

APPENDIX A: Solutions

CTAB Extraction Buffer (Stewart and Via, 1993)

2 % (w/v) of CTAB

100 mM of Tris-HCl pH 8.0

1.4 M of NaCl

20mM EDTA

0.2 % (v/v) of β -mercaptoethanol

Total RNA Extraction Buffer (Gao *et al.*, 2001)

200 mM of Tris-HCl pH 8.2

100 mM of LiCl

50 mM of EDTA

1.5 % (w/v) of SDS

2 % (w/v) of PVP

2 % (w/v) of BSA

10 mM of DTT

APPENDIX B: Amino Acid Sequences of Putative *RPK1* and Putative *CLV1*

>Oruf_RPK1

MAGVVTRAVAAAVLVVVVVVAAAELVAAEPPPSERSALLAFLAATPHERRLGWNSSTSACGWVGVTCDAGNATVVQ
VRLPGVGLIGAIPPGTLGRLTNLQVLSLRNRLGGIPDDVLQLPQLRLLFLQNNLLSGAIPPEVSKLAALERLVL
SSNNLSGPIPFITLNNLTSRLALRLDGNKLSGNIPSISIQSLAVFNVDNNLNGSIPASLASFPAEDFAGNLQLCGS
PLPPCKSFFPSPSPSPGVSPADVPGAASSSKRRRLSGAAIAGIVVGAVVLALLLVAAVLCVSKRRRGASEGPKS
TTAAAAGAGAAAARGVPPPGSGEGTGMTSSSKEDMGASGSAAAABAABAAPSRLVFGKGAGYSFDLEDLLRAS
AEVLGKGSVGTSTYKAVLEEGTTVVVKRLKDVAVARREFDAHMDALGKVEHRNVLPVRAYYFSKDEKLLVFDYLPNG
SLSAMLHSGRSGKTPLDWDARMRSALSAARGLARLHTVHSLVHGNVKSSNVLLRPDADAAALSDFCLHPIFAPSS
ARPGAGGYRAPEVVDTRRPTYKADVSLGVLLLELLTGKSPTHASLEGDGTLDLPRWVQSVVREEWTAEVFDVELV
RLGASAEEMVALLQVAMACVATVPDARPDAPDVVRMIEEIGGGHGRTTTEESEEGVRGTSEEERSRGTPPAAPT

>OsJ_RPK1(gi|53792194)

MAGVVTRAVAAAVLVVVVVVAAAELVAAEPPPSERSALLAFLAATPHERRLGWNSSTSACGWVGVTCDAGNATVVQ
VRLPGVGLIGAIPPGTLGRLTNLQVLSLRNRLGGIPDDVLQLPQLRLLFLQNNLLSGAIPPAVSKLAALERLVL
SSNNLSGPIPFITLNNLTSRLALRLDGNKLSGNIPSISIQSLVFNVDNNLNGSIPASLARFPAEDFAGNLQLCGS
PLPPCKSFFPSPSPSPGVSPADVPGAASSSKRRRLSGAAIAGIVVGAVVLALLLVAAVLCVSKRRRGASEGPKS
TTAAAAGAGAAAARGVPPPGSGEGTGMTSSSKEDMGASGSAAAABAABAAPSRLVFGKGAGYSFDLEDLLRAS
AEVLGKGSVGTSTYKAVLEEGTTVVVKRLKDVAVARREFDAHMDALGKVEHRNVLPVRAYYFSKDEKLLVFDYLPNG
SLSAMLHSGRSGKTPLDWDARMRSALSAARGLAHLHTVHSLVHGNVKSSNVLLRPDADAAALSDFCLHPIFAPSS
ARPGAGGYRAPEVVDTRRPTYKADVSLGVLLLELLTGKSPTHASLEGDGTLDLPRWVQSVVREEWTAEVFDVELV
RLGASAEEMVALLQVAMACVATVPDARPDAPDVVRMIEEIGGGHGRTTTEESEEGVRGTSEEERSRGTPPAAPT

>OsI_RPK1

MAGVVTRAVAAAVLVVVVVVAAAELVAAEPPPSERSALLAFLAATPHERRLGWNSSTSACGWVGVTCDAGNATVVQ
VRLPGVGLIGAIPPGTLGRLTNLQVLSLRNRLGGIPDDVLQLPQLRLLFLQNNLLSGAIPPAVSKLAALERLVL
SSNNLSGPIPFITLNNLTSRLALRLDGNKLSGNIPSISIQSLAVFNVDNNLNGSIPASLARFPAEDFAGNLQLCGS
PLPPCKSFFPSPSPSPGVSPADVPGAASSSKRRRLSGAAIAGIVVGAVVLALLLVAAVLCVSKRRRGASEGPKS
TTAAAAGAGAAAARGVPPPGSGEGTGMTSSSKEDMGASGSAAAABAABAAPSRLVFGKGAGYSFDLEDLLRAS
AEVLGKGSVGTSTYKAVLEEGTTVVVKRLKDVAVARREFDAHMDALGKVEHRNVLPVRAYYFSKDEKLLVFDYLPNG
SLSAMLHSGRSGKTPLDWDAQMRSAALSAARGLAHLHTVHSLVHGNVKSSNVLLRPDADAAALSDFCLHPIFAPSS
ARPGAGGYRAPEVVDTRRPTYKADVSLGVLLLELLTGKSPTHASLEGDGTLDLPRWVQSVVREEWTAEVFDVELV
RLGASAEEMVALLQVAMACVATVPDARPDAPDVVRMIEEIGGGHGRTTTEESEEGVRGTSEEERSRGTPPAAPT

>OsJ_CLV1(gi:125602183)

MAAAAVHVLALLPLATITSASSAPLPLALLSLRSSLGDPAGALRSWTYAAAASAGATRSLAPPWCAWPGVACDG
ATGEVVGVDLSRRNLSGTVSPTAARLLSPTLTSNLNLSGNAFAGELPPAVLLLRLVALDVSHNFFNSTFPDGIKAL
GSLAFLDAFSNCFVGELPRGIGELRRLEHLNLGGSFFNGSIPGEVGQLRRLRFLHLAGNALSGRLPRELGELTSVE
HLEIGYNAYDGGIPPEFGKMAQLRYLDIAAANVSGPLPELGELTRLESFLFKNRIAGAIPPRWSRLRALQVLDV
SDNHLAGAIPAGLGELTNLTTLNLSNLSGTIPAAIGALPSLEVLQLWNNSLAGRLPESLGASRRLVRDLVSTNS
LSGPIPPGVCAGNRLARLILFDNRFDASIPASLADCSSLWRVRLEANRLSGEIPAGFGAIRNLTYMDLSSNSLTGG
GIPADLVASPSLEYFNVSGLVGGALPDMAWRGPKLQVFAASRCGLVGELPAFGATGCANLYRLELAGNALGGGIP
GDIGSCKRLVSLRLQHNETGEIPAAIAALPSITEVDLSWNALTGTVPFGFTNCTTLETDFVSNHLAPAEPSSDA

GERGSPARHTAAMWVPAVAVAFAGMVVLGATARWLQWRGGDDTAAADALGPGGARHPDLVVGWPWRMTAFQRLSFTA
DDVARCVESDGIAGAGSSGTVYRAKMPNGEVIKVLWQAPAAQKEAAAPTEQNQKLQDSDGGGGGKRTVAEVE
VLGHLRHRNIVRLLGWCTNGESTMLLYEYMPNGSLDELLHGAAAKARPGWDARYKIAVGVAQGVSYLHHDCLPAIA
HRDIKPSNILLDDMEARVADFGVAKALQSAAPMSVAGSCGYIAPEYTYTLKVNEKSDVYSFGVVLLEILTGRRS
VEAEYEGGNNIVDWVRRKVAGGGVGDVIDAAAWADNDVGGTRDEMALARVALLCTSRCPQERPSMREVL SMLQEA
RPKRKNSAKKQVK

>RKN(W0/2000/004761)

