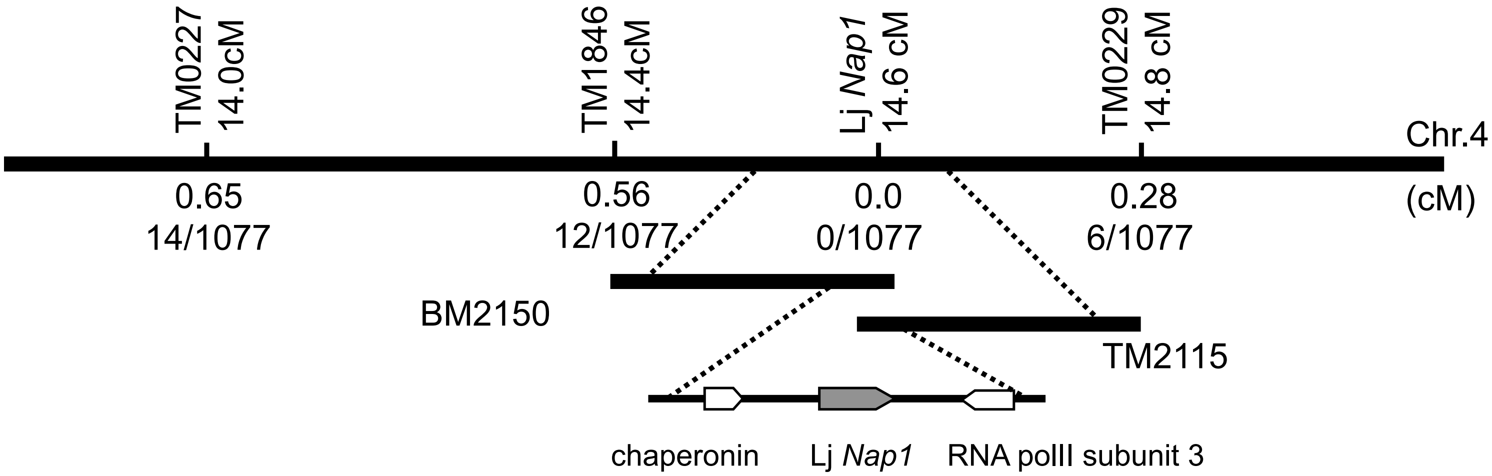
Map based cloning of Lj *Nap1*



Supplemental Figure 1. The genomic region surrounding Lj *Nap1* on linkage group 4 is shown with cM position. The cM distance from Lj *Nap1* to adjacent microsatellite markers, the fraction of recombinant plants and the BAC (BM)/TAC (TM) contig are indicated.

The two genes flanking Lj *Nap1* are shown. The orientation of the BM2150+TM2115 contig is not known.

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            . . . .10 . . . .20 . . . .30 . . . .40 . . . .50 . . . .60 . . . .70 . . . .80 . . . .90
LjNAP    1:MARSRQKLINQDSSLSPTAARSRELDGPSRWADYLGPDV..SSPVSSTSSRNLFHDGQSQGNTPSSQSGKGLNMQWVVQLTEVAEGLMAK:  88
MtNAP    1:MAKSRQKSSNQDSSLSPTAARSREWDGPSRWADYLGTETNTASPLSSTSSRNFGHDGQSQGSTPS.QPHKGLNMQWVVQLTDVADGLMAK:  89
AtNAP    1:MANSRQYYPSQDESMSPTSVRSREWEGPSRWTEYLGPEM..AASVSSTRSSKQI.DGHVGGST......KALNIQWVVQMIEVADGLMAK:  81

            . . . 100 . . . 110 . . . 120 . . . 130 . . . 140 . . . 150 . . . 160 . . . 170 . . . 180
LjNAP   89:MYRLNQLLDYPDPVNHVFSDGFWKAGVFPNHPRVCVLLSKKFPEHSSKLQIERIDKIAWDSMQDHAELHLQSLEPWVQLLLDLMVFREQA: 178
MtNAP   90:MYRLNQLLDYPDPINHVFSDGFWKAGVFPNHPRICVLLSKKFPEHFSKLQLERIDKIAWDSMQDHAELHLQSLEPWVQLLLDLMVFREQA: 179
AtNAP   82:MYRLNQILEYPDPVGHVFSEAFWKAGVFPNHPRICTLLSKKFPEHFSKLQLERIDKFSLDSLHDGAELHLQSLEPWIQLLLDLMAFREQA: 171

            . . . 190 . . . 200 . . . 210 . . . 220 . . . 230 . . . 240 . . . 250 . . . 260 . . . 270
LjNAP  179:LRLILDLSSTVITLLPHQNSLILHAFMDLFCSFVRVNLFSEKMPRKMLLQTYNLLHVMSRNERDCDFYHRLVQFIDSYDPPLKGLQEDLN: 268
MtNAP  180:LRLILDLSSTVITLLPHQNSLILHAFMDLFCSFVRVNLF...MPRKMLLQTYNLLHALSRNERDCDFYHRLVQFIDSYDPPLKGLQEDLN: 266
AtNAP  172:LRLILDLSSTVITLLPHQNSLILHAFMDLFCAFVRVNLFAEKIPRKMLLQVYNLLHALSRNDRDCDFYHRLVQFIDSYDPPLKGLQEDLN: 261