MPQPQCTTTATTFPASILPPPPPPPTTSTTSATAMAAAHVLLLLLPLATITSASSAPLPLLALLSLRSSLGDP
GALLRSWTYAAAASAGATRSLAPPWCAWPGVACDGTGEVGVLDLRRNLSGTVSPTAARLLSPTLTSLNLSGNGS
PASSRRVLLLRRLVALDVSHNFFNSTFPDGIKLGGAFLDAFSNCFVGELPRGIGELRRLEHLNLGGSFFNGSIP
GEVQQLRRLRFLHLAGNRLSGRLPRELGELTSVEHLEIGYNAYDGGIPEFGKMAQLRYLDIAAANVSGPVPELLG
LTRLESFLFKNRIGRRDPPRWSRLRALQVLDVSDNHLAGAIPALGELTNLTTLNLSNLSGTIPAAIGALPSLE
VLQLWNNSLAGRLPESLGASRRRLVRLDVSTNSLSGPIPPGVCAGNRLARLILFDNRFD SAIPASLADCSSLWRVRL
EANSLSGEIPAGFGAIRNLTYMDLSSNSLTGGGIPADLVASPSLEYFNVSGNLVGRPLPDMAWRGPKLQVFAASRC
GLVGELPAFGATGCANLYRLELAGNALGGGIPGDIGSCKRLVSLRLQHNELTGEIPAAIALPSITEVDLSGTRSPA
PSAGVHQLHDVETFDVSFNHLAPAEPSSDAGERGSPRGTTRRCGCPPWRCAFAGMVVLGATARWLQWRGGDDTAAA
DARGPGGARHPDLVVGWPWRMTAFQRLSFTADDVPRC VEGSDGVGAGSSGTVYRAKMPNGEVIKVLWQAAAQKEA
AAPTEQNQKLQDSDGGGGGKRTVAEVEVLGHLRHRNIVRLLGWCTNGESTMLLYEYMPNGSLDELLHARAKAPRA
GTPGTRSPSVAQGVSYLHHDCLPAIAHRDIKPSNILLSTTTWRHALADFGVAKALQSAAPMSVAGSCGYIAPEYTY
TLKVNEKSDVYSFGVVLLEILTGRRSVEAEYEGGNNIVDWVRRKVAGGGVGDVIDAAAWADNDVGGTRDEMALARG
WRCCHQVPVQERPSMREVL SMLQEAPRKRKNSAKKQVKZ

>OsI_CLV1

VNEKSDVYSFGVVLLEILTGRRSVEAEYEGGNNIVDWVRRKVAGGGVGDVIDAAAWADNDVGGTRDEMALARVAL
LCTSRCPQERPSMREVL SMLQEAPRKRKNSAKKQVK

>Oruf_CLV1

VNEKSDVYSFGVVLLEILTGRRSVEAEYEGGNNIVDWVRRKVAGGGVGDVIDAAAWADNDVGGTRDEMALARVAL
LCTSRCPQERPSMREVL SMLQEAPRKNSAKKQVK

APPENDIX C: Gblocks Cleaned of Orthologous RPK1 Amino Acid Sequences

>At_RKL1(At1g48480)

RVTALRLPGVALSGDIPEGIFLTQLRTLRLNLSGSLPKDLSTSSNLRHLYLQGNRFSGEIPLVRLNLASNSFTGEISS
GFTNLTLKTLFLENNQLSGSIPLNGSIPKNLQRFESDSFLQFDLEDLLRASAEVLGKGTGTAYKAVLDAVTVVAVKRLK
DVMMADEKFEKIELVGHENLVPLRAYYFSRDEKLLVYDFMPMGSLSALLHGNGRSPLNWDVRSRIAIGAARGLDYLHH
GNIKSSNILLTKSHDAGYRAPEVTDPKRVSQKGDVYSFGVVLELLITGKAPDLPRWVKSVARDEWRREVFDSSELLSEMA
EMVQLGLECTSQHDPQRPEMSEVVRKME

>At_RLK902(At3g17840)

RVTALRLPGETLSGHIPEGIFLTQLRTLRLNLTGSLPLDLGSCSDLRRLYLQGNRFSGEIPLVRLNLAENEFSGEISS
GFKNLTLKTLYLENNKLSGSLLLNGSIPKSLQKFDSDSFVGFLEDLLRASAEVLGKGTGTAYKAVLDAVTLVAVKRLK
DVTMADREFKEKIEVVGHENLVPLRAYYSGDEKLLVYDFMPMGSLSALLHGNGRPPNWEVRSIALGAARGLDYLHH
GNVKSNNILLTNSHDAGYRAPEVTDPRRVSQKADVYSFGVVLELLITGKAPDLARWVHSVAREEWRNEVFDSSELMSEMA
EMLQLGIDCTEQHPDKRPVMVEVVRRIQ

>At_TMKL1(_At3g24660)

SPLQCSDLSSPQWTNTSLFNDLHLLSLQLPSANLTGSLPREIGFESMLQSVFLNINSLSGSIPLSDVDLSGNALAGVLP
SIWNLCLVSFKIHGNNLSGVLFPFSGEFPEFITRFKGVKSLDLTDDVLNATGQVMEKTSYGTVYKAKLSDGGNIALRLR
EGTCKDRSSCLPVIRQLHENLVPLRAFYQKGKELLIIYDLPNISLHDLHESKRKPALNWARRHKIALGIARGLAYLHH
GNIRSKNVLDFFFAGYKAPELHKMKCNPRSDVYAFGILLLEILMGKKPDLPSLVKAAVLEETTMEVFDLEAMKEGLV
HALKLAMGCCAPVTTVRPSMEEVVKQLE

>OsJ_MARK(gi|108710729)

RVAVLRLPGAALAGRVPEGTLLTALHTLSRLNLGALPGDLTSAALRNVLNGNRLSGEFPLVRLAIGGNDLSGSIPP
ALGNLTLKVLLLENNRFSGEIPLNGSIPATLRTMPRSAFLGFDLEDLLRASAEVLGKGAFGTTYKAVLESATVAVKRLK
DVTLTEPEFRDRIADIGHEFIVPLRAYYYSKDEKLLVYDFMPMGSLSAVLHGNGRGTPLNWETRSSIALAAARGVEYIHH
GNIKSSNVLLNKSQYAGYRAPEVTDPRRVSQKADVYSFGVLLLELLITGKAPDLPRWVQSVVRSEWTAEVFDMELLREQMV
QLLQLAIDCVAQVPDARPSMPHVVLRIE

>Zm_MARK(gi|162459881)

RVAVLRLPGATLSGAVPAGTLLTALHTLSRLNLGALPADLASAAALRNVLNGNRLSGGFPLVRLSLGGNDLSGPIPA
ELGSLTLRVLLLENNRFSGEISLNGSIPASLRSQPRSAFLGFDLEDLLRASAEVLGKGAFGTTYKAVLESATVAVKRLK
DVTLSEAEFRERISEIGHEFIVPLRAYYYSKDEKLLVYDFMPMGSLSAVLHGNGRGTPLNWDLRSSIALAAARGVEYIHH
GNIKSSNVLLGKSQYAGYRAPEVIDSRVSQKADVYSFGVLLLELVTKAPDLPRWQSVNRSEWGSVDFMELMREPM
QLVLLAMDCTAQVPEARPSMAHVVMRIE

>At_TMK(At5g58300)

SVHALRLPGIGLLGPIPPNTLLESLRILSLRNLSGNLPPDIHSLPSLDYIYLQHNNFSGEVPLNILDLSFNSFTGKIPA
TFQNLKLTGLSLQNNKLSGPVPLNGSIPSALGGFPSSSFSGFDLEDLLRASAEVLGKGSYGTAYKAVLEESTTVVVKRLK
EVAAGKREFEQQMEIISHPSVPLRAYYYSKDEKLMVCDDYPAGNLSLLHGNGREKTPLDWDSRVKITLSAAKGIAHLHH
GNIKSSNVIMKQESDAGYRAPEVMETRKHTHKSVDVYSFGVLLILEMLTGKSPDLPRWQSVVREWTSEVFDIELMREEMV
QMLQIAMACVAQVPEVRPTMDDVVRMIE

>At_RLK(At4g23740)

RIIAVRLPGVGLNGQIPPNTILSALRVLSLRNSISGEFPKDFVELKDLAFLYLQDNNLSGPLPLTSVNLSNNGFNGTIPS
SLSRLKIQSLNLANNTLSGDIPLAGIPDWLRRFPFSSYTGFDEDLRASAIEVLGKGTGFTTYKAVLEDATSVAVKRLK
DVAAGKRDFEQMEIIGHENVVELKAYYYSKDEKLMVYDYFSRGSVASLLHGNRNRIPLDWETRMKIAIGAAGKGIARIHH
GNIKSSNIFLNSESNNGYRAPEVTDTRKSSQLSDVYSFGVVLLELLTGKSPHLVRWVHSVVEEWTAIEVFDIELLREEMV
EMLQIAMSCVVKAADQRPKMSDLVRLIE

>At_LRR1(At5g16590)

RVTALRLPGVGLSGPLPIAIGLTKLETLSFRFNNGPLPPDFANLTLLRYLYLQGNFSGEIPPIIRINLAQNNFLGRIPD
NVNSATLATLYLQDNQLTGPIPLNGSIPDPLSGMPKTAFLGFDLDGLLKASAIEVLGKGTGSSYKASFDHGLVVAVKRLR
DVVPEKEFREKLQVLGHANLVTLIAYYFSRDEKLVVFEYMSRGSLSALLHGNKGRSPLNWETRANIALGAARAIISYLHH
GNIKSSNILLSSEFEAGYRAPEVTDARKISQKADVYSFGVLILELLTGKSPDLPRWVSSITEQQSPSDVFDPELTRENMI
RLLNIGISCTTQYPDSRPTMPEVTRLIE

>Oruf_RPK1

TVVQVRLPGVGLIGAIPPGTLLTNLQVLSLRSNILGGIPDDVLQPLQLRLLFLQNNLLSGAIPLERLVSSNNLSGPIPF
TLNNLTLRALRLDGNKLSGNIPLNGSIPASLASFPAEDFAGFDLEDLLRASAIEVLGKGSVGTSTYKAVLEEGETTVVVKRLK
DVAVARREFDAHMDALGHRNVLPVRAYYFSKDEKLLVFDYLPNGSLSAMLHGSRGKTPLDWDARMRSALSAARGLARLHH
GNVKSSNVLLRPDADAGYRAPEVVDTRRPTYKADVYSLGVLLLELLTGKSPDLPRWVQSVVREEWTAIEVFDVELVREEMV
ALLQVAMACVATVPDARPDAPDVVRMIE

>OsJ_RPK1(gi|53792194)

TVVQVRLPGVGLIGAIPPGTLLTNLQVLSLRSNILGGIPDDVLQPLQLRLLFLQNNLLSGAIPLERLVSSNNLSGPIPF
TLNNLTLRALRLDGNKLSGNIPLNGSIPASLARFPAEDFAGFDLEDLLRASAIEVLGKGSVGTSTYKAVLEEGETTVVVKRLK
DVAVARREFDAHMDALGHRNVLPVRAYYFSKDEKLLVFDYLPNGSLSAMLHGSRGKTPLDWDARMRSALSAARGLAHLHH
GNVKSSNVLLRPDADAGYRAPEVVDTRRPTYKADVYSLGVLLLELLTGKSPDLPRWVQSVVREEWTAIEVFDVELVREEMV
ALLQVAMACVATVPDARPDAPDVVRMIE

>OsI_RPK1

TVVQVRLPGVGLIGAIPPGTLLTNLQVLSLRSNILGGIPDDVLQPLQLRLLFLQNNLLSGAIPLERLVSSNNLSGPIPF
TLNNLTLRALRLDGNKLSGNIPLNGSIPASLARFPAEDFAGFDLEDLLRASAIEVLGKGSVGTSTYKAVLEEGETTVVVKRLK
DVAVARREFDAHMDALGHRNVLPVRAYYFSKDEKLLVFDYLPNGSLSAMLHGSRGKTPLDWDQMRSAALSAARGLAHLHH
GNVKSSNVLLRPDADAGYRAPEVVDTRRPTYKADVYSLGVLLLELLTGKSPDLPRWVQSVVREEWTAIEVFDVELVREEMV
ALLQVAMACVATVPDARPDAPDVVRMIE

>OsJ_RLL_1(gi|7573610)

RVVALRLPGLGSGVPVPRGTLLTALQVLSLRANLSGEFPEELSLASLTGLHLQLNAFSGALPLQVLDLSFNNGFNGTLPA
ALSNTLTVALNLSNNSLSGRVPLDGPVPTSLLRFNDTAFAGFDLEDLLRASAIEVLGKGAFGTAYRAVEDATTVVVKRLK
EVSAGRRDFEQMELVGHANVAELRAYYYSKDEKLLVYDYFSRGSVSNMLHGKRDRTPLNWETRVRIALGAARGIAHIIHH
GNIKASNVLNNQYGGYCAPEVTDNRKASQCSDVYSFGVFILELLTGRSPHLVRWVQSVVREEWTAIEVFDVELMREEMV
EMLQIAMACVSRTPERRPKMSDVVRMLE

>OsJ_RLL_2(gi|15128407)

RVQTLRLPAVGLFGPLPSDTLLDALEVLSLRSNITVDLPPEVGSIPSLHSLYLQHNNLSGIIPLTFDLSYNTFDGEIPL

RVQNLTLTALLQNNLSGPIPLSGPIPPSLQRFPA NSFLGFDLEDLLRASA EVLGKGSYGT TYKAVLEDGTTVVVKRLK
E V V V G K K D F E Q Q M E I V G H Q N V V P L R A Y Y Y S K D E K L L V Y D Y I P S G S L A V V L H G N K G K A P L D W E T R V K I S L G V A R G I A H L H H
G N L K S S N I L L S Q N L D G G Y R A P E V L E T K K P T Q K S D V Y S F G V L V L E M L T G K A P H L P R W Q S V V R E E W T A E V F D V D L L R D E M V
Q M L Q V A M A C V A A P P D Q R P K M D E V I R R I V

>O s J _ R L L _ 3 (g i | 115464509)

R V R E L R L P A V G L F G P I P S D T L L D A L Q V L S L R S N L T I S L P P D V A S I P S L H S L Y L Q H N N L S G I I P L T F L D L S Y N S F D G E I P L
K V Q N I T L T A L L Q N N S L S G P I P L S G P I P P S L Q K F P A S S F F G F D L E D L L R A S A E V L G K G S Y G T T Y K A V L E D G T T V V V K R L K
E V V A G K R E F E Q Q M E I I G H Q N A V Q L R A Y Y Y S K D E K L L V Y D Y M T P G S L C A A L H G N R G R T T L D W A T R V K I S L E A A R G I A H L H H
G N I K S S N I L L S Q G L S A G Y R A P E V L E T K R Q T Q K S D V Y S Y G V L L L E M L T G K A P H L P R W Q S V V R E E W T S E V F D A D L L R D E M V
Q M L Q L A M A C V A I V P D Q R P R M E E V V R R I E

APPENDIX D: Gblocks Cleaned of Orthologous CLV1 Amino Acid Sequences

>At_BAM1(At5g65700)

VTSLDLSGLNLSGNLSLAENLISGPPIPEISSLSGLRHLNLSNNLTQLRHLHLGGNYFAGKIPPSYGSWPVIEYLAVSGN
ELVGIGNLTTLRELFDGANCGLTGEIPPEIGKLQKLDTLFLQVNVFGTLSSLKSMDSLNNMFNKLHGEIPEFIGDLPELE
VLQLWENNFTGSIPQKLGLENLNLVDLSSNKLGTLPNMCSGNKLETITLGNFLFGSIPDSLKGKCESLTRIRMGENFLF
GLPKLTQVELQDNYLSGLGQISLSNNQLSGPLPPAIGNFVQKLLLDGNKFQGPINLFSGRIAPEISRCKLLTFVDLSRN
ELSGEIPGSIPGSISSMLTSLDFSNNLSGLVPMSSAIAGSYGYIAPEYAYTLKVDEKS

>At_BAM2(At3g49670)

AIRLNHSSIPVSVSLPFSVGDWRGVSTFSGARPLVLAKVKLRAELVDEEIVHFEERDFAGTACVPVYVMLPLGVIDMNSE
VVEPLDQLRTLKSMVMDCWWGIVESHTPQVYNWSGYKKLFQMIRELLKIQVMSFHECGGNVDDVHIQIPEWVREIGQSN
PDIYFTDSAGRNRTECLTWGIDKQRVLRGRTALEVYFDYMRSFVEFDEFEEKIPEIEVGLGPCGELRYPSPYAQFGW
KYPGIGEFQCYDKYLMNKEAAEVRGHSFWGRGPDNTETYSTPHGTGFFRDGGDYDNWYSRVLIDHGDRVLAMANLAFEGT
CIAAKLSHWYKTASHALTAGFYNNSSNRDGYGPERFLKRMHGEAVPDLGLAPGTQETN

>At_BAM3(At4g20270)

ITRLDLSNLNISGFLDISSNSFSGELPKEIYELSGLEVLNISSNLTRLEHLDLGGNYFDGEIPRSYGSFSLKFLSLSGN
DLRGLANITTLVQLLDLANCSLKGSIPAEGLNKNLEVLFLQTNELGNMTSLKTLDLSNNFLNRLHGEIPEFVSELPDLQ
ILKLWHNNFTGKIPSKLGSNLIEIDLSTNKLTLGIPESLCFGRRLKILILFNNFLFGPLPEDLGQCEPLWRFRLGQNFLI
YLPNLSLLELQNNFLTGLTQINLSNNRLSGPIPGSIRNLLQILLGANRLSGQIPNNFSGKFPPEFGDCMSLTYLDSLHN
QISGQIPQSLPNELGYMLTSAFSSHNNFSGSVPMSSAIAGSYGYIAPEYAYTLRIDEKS