            . . . 280 . . . 290 . . . 300 . . . 310 . . . 320 . . . 330 . . . 340 . . . 350 . . . 360
LjNAP  269:FVSPRIGEVLEAVGPIIFLSTDTRKLRNEGFLSPYHPRYPDILTNSAHPLRAQDLANVTAYREWVLFGYLVCPDELRRVTSIDIALVVLK: 358
MtNAP  267:FVSPRIGEVLEAVGPIIFLSTDTKKLRNEGFISPYHPRFPDILTNSAHPLRAQDLANVTAYREWVLFGYLVCPDELRRVTSIDIALVVLK: 356
AtNAP  262:FVSPRIGEVLEAVGPSIFLSADTRKLRNEGFLSPYHPRFPDILTNSAHPMRAQDLANVTSYREWVLLGYLVCPDELLRVTSIDIALVVLK: 351

            . . . 370 . . . 380 . . . 390 . . . 400 . . . 410 . . . 420 . . . 430 . . . 440 . . . 450
LjNAP  359:ENLVLTLFRDEYILLHEDYQLYVLPRILESKKMAKSGRTKQKEADLEYNVAKQVEKMISEVHEQAILSCDAIHRERRILLKQEIGRMVLF: 448
MtNAP  357:ENLVLTLFRDEYILLHEEYQLYVLPRILESKKMAKSGRTKQKEADMEYNVAKQVEKMISEVHEQAILSCDAIHRERRILLKQEIGRMVLF: 446
AtNAP  352:ENLVVTLFRDEYILLHEDYQLYVLPRVLESKKMAKSGRTKQKEADLEYSVAKQVEKMISEVHEQALQLCDTIHRERRILLKQEIGRMVLF: 441

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LjNAP  449:FTDQPSLLAPNIQMVFSALALAQCEVIWFFQHVGVASSKSKTTRVVPVDIDPNDPTIGFLLDGMDHLCCLVRKYIAAIRGYSLSYLSSCA: 538
MtNAP  447:FTDQPSLLAPNIQMVFSALALAQCEVIWYFQHVGVASSKSKTTRVVPVDIDPNDPTIGFLLDGMDHLCCLVRKYIAAIRGYSLSYLSSCA: 536
AtNAP  442:FTDQPSLLAPNIQMVFSALALAQSEVLWYFQHAGIASSRSKAARVIPVDIDPNDPTIGFLLDGMDRLCCLVRKYISAARGYALSYLSSSA: 531

            . . . 550 . . . 560 . . . 570 . . . 580 . . . 590 . . . 600 . . . 610 . . . 620 . . . 630
LjNAP  539:GRIRFLLGTPGMVALDIDAFLKGLLQQIVHHLENLPKPQGENVSAITCDLSDFRKDWLSILLIVTSSRSSINIRHLEKATVSTGKEGLLS: 628
MtNAP  537:GRIRFLLGTPGMVALDIDASLKGLLQQIVHHLEHLPKPQSENISAITCDLSDFRKDWLSILLMVTSSRSSINIRHLEKATVSTGKEGLLS: 626
AtNAP  532:GRIRYLMGTPGIVALDLDPTLKGLFQRIVQHLESIPKAQGENVSAITCDLSDFRKDWLSILMIVTSSRSSINIRHLEKATVSTGKEGLLS: 621

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LjNAP  629:EGNSAYNWSRCVDELESVLSKHGSLRKLYFYHQHLTAVFRNTMFGPEGRPQHCCAWLGIASSFPECSSPIVPEEVTKIGRDAVLYVESLI: 718
MtNAP  627:EGNAAYNWSRCVDELESLLSKHGSLRKLYFYHQQLKVVFRNTMFGPEGRPQHCCAWLGIASSFPECASPVVPEEVTKFGRDAVLYVESLI: 716
AtNAP  622:EGNAAYNWSRCVDELESQLSKHGSLKKLYFYHQHLTTVFRNTMFGPEGRPQHCCAWLSVASSFPECASLIIPEEVTKFGRDAVLYVESLI: 711

            . . . 730 . . . 740 . . . 750 . . . 760 . . . 770 . . . 780 . . . 790 . . . 800 . . . 810
LjNAP  719:ESIMGGLEGLINILDSEGGFGALENQLFPEQAASHLNYASRVAIPSYKSPKGTAGVPLPGHESYPENNNSIKMLEAAMQRLTNLCSVLND: 808
MtNAP  717:ESIMGGLEGLINILDSEGGFGALENQLLPEQAASYLNYASRVSIPSYKSPKGTAGFPLPGHESFPENNSSIKMLEAAMQRLTNLCSVLND: 806
AtNAP  712:ESIMGGLEGLINILDSEGGFGALESQLLPEQAAAYLNNASRISAPSVKSPRVVGGFTLPGHESYPENNKSIKMLEAAIQRLTNLCSILND: 801

            . . . 820 . . . 830 . . . 840 . . . 850 . . . 860 . . . 870 . . . 880 . . . 890 . . . 900
LjNAP  809:MEPICVLNHVFVLREYMRECILGNFRRRLLGVLKTDNDLQRPSVLESLIQRHVSIMHLAEQHISMDITQGIREVLLSEAFSGPVSSLHLF: 898
MtNAP  807:MEPICVLNHVFVLREYMRECILGNFRRRLLGVLKTDNDLQRPSVLESLILRHVSIVHLAEQHISMDITQGIREVLLSEAFSGPVSSLHLF: 896
AtNAP  802:MEPICVINHVFVLREYMRECILGNFKRRFLTALQTDNDLQRPSVLESLIRRHMGIVHLAEQHVSMDLTQGIREILLTEAFSGPVSSLHTF: 891

            . . . 910 . . . 920 . . . 930 . . . 940 . . . 950 . . . 960 . . . 970 . . . 980 . . . 990
LjNAP  899:EKPTDQH..TGSATESVCNWYIENIIKDVSGAGILFVPIHKCFRSTRPVGGYFAESVTDLRELQAFVRIFGGYGVDRLDRMLKEHTAALL: 986
MtNAP  897:EKPTDQH..TGSATESVCNWYIENIIKDVSGAGILFVPIHKCFRSTRPVGGYFAESVTDLSELQAFVRIFGGYGVDRLDRMLKEHTAALL: 984
AtNAP  892:EKPAEQQQTTGSAVEVVCNWYMDNIIKDVSGAGILFAPRHKYFKSTRPVGGYFAESVTDLKELQAFVRIFGGYGVDRLDRMMKVHTAALV: 981

            . . .1000 . . .1010 . . .1020 . . .1030 . . .1040 . . .1050 . . .1060 . . .1070 . . .1080
LjNAP  987:NCIDTTLRSNRDVLEAVATSLHAGDRIEREASMRQIVDLETVIGFCVQAGLALAFDRLLAEASGAILEEGAPLIHSLLAGMVKHLPDGVP:1076
MtNAP  985:NCIDTSLRSNRDVLEAVASSLHAGDRIEREASMKQIVDLETVIDFCIQAGLALAFDRLLSEASGAILEEGAPLIHSLLTGVVNHLPDGVP:1074
AtNAP  982:NCIETSLRSNRELIEAAAASMHSGDRVERDASVRQIVDLDTVIGFCIEAGQALAFDDLLAEASGAVLEDNASLIHSMISGIVEHIPEEIP:1071

            . . .1090 . . .1100 . . .1110 . . .1120 . . .1130 . . .1140 . . .1150 . . .1160 . . .1170
LjNAP 1077:EKEEIRRMRSVANTAGVVSDHDSIWVRSILEEVGGASDGSWSLLPYLFATFMTSNIWSTTAFNVDTEGFSNNIHCLARCISAVIAGSEFV:1166
MtNAP 1075:EKEEIKRMRTVANTAGVVNDHDSIWVRSILEDVGGASDGSWSLLPYLFATFMTSNIWSTTAFNVDTEGFSNNIHCLARCISAVVAGSEFV:1164
AtNAP 1072:EKKEIRRIKGVANGVGVAGDHDSEWVRLILEEVGGANDNSWSLLPYFFASFMTSNAWNTTGFNIETGGFSNNIHCLARCISAVIAGSEYV:1161

            . . .1180 . . .1190 . . .1200 . . .1210 . . .1220 . . .1230 . . .1240 . . .1250 . . .1260
LjNAP 1167:RLEREYQHR.QSLTNGH..AEGMDPELASHTSAEASIKSTLQLFVKFSAEIILDSWSETQRAHLVAQLIFLDQLCEISPYLPRSSLETHV:1253
MtNAP 1165:RLEREHQHR.QSLSNGH.ASEGMDPELSGHMSAEASINSTLQLFVKLSAEMILDSWSETHRSHLVAQLIFLDQLCEISPYLPRSSLETHV:1252
AtNAP 1162:RLQREYQQQHQSLSNGHHSSENLDSEFPPRVTAEASIKSSMLLFVKFAASIVLDSWSEANRSHLVAKLIFLDQLCEISPYLPRSSLESHV:1251

            . . .1270 . . .1280 . . .1290 . . .1300 . . .1310 . . .1320 . . .1330 . . .1340 . . .1350
LjNAP 1254:PYAILRSIYSQYYADTPSTPLAMLNASPRHSPAILLAHASPGLRH...P.RGDS..TPPYYGNDSGYFKGGSSS.HSQEHLYDADIGSIR:1336
MtNAP 1253:PYAILRSVYSHYYADTPSTPLAIMNASPRQSPAL.LAHASPVLRH...P.RGDS..TPPYYGNDSGYFKG.SSS.HSQDHLYDADISSIR:1333
AtNAP 1252:PYTILRSIYTQYYSNTPSTPLS..TASPYHSPSVSLIHASPSMKNSTTPQRGSGSGSSSTAAPDSGYFKGSSSSLYGQEHYTESETGNSR:1339