>At_CLV1(At1g75820)

VISLNVSFPTPLFGNLTAAANNFTGELPLEMKSLTSLKVLNISNNLKKLYLSFGGNFFSGEIPESYGDIQSLEYLGLNGA
GLSGLSRLKNLREMLDMASCTLTGEIPTSLSNLKHHLTLFLHINNLSGLVSLKSLDLSINQLNNLYGQIPEAIGELPKLE
VFEVWENNFTLQLPANLGRNLIKLDVSDNHLTGLIPKDLCRGEKLEMLILSNNFFFGRPIPEELGKCKSLTKIRIVKNLLF
NLPLVTIIELTDNFFSGLDQIYLSNNWFSGEIPPAIGNFLQTLFLDRNRFRGNIPNNITGGIPDSISRCSTLISVDLSRN
RINGEIPGSIPTGIGNMLTTLDFNDLSGRVPMSSAIAGSYGYIAPEYAYTLKVDEKS

>Gm_CLL1(gi|25956280)

VVAINVSFVPLFGNLTVSQNNLTGVLPKELAALTSKHLNISHNLEKLYLKLDGNYFSGSIPESYSEFKSLEFLSLSTN
SLSGLSKLKTLYLLDLSSCNLSGEIPPSLANLTNLDTLFLQINNLSAMVSLMSLDLSINDLNNLRGSVPSFVGELPNLE
TLQLWDNNFSFVLPNGLQNLKFFDVIKNHFTGLIPRDLCCKSGRLQTIMITDNFFRGPIPEIGNCKSLTKIRASNNYLF
KLPSVTIIELANNRFNGLGILTLSSNNLFSGKIPPALKNLLQTLSDANEFVGEIPNNLTGPIPTTLTRCVSLTAVDLSRN
MLEGKIPGPVPEEIRFMLTTLDSLNNNFIGKVPMSAIAGSYGYIAPEYAYTLKVDEKS

>Gm_CLL2(gi|7329124)

VVAINVSFVPLFGNLTVSQNNLTGVLPKELAALTSKHLNISHNLEKLYLKLDGNYFSGSIPESYSEFKSLEFLSLSTN
SLSGLSKLKTLYLLDLSSCNLSGEIPPSLANLTNLDTLFLQINNLSAMVSLMSLDLSINDLNNLRGSVPSFVGELPNLE
TLQLWDNNFSFVLPNGLQNLKFFDVIKNHFTGLIPRDLCCKSGRLQTIMITDNFFRGPIPEIGNCKSLTKIRASNNYLF
KLPSVTIIELANNRFNGLGILTLSSNNLFSGKIPPALKNLLQTLSDANEFVGEIPNNLTGPIPTTLTRCVSLTAVDLSRN
MLEGKIPGPVPEEIRFMLTTLDSLNNNFIGKVPMSAIAGSYGYIAPEYAYTLKVDEKS

>Gm_CLL3(gi|9651943)

VTALNLTGLDLSGNLSLAANKFSGPIPPSLSALSGLRYLNLSNNMQNLRHLHLGGNFFSGQIPPEYGRWQRLQYLAVSGN
ELDGIGNLTSLRELLDVAAYCALSGEIPAALGKLQKLDTLFLQVNALGNLKSLSMDLSNNMLNKLHGAIPFIFIGELPALE
VVQLWENNLTGSIPEGLGKNLNLVDLSSNKLGTLPYLCSGNTLQTLITLGNFLFGPIPESLGTCESTRIRMGENFLF
GLPKLTQVELQDNYLSGLGQITLSNNQLSGALSPSIGNFVQKLLLDGNMFTGRIPNKFSGPIAPEISQCKLLTFLDLSRN
ELSGDIPGSIPSSISSMLTSVDFSYNLNSGLVPMSAIAAGSYGYIAPEYAYTLKVDEKS

>Gm_CLL4(gi|9651945)

VTSLDLTGLDLSGNLSLASNKFSGPIPPSLSALSGLRFLNLSNNMQNLRHLHLGGNFFSGQIPPEYGRWQRLQYLAVSGN
ELEGIGNLSSLRELLDAAYCGLSGEIPAALGKLQKLDTLFLQVNALGNLKSLSMDLSNNMLNKLHGAIPFIFIGELPALE
VVQLWENNLTGSIPEGLGKNLNLVDLSSNKLGTLPYLCSGNTLQTLITLGNFLFGPIPESLGSCESLIRMGENFLF
GLPKLTQVELQDNYLSGLGQITLSNNQLSGVLPPSIGNFVQKLLLDGNMFTGRIPNKFSGPIVPEISQCKLLTFLDLSRN
ELSGDIPGGIPSSISSMLTSVDFSYNLNSGLVPMSAIAAGSYGYIAPEYAYTLKVDEKS

>Mt_CLL1(gi|58372544)

VIALNVTQVPLFGSLTITMDNLTGELPTELSKLTSLRILNISHNLMKLKYL SFAGNFFSGTIPESYSEFQKLEILRLNYN
SLTGLSKLKMKELEISNANLTGEIPPSLGNLENLDSFLQMNLSMMSRSLMSDLSINGLNKLRGSIPAFIGDLPNLE
TLQWENNFSFVLPQNLSNFIYFDVTKNHLTGLIPPELCKSKKLTFTIVTDNFFRGPIPNIGPCKSLEKIRVANNYLF
QLPSVQIIELGNNRFNGLGNLALSNNLFTGRIPASMKNLLQTLLLDANQFLGEIPNNLTGGIPKTVTQCSSLTAVDFSRN
MLTGEVPGKIPDEIRFMTTLDLSYNNTGIVPMSSIAAGSYGYIAPEYAYTLKVDEKS

>OsJ_CLL1(gi|50726262)

VVGVDLSRRNLSGSLNLSGNAFAGELPPAVLLLRLVALDVSHNLRREHLNLGGSFNNGSIPGEVQQLRRLRFLHLAGN
ALSGLGELTSVEHLLDIAAANVSGLPPELGELTRLESFLFKNRISRLRALQVLDVSDNHLNLSLGTIPAAIGALPSLE
VLQLWNNLAGRLPESLGASLVRLDVSTNSLGPVPGVACGNRLARLILFDNRFDSAIPASLADCSSLWRVRLEANRLG
AIRNLTYMDLSSNSLTGLEIFYNVSIGNLVGGALPDMAWRGLQVFAASRCGLVGELPNALGGGIPGDIGSCKRLVSLRLQHN
ELTGEIPGTVPVPGFTNCLETDFVSFNLAPAEPSPRTATSSPATSSSTTTWRHASPTS

>OsJ_FON1(gi|113596633)

VVAINLTALPLHSNLTIAACCLPGHVPLEPTLPSLRHLNLSNNHARLYLHLGGNYFTGAIPDSYGDAALEYLGLNGN
TSLGSLRLTRLREMLDMSSCNLTGPVPELGRLQRLDTLFLQWNRLGDLSSLASLDLSVNDLNHLRGSIPDFVAGFAQLE
VLQLWNNLTGNIPAGLGKNLKTLDLATNHLTGPIPADLCAGRRLEMLVLMENGLFGPIPDSDLGCKTLTRVRLAKNFLF
NLPQANMVVELTDNLTGIGMLLLGNNIGGRIPPAIGNLLQTLLESNNFSGALPNALTGAIPDELIRCASLAAVDLSRN
GFSGEIPGELPPMSNMLTTLDVSYNSLSGPVPMMSAIAAGSYGYIAPEYAYTLRVDEKS

>OsJ_RLL1(gi|31745227)

VVGLDVSGNLNSGRLSVGANAFSGPIPASLGRLQFLTYLNLSNNMPLLRHLHLGGNFFSGEIPPEYGRWGRMQYLAVSGN
ELSGLGNLTSLRELLDAANCGLSGEIPPELGKLQNLDTLFLQVNSLGYLKSLSLDLSNNVLNKLRGDIPDFVGDLPSE
VLQLWENNLTGGVPRRLGRNLQLDLSSNRLGTLPPELCAGGKMHTLIALGNFLFGAIPDSLGECKSLSRVRLGENYLF
ELPKLTQVELQDNLLTGLGEISLNNQLTGALPASIGNFVQKLLDRNSFSGVVPNALEGGVPPEIGKCRLLTYLDLSRN
NISGKIPGEIPPSIATMLTAVDFSYNLNSGLVPMSAIAAGSYGYIAPEYAYTLKVDEKS

>Pg_CLL1(gi|104642235)

VEEVDSLNTNIIGKLPLADNYVNGSIPADLRRCKLGYLDLSQSLELQVLNLVFNLLNTTIPFLGNLPNLLQFNLAYN

PFTGLGNLTKLQNLLDLSINRLSGSIPESITKLDKVAQIELYQNLLGELKALKRFDASMNMLNDLVGEIPPGLGSFASLT
ELKLFSNRLTGRLPESLGRYLQALDIADNLLSGSLPPDLCKNKKLEILSIFNNVFAGNIPESLGTCTSLNRVRLGGNKFW
GLPHISLLELKDNNEGLSQLVINGNTFTGSLPTEIGELLSEIIASNNFLT GALPNQLSGELPAEISSCKQLGEINLSKN
QFSGSIPGLIPSEFGNLLNTFDVSNRLSGAVPMSAIAGSYGYIAPEYAYTLKVNEKS

>Ps_CLL1(gi|24940244)

VITLNVTVPLFGRLIITMDNLTGELPFEISNLTSKILNISHNLKELTILCLAGNYFTGTIPESYSEFQKLEILSINAN
SLSGLSKLKTLKELLEVSNCNLTEIPPSFGNLENLDSLFLQMNLSMKSLSLDLSNNALNKFRGSIPAFIGDLPNLE
TLQWENNFSFVLPQNLGSNFIFFDVTKNHLTGLIPDLCKSKKLQTFIVTDNFFHGPIPKGIGACKSLLKIRVANNYLF
QMPSVTIIELGNNRFNGLGILTISNNLFTGRIPASMKNLQTLWLDANQFVGEIPNNLTGVIPTTVSQCRSLTAVDFSRN
MITGEVPGLIPDEIRFMLTTLDSYNNFTGIVPMSSIAGSYGYIAPEYAYTLKVDEKS

>Vv_CLL1(gi|225424960)

VVSLDISNSNISGNLSVCNNLAGSFPEIHKLSRLQYLNISNNLPKLNKHLDFGGNYFSGKIPRNYGGMVQLTYLSLAGN
DLGGLGNLTNLKRLLDLSSCGLEGPPELGNLKHLDLTLFLQTNQLGNLSSLKSLDLSNNGLNKFHGEIPHFAELPKLE
VLKLWQNNFTGTIPSKLGRNLSELDLSTNKLTLGLIPKSLCFGRRLKILILLNNFLFGPLPDDLGRCELTQRVRLGQNYLL
YLPQLSLMELQNNYLTGVGQLNLSNNRLSGSLPTSIGNFLQILLNNGNRFTGNIPNNFSGIIPPEIGHCLSLTYLDLSQN
QISGPQPQLPKEIGFMLTSVDFSHNNFSGWIPMSAIAGSYGYIAPEYAYTLKVDEKS

>OsJ_CLV1(gi|125602183)

VVGVDLSRRNLSGSLNLSGNAFAGELPPAVLLLRRRLVALDVSHNLRREHLNLGGSFFNGSIPGEVQQLRRRLRFLHLAGN
ALSGLGELTSVEHLLDIAAANVSGPLPELGELTRLESFLFKNRISRLRALQVLDVSDNHLNSLSGTIPAAIGALPSLE
VLQLWNNLAGRLPESLGASLVRLDVSTNSLSGPIPPVCAGNRLARLILFDNRFDSAIPASLADCSSLWRVRLEANRLG
AIRNLTYMDLSSNSLTGLETFNVSGNLVGGALPDMAWRGLQVFAASRCGLVGELPNALGGGIPGDIGSCKRLVSLRLQHN
ELTGEIPGTVPFGFTNCLETDFVSFNLAPAEPMSVAVAGSCGYIAPEYTYTLKVNEKS

APPENDIX E: ClustalW Alignment of Gblocks Cleaned of Orthologous RPK1 Amino Acid Sequences

	10	20	30	40	50	60
At_RKL1_At1g48480	R	V	T	A	L	R
At_RLK902_At3g17840	R	V	T	A	L	R
At_LRR1_At5g16590	R	V	T	A	L	R
OsJ_MARK_gi108710729	R	V	A	V	L	R
Zm_MARK_gi162459881	R	V	A	V	L	R
OsJ_RLL_2_gi15128407	R	V	Q	T	L	R
OsJ_RLL_3_gi115464509	R	V	R	E	L	R
At_TMK_At5g58300	S	V	H	A	L	R
At_RLK_At4g23740	R	I	I	A	V	R
OsJ_RLL_1_gi7573610	R	V	V	A	L	R
OsJ_RPK1_gi53792194	T	V	V	Q	V	R
OsI_RPK1	T	V	V	Q	V	R
Oruf_RPK1	T	V	V	Q	V	R
At_TMKL1_At3g24660	-	-	S	P	L	Q
Clustal Consensus	..	..	..	..	..	..
	70	80	90	100	110	120
At_RKL1_At1g48480	F	S	G	E	I	P
At_RLK902_At3g17840	F	S	G	E	I	P
At_LRR1_At5g16590	F	S	G	E	I	P
OsJ_MARK_gi108710729	L	S	G	E	F	P
Zm_MARK_gi162459881	L	S	G	E	F	P
OsJ_RLL_2_gi15128407	L	S	G	E	F	P
OsJ_RLL_3_gi115464509	L	S	G	E	F	P
At_TMK_At5g58300	F	S	G	E	V	P
At_RLK_At4g23740	L	S	G	E	V	P
OsJ_RLL_1_gi7573610	F	S	G	E	V	P
OsJ_RPK1_gi53792194	L	S	G	E	V	P
OsI_RPK1	L	S	G	E	V	P
Oruf_RPK1	L	S	G	E	V	P
At_TMKL1_At3g24660	L	S	G	E	V	P
Clustal Consensus	..	..	..	..	..	..
	130	140	150	160	170	180
At_RKL1_At1g48480	S	F	L	Q	F	D
At_RLK902_At3g17840	S	F	V	G	F	D
At_LRR1_At5g16590	A	F	L	G	F	D
OsJ_MARK_gi108710729	A	F	L	G	F	D
Zm_MARK_gi162459881	A	F	L	G	F	D
OsJ_RLL_2_gi15128407	S	F	L	G	F	D
OsJ_RLL_3_gi115464509	S	F	F	G	F	D
At_TMK_At5g58300	S	F	S	G	F	D
At_RLK_At4g23740	S	F	T	G	F	D
OsJ_RLL_1_gi7573610	A	F	A	G	F	D
OsJ_RPK1_gi53792194	D	F	A	G	F	D
OsI_RPK1	D	F	A	G	F	D
Oruf_RPK1	D	F	A	G	F	D
At_TMKL1_At3g24660	K	S	L	D	L	T
Clustal Consensus	..	..	..	..	..	..
	190	200	210	220	230	240
At_RKL1_At1g48480	H	E	N	L	V	P
At_RLK902_At3g17840	H	E	N	L	V	P
At_LRR1_At5g16590	H	A	N	L	V	T
OsJ_MARK_gi108710729	H	E	F	I	V	P
Zm_MARK_gi162459881	H	E	F	I	V	P
OsJ_RLL_2_gi15128407	H	E	F	I	V	P
OsJ_RLL_3_gi115464509	H	Q	N	A	V	Q
At_TMK_At5g58300	H	P	S	V	V	P
At_RLK_At4g23740	H	E	N	V	E	L
OsJ_RLL_1_gi7573610	H	A	N	V	A	E
OsJ_RPK1_gi53792194	H	R	N	V	L	P
OsI_RPK1	H	R	N	V	L	P
Oruf_RPK1	H	R	N	V	L	P
At_TMKL1_At3g24660	H	E	N	L	V	P
Clustal Consensus	..	..	..	..	..	..