            . . .1360 . . .1370 . . .1380 . . .1390 . . .1400 . . .1410 .
LjNAP 1337:N............TRRSGPLDYSASRNRVKSVEGSTSGSTGPSPLPRFAVSRSGPLAYK...:1383
MtNAP 1334:N............TRRSGPLDYGAGRHKVKSVESSNSGSTGPSPLPRFAVSRSGPLAYK...:1380
AtNAP 1340:NNENNNNNKQRGSSRRSGPLDYSSSH...K..GGSGSNSTGPSPLPRFAVSRSGPISYKQHN:1396
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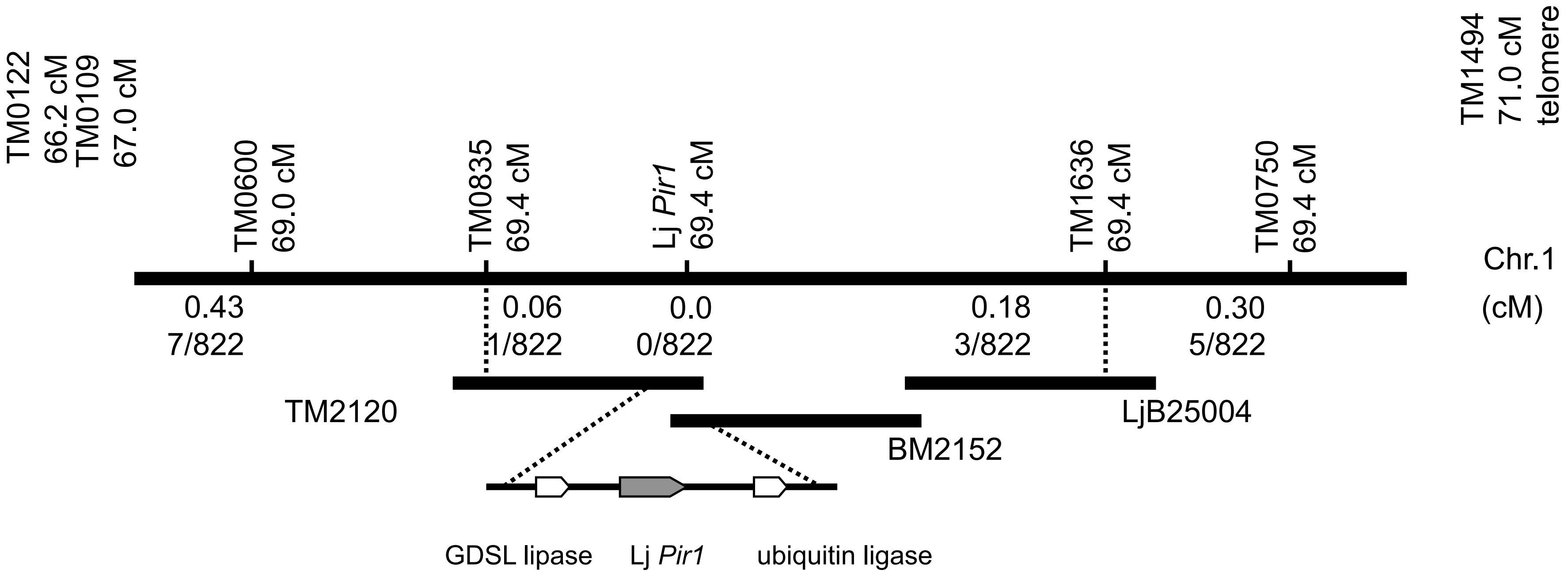
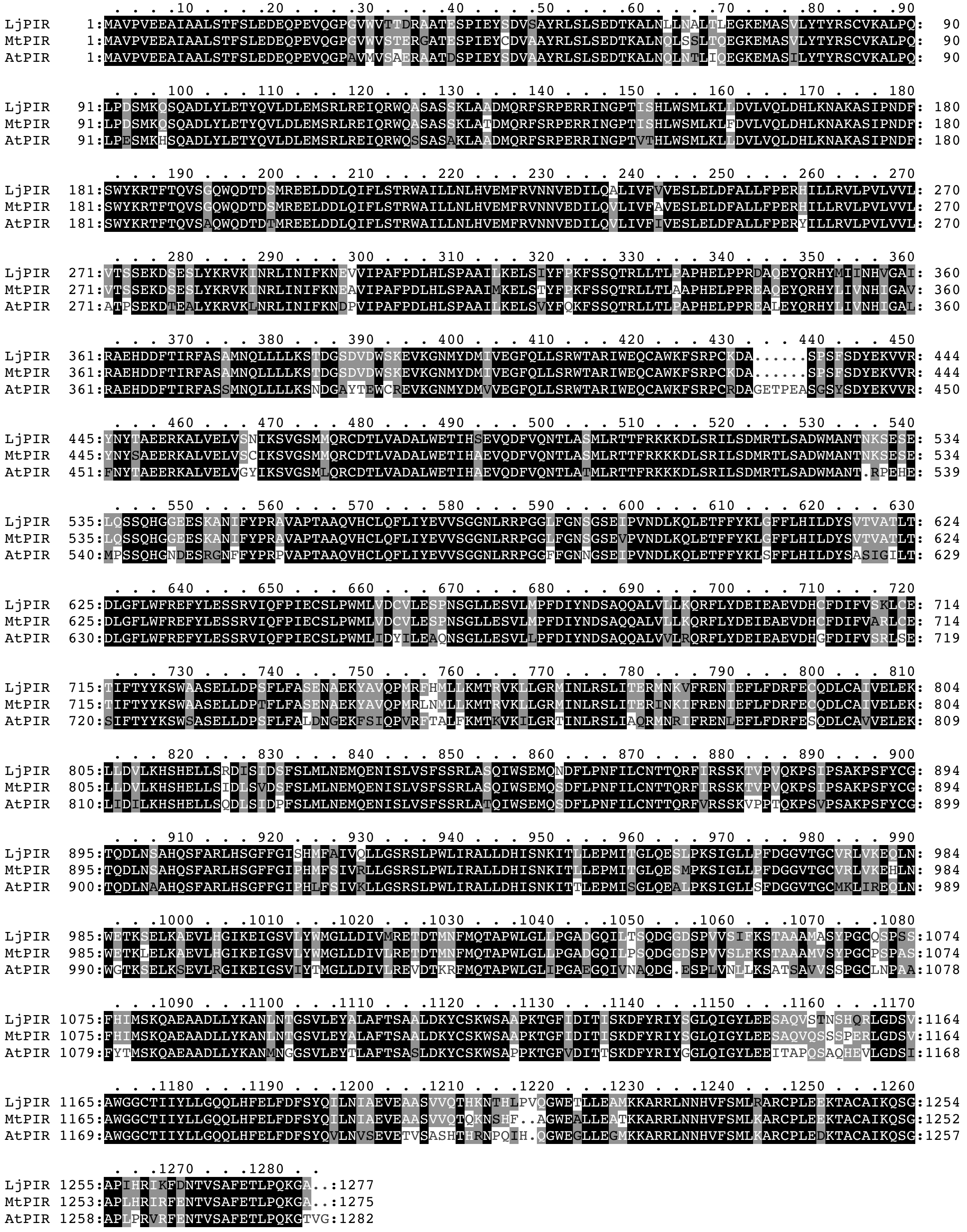
Supplemental figure 2. Alignment of *Lotus japonicus*, *Medicago truncatula* and *Arabidopsis thaliana* NAP proteins. *Lotus japonicus* sequence based on BP052201, but modified according to alternative splicing in other cDNAs. *Medicago truncatula* sequence based on AC147481 genome sequence with predicted amino acid sequence ABN0489.1 + ABN04850.1. In agreement with exon intron border sequences for Lotus and Arabidopsis, the amino acid sequence ILNYSIHSTMQ was removed from the predicted amino acid sequence ABN04850.1. The *Arabidopsis thaliana* sequence corresponds to AY496700.