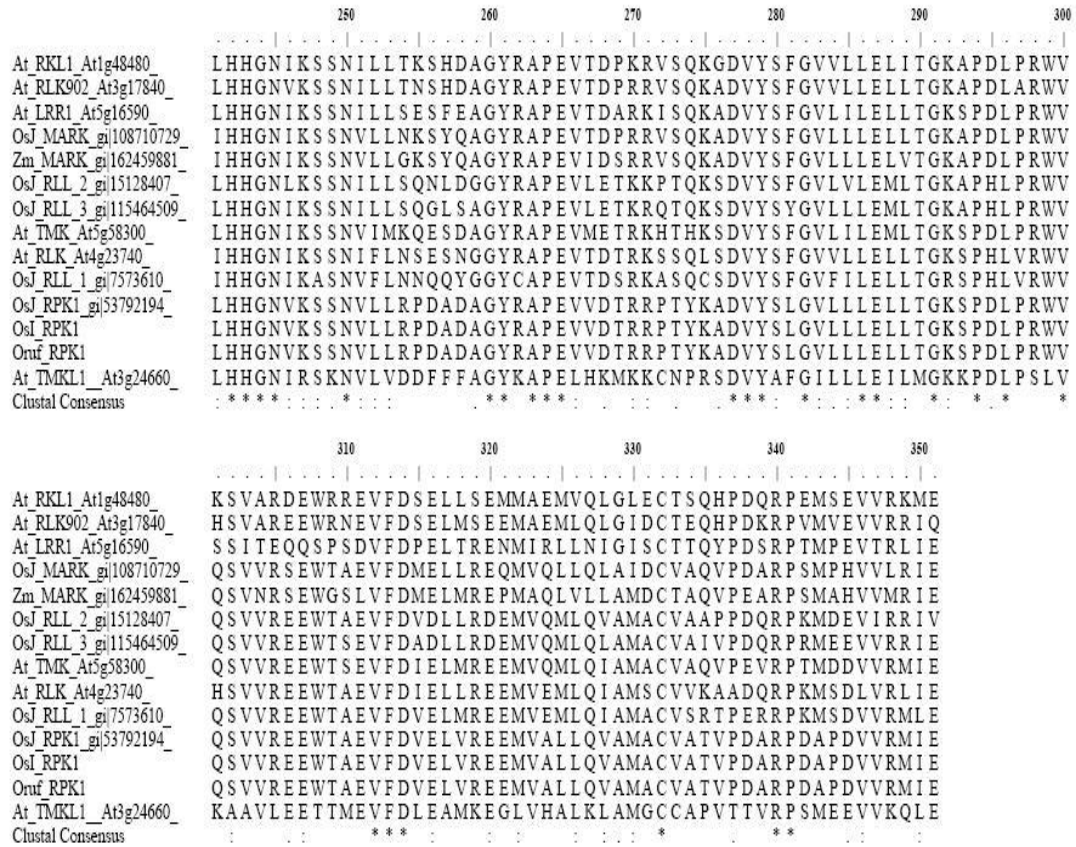


Figure A.1: ClustalW alignment of Gblocks cleaned of orthologous *RPK1* amino acid sequences. At_LRR1 (At5g16590), At_RKL1 (At1g48480), At_RLK (At4g23740), At_RLK902 (At3g17840), At_TMK (At5g58300) and At_TMKL1 (At3g24660) from *Arabidopsis thaliana*; OsJ_MARK (gi:108710729), OsI_RPK1, OsJ_RPK1 (gi:18677097), OsJ_RLL1 (gi:7573610), OsJ_RLL2 (gi:15128407) and OsJ_RLL3 (gi:115464509) from *Oryza sativa*; Oruf_RPK1 from *Oryza rufipogon*; Zm_MARK (gi:226498594) from *Zea mays*.

APPENDIX F: ClustalW Alignment of Gblocks Cleaned of Orthologous CLV1 Amino Acid Sequences

	10	20	30	40	50	60
Gm_CLL3_gi 9651943	VTALNLTGLDLSGNLSLAANKFSGPIPPSLSALSGLRYLNL	SNNMQNLRHLHLGGNFFSG				
Gm_CLL4_gi 9651945	VTSLDLTGLDLSGNLSLASNKFSGP	IPPSLSALSGLRFLNL	SNNMQNLRHLHLGGNFFSG			
At_BAM1_At5g65700	VTSLDLSGLNLSGNLSLAENLISGP	IPPEISSLSGLRHLNL	SNNLTQLRHLHLGGNYFAG			
OsJ_RLL1_gi 31745227	VVGGLDVSGNLSGRLSVGANAFSGPI	PASLGRQLFTYLNLSNNMPLLRHLHLGGNFFSG				
At_BAM3_At4g20270	ITRLDLSNLSISGFLDISSNSFS	GELPKEIYELSGLEVNL	ISSNLTRLEHLDLGGNYFDG			
Vv_CLL3_gi 225424960	VVSLDISNSNISGNLSVCGNNLAGS	FPPEIHKLSRLQYLNISNNLPKLKHLDFGGNYFSG				
Pt_CLL1_gi 224085908	VVSLNVSFRHLPGNLTLSGNLT	TGGFPVEIAMLTSLRILNISNNLKNLKHVHLGGNFFSG				
Pt_CLL2_gi 224061985	VVSLNLSFRHLPGNLTLANDNLT	TGELPAEIAMLSLRILNISGNLKKLKHHLGGNFFSG				
Vv_CLL2_gi 225457925	VVSLNLSFVTLFGNLTACDNLT	TGKLPMEMAKLTSLKLVNL	SNNLKKLKHMHHLGGNYFSG			
At_CLV1_At1g75820	VISLNVSFVTLFGNLTAAANFT	TGELPLEMKS	LTSLKVLNISNNLKKLKYLSFGGNFFSG			
Gm_CLL1_gi 25956280	VVAINVSVFVPLFGNLT	TVSQNNLTGVL	PKELAALTSKHLNISHNLEKLYLKL	DGNFYSG		
Gm_CLL2_gi 7329124	VVAINVSVFVPLFGNLT	TVSQNNLTGVL	PKELAALTSKHLNISHNLEKLYLKL	DGNFYSG		
Mt_CLL1_gi 58372544	VIALNVTQVPLFGSLTITMDNLT	TGELPTELSKLTSLRILNISHNLMKLYLSFAGNFFSG				
Ps_CLL1_gi 24940244	VITLNVITQVPLFGRLIITMDNLT	TGELPFEISNLTSLKILNISHNLKELTILCLAGNYFTG				
OsJ_FON1_gi 113596633	VVAINTALPLHSNLTIAACCL	PGHVPLELPTLPSLRHLNL	SNNHARLRYLHLGGNYFTG			
OsJ_CLL1_gi 50726262	VVGVDLSRRNLSGSLNLSGNAFAGEL	PPAVLLRRLVALDVSHNLRLEHLNLGGSFFNG				
OsJ_CLV1_gi 125602183	VVGVDLSRRNLSGSLNLSGNAFAGEL	PPAVLLRRLVALDVSHNLRLEHLNLGGSFFNG				
Pg_CLL1_gi 104642235	VEEVDLSNTNIIIGKLPLADNYVNGS	I PADLRRCRKLGYLDLSQS	LSLELQVLNLVFNLLNT			
At_BAM2_At3g49670	AIRLNHSVIPVSVSLPFSVGDWRGVST	FSGARPLVLAKVKLRAELVDEEIVHFEERDFAG				
Clustal Consensus	::: : *	*	*	::: :	::: :	
	70	80	90	100	110	120
Gm_CLL3_gi 9651943	QIPPEYGRWQRLQYLAVSGNELD	IGNLTSLRELLDVAYCALSGEIP	PAALGKLQKLDTLF			
Gm_CLL4_gi 9651945	QIPPEYGRWQRLQYLAVSGNELEG	IGNLTSLRELLDAAYCGLSGEIP	PAALGKLQKLDTLF			
At_BAM1_At5g65700	KIPPSYGSWPVIEYLAVSGNELV	IGNLTSLRELLFDGANCGLTGEI	PEIGKLQKLDTLF			
OsJ_RLL1_gi 31745227	EIPPEYGRWGRMQYLAVSGNELS	GLGNLTSLRELLDAANCGLSGEIP	PELGLQNLDTLF			
At_BAM3_At4g20270	EIPRSYGSFLSLKFLSLSGNDLR	GLANITTLVQLDLANC	SLKGSIPAEGLNKNLEVL			
Vv_CLL3_gi 225424960	KIPRNYGGMVQLTYLSLAGNDL	GGLGNLTNLKRLLDLSSCGLE	GPIPELGNLKHLDTLF			
Pt_CLL1_gi 224085908	TIPEEYSEILSLEYLGLNGNAL	SGLSRKLNLSLDMASCNLDGEI	PSALSQTLHLHS			
Pt_CLL2_gi 224061985	KIPEEYSEIMILEFLGLNGNDL	SGLSKLNLSLDMGSCNNGEIP	STLGLQTLHLHS			
Vv_CLL2_gi 225457925	DIPDVFSDIHLSLELLGLNGNLS	GLVRLSNLQGLLDLGS	CNLTGEIPPSLGRKMLHSL			
At_CLV1_At1g75820	EIPESYGDIIQSLEYLGLNGAGL	SGLSRKLNREMLDMASCTLTGEI	PTSLSNLKHLHTLF			
Gm_CLL1_gi 25956280	SIPESYSEFKSLEFLSLSTNSL	SGLSKLKTLYLLDLSSCNLSGEI	PPSLANLTNLDTLF			
Gm_CLL2_gi 7329124	SIPESYSEFKSLEFLSLSTNSL	SGLSKLKTLYLLDLSSCNLSGEI	PPSLANLTNLDTLF			
Mt_CLL1_gi 58372544	TIPESYSEFQKLEILRLNYS	LTLSGLKMLKELLEISNANLTGEI	PPSLGNLENLDSLF			
Ps_CLL1_gi 24940244	TIPESYSEFQKLEILSINANS	LSGLSKLKTLELVSNCNLTGEI	PPSFGNLENLDSLF			
OsJ_FON1_gi 113596633	AIPDSYGDIAALEYLGLNGNTL	SGLSRLTRLREMLDMSSCNLTGP	VPELGRQLRLDTLF			
OsJ_CLL1_gi 50726262	SIPGEVQGLRRLRFLHLAGNAL	SGLGELTSVEHLLDIAAANVSG	PLPELGELTRLES			
OsJ_CLV1_gi 125602183	SIPGEVQGLRRLRFLHLAGNAL	SGLGELTSVEHLLDIAAANVSG	PLPELGELTRLES			
Pg_CLL1_gi 104642235	TIPPLGNLPNLLQFNLAYNP	FTGLGNLT	TKLQNLDDL SINRLSGSIPESITKLDKVAQIE			
At_BAM2_At3g49670	TACVPVYVMLPLGVIDMNS	EVVEPLDQLRTLKSV	VMVDCWWGIVESHTPQVYNWSGYKKLF			
Clustal Consensus	::: : :	::: : :	::: : :	::: : :	::: : :	
	130	140	150	160	170	180
Gm_CLL3_gi 9651943	LQVNALGNLKSLSKSMDSL	SNNMLNKLHGAIPEF	IGELPALEVVQLWENNLTGS	IPEGLGKN		
Gm_CLL4_gi 9651945	LQVNALGNLKSLSKSMDSL	SNNMLNKLHGAIPEF	IGELPALEVVQLWENNFTGS	IPEGLGKN		
At_BAM1_At5g65700	LQVNVFGTSLSLKSMDL	SNNMFNKLHGEIPEF	IGDLPLEVLQLWENNFTGS	IPQKLGEN		
OsJ_RLL1_gi 31745227	LQVNSLGYLKSLSLSDL	SNNVNLKLRGDI	PDFVGDLP	SLEVLQLWENNFTGGVPRRLGRN		
At_BAM3_At4g20270	LQTNELGNMTSLKTLDL	SNNFLNRLHGEIPEF	VSEL	PDLQILKLWHNNFTGKIPSKLGSN		
Vv_CLL3_gi 225424960	LQTNQLGNLSLSKSLDL	SNNGLNKFHGEI	PHFIAELPKLEVLKLWQNNFTGT	IPSKLGRN		
Pt_CLL1_gi 224085908	LQVNNLSGLISLKSDDL	SINNKLHGP	IPEFFGDFPNLEVLQVWGNNTFEL	PQNLGRN		
Pt_CLL2_gi 224061985	LQFNNSGLISLKSDDL	SINNKLHGP	IPEFFGDFPNLEVLQVWGNNTFEL	PKQLGRN		
Vv_CLL2_gi 225457925	LQNLQSLGLVNLKSLDL	SNNVNLKLRGDI	PDFVGDLP	SLEVLQLWENNFTGGVPRRLGRN		
At_CLV1_At1g75820	LHINNLSGLVSLKSLDL	SINQLNNLYGQIPEA	IGELPKLEVFEVWENNFTLQLPANLGRN			
Gm_CLL1_gi 25956280	LQINNLSAMVSLMSLDL	SINDLNNLRGSVPS	FVGELPNLETLQLWNNFSFVLP	PNNLQGN		
Gm_CLL2_gi 7329124	LQINNLSAMVSLMSLDL	SINDLNNLRGSVPS	FVGELPNLETLQLWNNFSFVLP	PNNLQGN		
Mt_CLL1_gi 58372544	LQMNNLSMRSNLKSLDL	SINGLNKLRGSI	PAFIGDLPNLETLQVWENNFSFVLP	PQNLGSN		
Ps_CLL1_gi 24940244	LQMNNLSMKSLSLDL	SNNALNKFGRS	I PAFIGDLPNLETLQVWENNFSFVLP	PQNLGSN		
OsJ_FON1_gi 113596633	LQWNRLGDLSSLASLDL	SVNDLNHLRGS	IPDFVAGFAQLEVLQLWNNLTGN	I PAGLGKN		
OsJ_CLL1_gi 50726262	LFKNRI	SRLRALQVLDVSDNHLNLS	SGTIPAAIGALPSLEVLQLWNNSLAGRL	PESLGAS		
OsJ_CLV1_gi 125602183	LFKNRI	SRLRALQVLDVSDNHLNLS	SGTIPAAIGALPSLEVLQLWNNSLAGRL	PESLGAS		
Pg_CLL1_gi 104642235	LYQNLLGELKALKRF	DASMMMLNDLVGEI	PPGLGSFASLT	TELKLF	SNRLTGRLP	SGRY
At_BAM2_At3g49670	QMIRELLKIQVMS	FHECGGNVDDVHIQI	PEWVREIGQSNPDIYFTDS	AGRRNTECL	TW	
Clustal Consensus	::: : :	::: : :	::: : *	::: : :	::: : *	