Map based cloning of Lj *Pir1*



Supplemental Figure 3. The genomic region surrounding Lj *Pir1* on linkage group 1 is shown with cM position. The cM distance to adjacent microsatellite markers, the fraction of recombinant plants and the BAC (BM)/TAC (TM) contig are indicated. Only the end sequences are known for BAC clone LjB25O04. Two genes flanking Lj *Pir1* are shown.



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            . . . .10 . . . .20 . . . .30 . . . .40 . . . .50 . . . .60 . . . .70 . . . .80 . . . .90
LjPIR    1:MAVPVEEAIAALSTFSLEDEQPEVQGPGVWVTTDRAATESPIEYSDVSAYRLSLSEDTKALNLLNALTLEGKEMASVLYTYRSCVKALPQ:  90
MtPIR    1:MAVPVEEAIAALSTFSLEDEQPEVQGPGVWVSTERGATESPIEYCDVAAYRLSLSEDTKALNQLSSLTQEGKEMASVLYTYRSCVKALPQ:  90
AtPIR    1:MAVPVEEAIAALSTFSLEDEQPEVQGPAVMVSAERAATDSPIEYSDVAAYRLSLSEDTKALNQLNTLIQEGKEMASILYTYRSCVKALPQ:  90

            . . . 100 . . . 110 . . . 120 . . . 130 . . . 140 . . . 150 . . . 160 . . . 170 . . . 180
LjPIR   91:LPDSMKQSQADLYLETYQVLDLEMSRLREIQRWQASASSKLAADMQRFSRPERRINGPTISHLWSMLKLLDVLVQLDHLKNAKASIPNDF: 180
MtPIR   91:LPDSMKQSQADLYLETYQVLDLEMSRLREIQRWQASASSKLATDMQRFSRPERRINGPTISHLWSMLKLFDVLVQLDHLKNAKASIPNDF: 180
AtPIR   91:LPESMKHSQADLYLETYQVLDLEMSRLREIQRWQSSASAKLAADMQRFSRPERRINGPTVTHLWSMLKLLDVLVQLDHLKNAKASIPNDF: 180

            . . . 190 . . . 200 . . . 210 . . . 220 . . . 230 . . . 240 . . . 250 . . . 260 . . . 270
LjPIR  181:SWYKRTFTQVSGQWQDTDSMREELDDLQIFLSTRWAILLNLHVEMFRVNNVEDILQALIVFVVESLELDFALLFPERHILLRVLPVLVVL: 270
MtPIR  181:SWYKRTFTQVSGQWQDTDSMREELDDLQIFLSTRWAILLNLHVEMFRVNNVEDILQVLIVFAVESLELDFALLFPERHILLRVLPVLVVL: 270
AtPIR  181:SWYKRTFTQVSAQWQDTDTMREELDDLQIFLSTRWAILLNLHVEMFRVNNVEDILQVLIVFIVESLELDFALLFPERYILLRVLPVLVVL: 270

            . . . 280 . . . 290 . . . 300 . . . 310 . . . 320 . . . 330 . . . 340 . . . 350 . . . 360
LjPIR  271:VTSSEKDSESLYKRVKINRLINIFKNEVVIPAFPDLHLSPAAILKELSIYFPKFSSQTRLLTLPAPHELPPRDAQEYQRHYMIINHVGAI: 360
MtPIR  271:VTSSEKDSESLYKRVKINRLINIFKNEAVIPAFPDLHLSPAAIMKELSTYFPKFSSQTRLLTLAAPHELPPREAQEYQRHYLIVNHIGAV: 360
AtPIR  271:ATPSEKDTEALYKRVKLNRLINIFKNDPVIPAFPDLHLSPAAILKELSVYFQKFSSQTRLLTLPAPHELPPREALEYQRHYLIVNHIGAL: 360

            . . . 370 . . . 380 . . . 390 . . . 400 . . . 410 . . . 420 . . . 430 . . . 440 . . . 450
LjPIR  361:RAEHDDFTIRFASAMNQLLLLKSTDGSDVDWSKEVKGNMYDMIVEGFQLLSRWTARIWEQCAWKFSRPCKDA......SPSFSDYEKVVR: 444
MtPIR  361:RAEHDDFTIRFASAMNQLLLLKSTDGSDVDWSKEVKGNMYDMIVEGFQLLSRWTARIWEQCAWKFSRPCKDA......SPSFSDYEKVVR: 444
AtPIR  361:RAEHDDFTIRFASSMNQLLLLKSNDGAYTEWCREVKGNMYDMVVEGFQLLSRWTARIWEQCAWKFSRPCRDAGETPEASGSYSDYEKVVR: 450

            . . . 460 . . . 470 . . . 480 . . . 490 . . . 500 . . . 510 . . . 520 . . . 530 . . . 540
LjPIR  445:YNYTAEERKALVELVSNIKSVGSMMQRCDTLVADALWETIHSEVQDFVQNTLASMLRTTFRKKKDLSRILSDMRTLSADWMANTNKSESE: 534
MtPIR  445:YNYSAEERKALVELVSCIKSVGSMMQRCDTLVADALWETIHAEVQDFVQNTLASMLRTTFRKKKDLSRILSDMRTLSADWMANTNKSESE: 534
AtPIR  451:FNYTAEERKALVELVGYIKSVGSMLQRCDTLVADALWETIHAEVQDFVQNTLATMLRTTFRKKKDLSRILSDMRTLSADWMANT.RPEHE: 539

            . . . 550 . . . 560 . . . 570 . . . 580 . . . 590 . . . 600 . . . 610 . . . 620 . . . 630
LjPIR  535:LQSSQHGGEESKANIFYPRAVAPTAAQVHCLQFLIYEVVSGGNLRRPGGLFGNSGSEIPVNDLKQLETFFYKLGFFLHILDYSVTVATLT: 624
MtPIR  535:LQSSQHGGEESKANIFYPRAVAPTAAQVHCLQFLIYEVVSGGNLRRPGGLFGNSGSEVPVNDLKQLETFFYKLGFFLHILDYSVTVATLT: 624
AtPIR  540:MPSSQHGNDESRGNFFYPRPVAPTAAQVHCLQFLIYEVVSGGNLRRPGGFFGNNGSEIPVNDLKQLETFFYKLSFFLHILDYSASIGILT: 629

            . . . 640 . . . 650 . . . 660 . . . 670 . . . 680 . . . 690 . . . 700 . . . 710 . . . 720
LjPIR  625:DLGFLWFREFYLESSRVIQFPIECSLPWMLVDCVLESPNSGLLESVLMPFDIYNDSAQQALVLLKQRFLYDEIEAEVDHCFDIFVSKLCE: 714
MtPIR  625:DLGFLWFREFYLESSRVIQFPIECSLPWMLVDCVLESPNSGLLESVLMPFDIYNDSAQQALVLLKQRFLYDEIEAEVDHCFDIFVARLCE: 714
AtPIR  630:DLGFLWFREFYLESSRVIQFPIECSLPWMLIDYILEAQNSGLLESVLLPFDIYNDSAQQALVVLRQRFLYDEIEAEVDHGFDIFVSRLSE: 719