	190	200	210	220	230	240
Gm_CLL3_gi9651943	LNLVDLS	SNKLTG	TLPPYLC	SGNTLQ	TLITLGN	FLFGPIPE
Gm_CLL4_gi9651945	LNLVDLS	SNKLTG	TLPTYLC	SGNTLQ	TLITLGN	FLFGPIPE
At_BAM1_At5g65700	LNLVDLS	SNKLTG	TLPPNMC	SGNKLET	ITLITLGN	FLFGSIPD
OsJ_RLL1_gi31745227	LQLDL	SSNRLT	GTLPPEL	CAGGKMHT	LIALGN	FLFGAIPD
At_BAM3_At4g20270	LIEIDL	STNKLT	GLIPESL	CFGRRLK	ILILFNN	FLFGPLPE
Vv_CLL3_gi225424960	LSELDL	STNKLT	GLIPKSL	CFGRRLK	ILILN	FLFGPLPD
Pt_CLL1_gi224085908	LMMLDV	SINHLT	TGLVPR	DLCKGGK	LTTLILM	NNFFLG
Pt_CLL2_gi224061985	LMYLDV	SYNHLT	TGLVPR	DLCKGGK	LTTLILM	NNFFIG
Vv_CLL2_gi225457925	LKNLDV	ATNHLT	TGTIPR	DLCKGGK	LTTLILM	ENYFFG
At_CLV1_At1g75820	LIKLDV	SDNHLT	TGLIPK	DLERGE	KLEMLIL	SNFFFG
Gm_CLL1_gi25956280	LKFFDV	IKNHFT	GLIPRDL	CKSGRLQ	TIMITDN	FFRGPI
Gm_CLL2_gi7329124	LKFFDV	IKNHFT	GLIPRDL	CKSGRLQ	TIMITDN	FFRGPI
Mt_CLL1_gi58372544	FIFYDV	TKNHLT	TGLIPPEL	CKSKKLT	FTIVTD	FFRGPI
Ps_CLL1_gi24940244	FIFYDV	TKNHLT	TGLIPPEL	CKSKKLT	FTIVTD	FFRGPI
OsJ_FON1_gi113596633	LKTLDL	ATNHLT	TGTIPADL	CAGRRLE	MLVLMEN	GLFGPI
OsJ_CLL1_gi50726262	LVRLDV	STNSLS	GPIPPG	VCAGNRL	LARLILF	DNRFDS
OsJ_CLV1_gi125602183	LVRLDV	STNSLS	GPIPPG	VCAGNRL	LARLILF	DNRFDS
Pg_CLL1_gi104642235	LQALDI	ADNLLS	GSLLP	DLCKNKK	LEILSIF	NNVFAG
At_BAM2_At3g49670	IDKQVR	LRGRTA	LEVYFD	YMRSFR	VEFDEF	FEKKI
Clustal Consensus	:	:	:	:	:	:
	250	260	270	280	290	300
Gm_CLL3_gi9651943	GLPKLTQ	VELQDNY	LSGLGQ	ITLSNN	QLSGAL	SPSIGN
Gm_CLL4_gi9651945	GLPKLTQ	VELQDNY	LSGLGQ	ITLSNN	QLSGVL	PPSIGN
At_BAM1_At5g65700	GLPKLTQ	VELQDNY	LSGLGQ	ITLSNN	QLSGVL	PPSIGN
OsJ_RLL1_gi31745227	ELPKLTQ	VELQDNL	LTLGLGE	ISLNN	QLTGAL	PASIGN
At_BAM3_At4g20270	YLPNLS	LLELQNN	FLTGLT	QINLSNN	RLSGPI	PGSIRN
Vv_CLL3_gi225424960	YLPQLS	LMELQNN	YLTGVG	QLNLSNN	RLSGSL	PTSIGN
Pt_CLL1_gi224085908	NLPLAT	LVELSNN	LFSGLG	LLSVSNN	RLITGKI	PPAIGN
Pt_CLL2_gi224061985	NLPLVT	QIELSH	NYFSG	LGSLSV	SDNRIT	GRIPRA
Vv_CLL2_gi225457925	NLPLVN	MLEDDN	LFTGLG	IFTVSNN	LITGKI	PPAIGN
At_CLV1_At1g75820	NLPLVT	IIELTD	NFFSG	LQDIYLS	NNWFS	GEPPIA
Gm_CLL1_gi25956280	KLPSTV	IIELANN	RFNGLG	ILITLSNN	LFSGKI	PPALKN
Gm_CLL2_gi7329124	KLPSTV	IIELANN	RFNGLG	ILITLSNN	LFSGKI	PPALKN
Mt_CLL1_gi58372544	QLPSVQ	IIELGNN	RFNGLG	NLALSN	NLFTGRI	PASMKN
Ps_CLL1_gi24940244	QMPSTV	IIELGNN	RFNGLG	ILITLSNN	LFSGKI	PPALKN
OsJ_FON1_gi113596633	NLPQAN	MVELTD	NLLTGIG	MLLLGNN	GIGGRI	PPAIGN
OsJ_CLL1_gi50726262	AIRNLT	TYMDLS	SNSLTG	LEYFN	VSNGLV	GGALPD
OsJ_CLV1_gi125602183	AIRNLT	TYMDLS	SNSLTG	LEYFN	VSNGLV	GGALPD
Pg_CLL1_gi104642235	GLPHIS	LLELKD	NNFEGL	SQLVING	NTFTGS	LPTEIG
At_BAM2_At3g49670	KYPGIG	EFQCYD	KYLMNKE	AAEVRG	HSFWGR	GPDNTE
Clustal Consensus	:	:	:	:	:	:
	310	320	330	340	350	360
Gm_CLL3_gi9651943	PIAPEIS	QCKLLT	FLDLSR	NELSGD	IPGSI	SSIS
Gm_CLL4_gi9651945	PIVPEIS	QCKLLT	FLDLSR	NELSGD	IPGGI	SSIS
At_BAM1_At5g65700	RIAPEIS	RCKLLT	TFVDL	SRNELS	GEPGSI	PGSISS
OsJ_RLL1_gi31745227	GVPPEI	IGKCR	LLTYL	DLSRNN	ISGKI	PPSIAT
At_BAM3_At4g20270	KFPPEF	GDCML	SLTYL	DLSHNQ	ISGQIP	QSLPN
Vv_CLL3_gi225424960	IIPPEI	IGHCL	SLTYL	DLSNQ	ISGIPQ	NLPKEI
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Pt_CLL2_gi224061985	EIPASMF	HCTSLT	SVDFS	QNSLSG	EIPGQ	LPSEI
Vv_CLL2_gi225457925	EIPACIV	SCTSLT	SIDFS	QNSLNG	EIPGQ	IPSEI
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Gm_CLL1_gi25956280	PIPTTL	TRCVSL	TAVDL	SRNM	LEGKIP	GPVP
Gm_CLL2_gi7329124	PIPTTL	TRCVSL	TAVDL	SRNM	LEGKIP	GPVP
Mt_CLL1_gi58372544	GIPKTV	TQCSSL	TAVDF	SRNML	TGEV	PGKIP
Ps_CLL1_gi24940244	VIPTTV	SQCRSL	TAVDF	SRNMI	TGEV	PGLIP
OsJ_FON1_gi113596633	AIPDEL	IRCAS	LA	AVDL	SRNGF	S
OsJ_CLL1_gi50726262	GIPGDI	GSCKRL	VSRL	QHNE	L	TGEI
OsJ_CLV1_gi125602183	GIPGDI	GSCKRL	VSRL	QHNE	L	TGEI
Pg_CLL1_gi104642235	ELPAEIS	SCKQL	GEINL	SKNQ	FSGSI	PGLIP
At_BAM2_At3g49670	VLIDHG	DRVL	AMAN	LA	FE	GT
Clustal Consensus	:	:	:	:	:	:

370

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Gm_CLL3_gi9651943_ . . . . | . . . . | . . . .
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OsJ_RLL1_gi31745227_ . . . . | . . . . | . . . .
At_BAM3_At4g20270_ . . . . | . . . . | . . . .
Vv_CLL3_gi225424960_ . . . . | . . . . | . . . .
Pt_CLL1_gi224085908_ . . . . | . . . . | . . . .
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Vv_CLL2_gi225457925_ . . . . | . . . . | . . . .
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Gm_CLL2_gi7329124_ . . . . | . . . . | . . . .
Mt_CLL1_gi58372544_ . . . . | . . . . | . . . .
Ps_CLL1_gi24940244_ . . . . | . . . . | . . . .
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Pg_CLL1_gi104642235_ . . . . | . . . . | . . . .
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Clustal Consensus . . . . | . . . . | . . . .

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Figure A.2: ClustalW alignment of Gblocks cleaned of orthologous CLV1 amino acid sequences. At_BAM1 (At5g65700), At_BAM2 (At3g49670), At_BAM3 (At4g20270) and At_CLV1 (At1g75820) from *Arabidopsis thaliana*; Gm_CLL1 (gi:25956280), Gm_CLL2 (gi:7329124), Gm_CLL3 (gi:9651943) and Gm_CLL4 (gi:9651945) from *Glycine max*; Mt_CLV1 (gi:58372544) from *Medicago truncatula*; OsJ_CLL1 (gi:50726262), OsJ_CLV1 (gi:125602183), OsJ_FON1 (gi:113596633) and OsJ_RLL1 (gi:31745227) from *Oryza sativa*; Pg_CLL1 (gi:104642235) from *Picea glauca*; Ps_CLL1 (gi:24940244) from *Pisum sativum*. Vv_CLL1 (gi:225424960) from *Vitis vinifera*.

APPENDIX G: DNA Sequences of *pANDA_CLV1* and *pANDA_RPK1* Inserts

>pENTR/D-TOPO containing putative *CLV1*

CACCAGTGAACGAGAAGAGCGATGTGTACAGCTTCGGTGTGGTACTATTGGAGATCCTGACGGGACGGCGGTCGGT
GGAGGCGGAGTACGGGGAGGGGAACAAC

>pENTR/D-TOPO containing putative *RPK1*

CACCAGGTTCTTTGGCTGCCTGTATGCCAATGCTCTGTTCTTTGCCAATTTTTTTCTCTTCTCTTCTTCTTCA
GTTTCTTTTCTGGGTATTGTTTTGTTGG

>*pANDA_CLV1*

CACCAGTGAACGAGAAGAGCGATGTGTACAGCTTCGGTGTGGTACTATTGGAGATCCTGACGGGACGGCGGTCGGT
GGAGGCGGAGTACGGGGAGGGGAACAAC

>*pANDA_RPK1*

CACCAGGTTCTTTGGCTGCCTGTATGCCAATGCTCTGTTCTTTGCCAATTTTTTTCTCTTCTCTTCTTCTTCA
GTTTCTTTTCTGGGTATTGTTTTGTTGG

APPENDIX H: Preliminary Yield Components

Line Characteristic	<i>Oryza rufipogon</i>	<i>Oryza sativa</i> ssp. <i>indica</i> cv. MR219	BC ₂ F ₇ line 7	BC ₂ F ₇ line 23
Yield per plot	2.8 kg	5.44 kg	5.82 kg	4.81 kg
Yield per plant	31.73 gm	48.08 gm	51.25 gm	40.49 gm
Tiller per plant	39	17.38	19.11	18.66
Panicles per plant	32	17.11	18.33	17.22
Spikelet per plant	1514	2314	2400	2074
Grains per plant	1207.0	1847.6	2014.2	1516.1

Table A.1: Preliminary yield components of *Oryza rufipogon*, *Oryza sativa* ssp. *indica* cv. MR219, BC₂F₇ line 7 and BC₂F₇ line 23 (Wickneswari pers. comm. 2010). *Oryza rufipogon*, *Oryza sativa* ssp. *indica* cv. MR219, BC₂F₇ line 7 and BC₂F₇ line 23 were grown at three location trial over two growing seasons (Wickneswari pers. comm. 2010).

APPENDIX I: Gene Sequences of Putative *RPK1* and Putative *CLV1*

>Genomic DNA *Oruf_RPK1* (Song et al., 2009)

[illegible]

>ORF *Oruf* RPK1

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>cDNA *Oruf_CLV1*

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