            . . . 730 . . . 740 . . . 750 . . . 760 . . . 770 . . . 780 . . . 790 . . . 800 . . . 810
LjPIR  715:TIFTYYKSWAASELLDPSFLFASENAEKYAVQPMRFHMLLKMTRVKLLGRMINLRSLITERMNKVFRENIEFLFDRFECQDLCAIVELEK: 804
MtPIR  715:TIFTYYKSWAASELLDPTFLFASENAEKYAVQPMRLNMLLKMTRVKLLGRMINLRSLITERINKIFRENIEFLFDRFECQDLCAIVELEK: 804
AtPIR  720:SIFTYYKSWSASELLDPSFLFALDNGEKFSIQPVRFTALFKMTKVKILGRTINLRSLIAQRMNRIFRENLEFLFDRFESQDLCAVVELEK: 809

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LjPIR  805:LLDVLKHSHELLSRDISIDSFSLMLNEMQENISLVSFSSRLASQIWSEMQNDFLPNFILCNTTQRFIRSSKTVPVQKPSIPSAKPSFYCG: 894
MtPIR  805:LLDVLKHSHELLSIDLSVDSFSLMLNEMQENISLVSFSSRLASQIWSEMQSDFLPNFILCNTTQRFIRSSKTVPVQKPSIPSAKPSFYCG: 894
AtPIR  810:LIDILKHSHELLSQDLSIDPFSLMLNEMQENISLVSFSSRLATQIWSEMQSDFLPNFILCNTTQRFVRSSKVPPTQKPSVPSAKPSFYCG: 899

            . . . 910 . . . 920 . . . 930 . . . 940 . . . 950 . . . 960 . . . 970 . . . 980 . . . 990
LjPIR  895:TQDLNSAHQSFARLHSGFFGISHMFAIVQLLGSRSLPWLIRALLDHISNKITLLEPMITGLQESLPKSIGLLPFDGGVTGCVRLVKEQLN: 984
MtPIR  895:TQDLNSAHQSFARLHSGFFGIPHMFSIVRLLGSRSLPWLIRALLDHISNKITLLEPMITGLQESMPKSIGLLPFDGGVTGCVRLVKEHLN: 984
AtPIR  900:TQDLNAAHQSFARLHSGFFGIPHLFSIVKLLGSRSLPWLIRALLDHISNKITTLEPMISGLQEALPKSIGLLSFDGGVTGCMKLIREQLN: 989

            . . .1000 . . .1010 . . .1020 . . .1030 . . .1040 . . .1050 . . .1060 . . .1070 . . .1080
LjPIR  985:WETKSELKAEVLHGIKEIGSVLYWMGLLDIVMRETDTMNFMQTAPWLGLLPGADGQILTSQDGGDSPVVSIFKSTAAAMASYPGCQSPSS:1074
MtPIR  985:WETKLELKAEVLHGIKEIGSVLYWMGLLDIVLRETDTMNFMQTAPWLGLLPGADGQILPSQDGGDSPVVSLFKSTAAAMVSYPGCPSPAS:1074
AtPIR  990:WGTKSELKSEVLRGIKEIGSVIYTMGLLDIVLREVDTKRFMQTAPWLGLIPGAEGQIVNAQDG.ESPLVNLLKSATSAVVSSPGCLNPAA:1078

            . . .1090 . . .1100 . . .1110 . . .1120 . . .1130 . . .1140 . . .1150 . . .1160 . . .1170
LjPIR 1075:FHIMSKQAEAADLLYKANLNTGSVLEYALAFTSAALDKYCSKWSAAPKTGFIDITISKDFYRIYSGLQIGYLEESAQVSTNSHQRLGDSV:1164
MtPIR 1075:FHIMSKQAEAADLLYKANLNTGSVLEYALAFTSAALDKYCSKWSAAPKTGFIDITISKDFYRIYSGLQIGYLEESAQVQSSSPERLGDSV:1164
AtPIR 1079:FYTMSKQAEAADLLYKANMNGGSVLEYTLAFTSASLDKYCSKWSAPPKTGFVDITTSKDFYRIYGGLQIGYLEEITAPQSAQHEVLGDSI:1168

            . . .1180 . . .1190 . . .1200 . . .1210 . . .1220 . . .1230 . . .1240 . . .1250 . . .1260
LjPIR 1165:AWGGCTIIYLLGQQLHFELFDFSYQILNIAEVEAASVVQTHKNTHLPVQGWETLLEAMKKARRLNNHVFSMLRARCPLEEKTACAIKQSG:1254
MtPIR 1165:AWGGCTIIYLLGQQLHFELFDFSYQILNIAEVEAASVVQTQKNSHF..AGWEALLEATKKARRLNNHVFSMLKARCPLEEKTACAIKQSG:1252
AtPIR 1169:AWGGCTIIYLLGQQLHFELFDFSYQVLNVSEVETVSASHTHRNPQIH.QGWEGLLEGMKKARRLNNHVFSMLKARCPLEDKTACAIKQSG:1257

            . . .1270 . . .1280 . .
LjPIR 1255:APIHRIKFDNTVSAFETLPQKGA..:1277
MtPIR 1253:APLHRIRFENTVSAFETLPQKGA..:1275
AtPIR 1258:APLPRVRFENTVSAFETLPQKGTVG:1282
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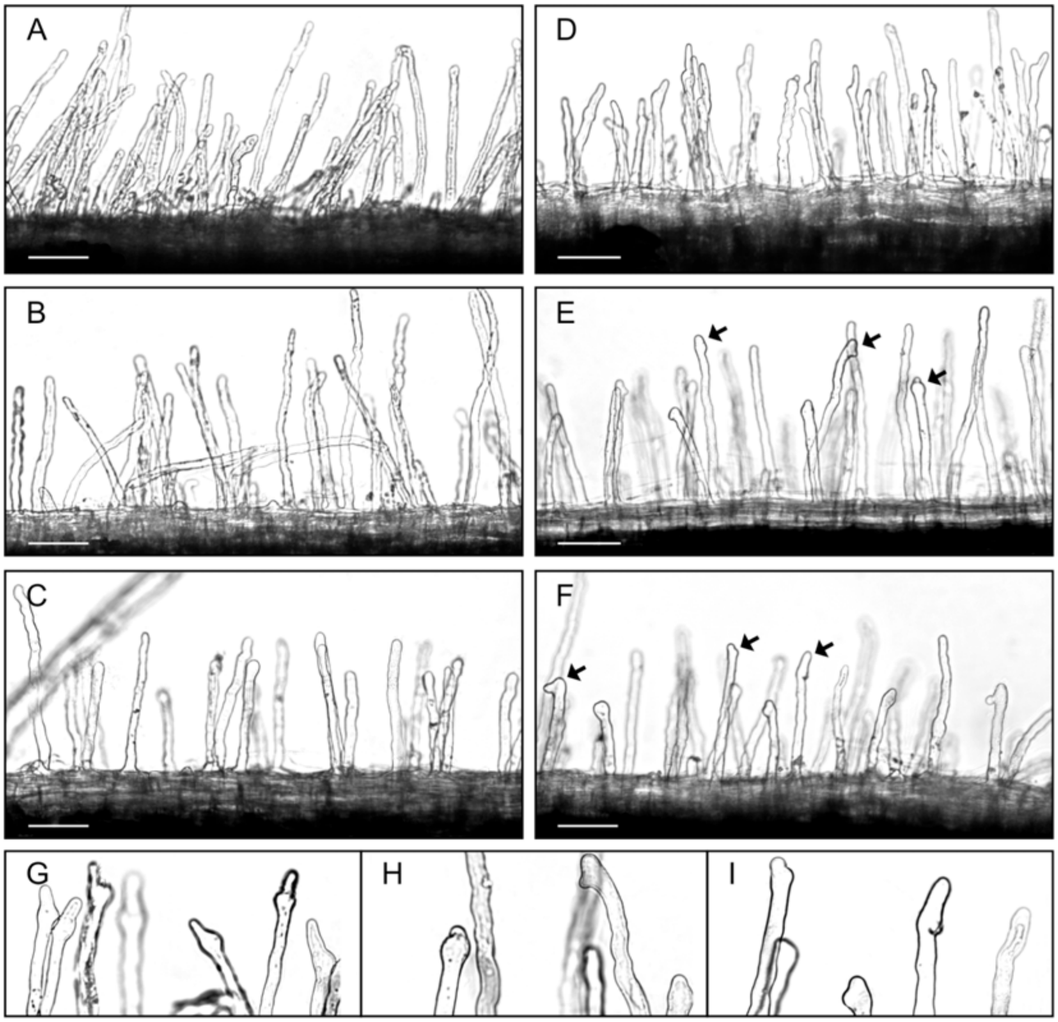
Supplemental Figure 4. Alignment of *Lotus japonicus*, *Medicago truncatula* and *Arabidopsis thaliana* PIR proteins. Lj PIR and At PIR (AAS78644.1) are based on full length cDNA sequences and Mt PIR is based on the genome sequence (AC146587) and EST sequence AW697392, tentative clusters TC110992, TC108945 and TC98507 and alignment of exons with Lj *Pir* and At *Pir*.



Supplemental Figure 5

Root hair deformations in *Lotus japonicus* wild-type and *nap1-1* and *pir1-1* mutants.

2 day old wild type Gifu (**A** and **D**), *nap1-1* (**B** and **E**), and *pir1-1* (**C** and **F**) seedlings were incubated in the absence (**A**, **B**, and **C**) or presence (**D**, **E**, and **F**) of the *M. loti* nodulation (Nod) factor (approx. 10 nM).

The root hair responses were scored and photographed 16 hours after Nod factor addition.

Panels **G**, **H,** and **I** represent close-ups of root hair deformations shown in **D**, **E**, and **F**, respectively.

Scale bars: 100μm.