Supplementary Figure S1

Protein sequence of D-type cyclins in mammals and plants. Light and dark grey boxes identify individual exons. The cyclin box is shown in red bold to illustrate that in most cases (other than plant CYCD3) it is found at the end of exon 1 and beginning of exon 2.

Human CYCD

>HsCYCD1 (NM_053056)
MEHQLLCCEVETIRRAYPDANLLNDRVLRAMLKAEETCAPSVSYFKCVQKEVLPSMRKIVATW**MLEVCEEQ**K
CEEEVFPLAMNYLDRFLSLEPVKKSRLQLLGATCMFVASKMKETIPLTAEKLCIYTDNSIRPEELLQMELLL
VNKLKWNLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCATDVKFISNPPSMVAAGSVVAAVQGLN
LRSPNNFLSYYRLTRFLSRVIKCDPDCLRACQEQIEALLESSLRQAQQNMDPKAAEEEEEEEEEVDLACTPT
DVRDVDI*

>HsCYCD2 (NM_001759)
MELLCHEVDPVRRAVRDRNLLRDDRVLQNLLTIEERYLPQCSYFKCVQKDIQPYMRRMVATW**MLEVCEEQ**KC
EEEVFPLAMNYLDRFLAGVPTPKSHLQLLGAVCMFLASKLKETSPLTAEKLCIYTDNSIKPQELLEWELVVL
GKLKWNLAAVTPHDFIEHILRKLPQQREKLSLIRKHAQTFIALCATDFKFAMYPPSMIATGSVGAAICGLQQ
DEEVSSLTCDALTELLAKITNTDVDCLKACQEQIEAVLLNSLQQYRQDQRDGSKSEDELDQASTPTDVRDID
L*

>HsCYCD3 (NM_001760)
MELLCCEGTRHAPRAGPDPRLLGDQRVLQSLLRLEERYVPRASYFQCVQREIKPHMRKMLAYW**MLEVCEEQ**R
CEEEVFPLAMNYLDRYLSCVPTRKAQLQLLGAVCMLLASKLRETTPLTIEKLCIYTDHAVSPRQLRDWEVLV
LGKLKWDLAAVIAHDFLAFILHRLSLPRDRQALVKKHAQTFLALCATDYTFAMYPPSMIATGSIGAAVQGLG
ACSMSGDELTELLAGITGTEVDCLRACQEQIEAALRESLREASQTSSSPAPKAPRGSSSQGPSQTSTPTDVT
AIHL*

Moss CYCD

>Phypa;CYCD (AJ488282)
MSPSVDCLASLYCAEDVSGTAWNESEMCGAADRVFESQPAVFMDFPVEDDEAIATLLMKEAQFMPEADYLER
YQSRKLSLEARLAAIEW**ILKVHSFY**NYSPLTVALAVNYMDRFLSRYYFPEGKEWMLQLLSVACISLAAKMEE
SDVPILLDFQVEQEEHIFEAHTIQRMELLVLSTLEWRMSGVTPFSYVDYFFHKLGVSDLLLRALLSRVSEII
LKSIRVTTSLQYLPSVVAAASIICALEEVTTIRTGDLLRTFNELLVNVESVKDCYIDMRQSEIGPYCVRMGL
KRKILHASEPQSPVGVLEAADVSSPSGTVLGFSSRESSPDVTDSPPSTNSQRKRRKLCLHNESCLHVESASL
*

Arabidopsis CYCD

>Arath;CYCD1;1 (AT1G70210)
MRSYRFSDYLHMSVSFSNDMDLFCGEDSGVFSGESTVDFSSSEVDSWPGDSIACFIEDERHFVPGHDYLSRF
QTRSLDASAREDSVAW**ILKVQAYY**NFQPLTAYLAVNYMDRFLYARRLPETSGWPMQLLAVACLSLAAKMEEI
LVPSLFDFQVAGVKYLFEAKTIKRMELLVLSVLDWRLRSVTPFDFISFFAYKIDPSGTFLGFFISHATEIIL
SNIKEASFLEYWPSSIAAAAILCVANELPSLSSVVNPHESPETWCDGLSKEKIVRCYRLMKAMAIENNRLNT
PKVIAKLRVSVASSTLTRPSDESSFSSSSPCKRRKLSGYSWVGDETSTSN*

>Arath;CYCD2;1 (AT2G22490)
MAENLACGETSESWIIDNDDDDINYGGGFTNEIDYNHQLFAKDDNFGGNGSIPMMGSSSSSLSEDRIKEMLV
REIEFCPGTDYVKRLLSGDLDLSVRNQALDW**ILKVCAHY**HFGHLCICLSMNYLDRFLTSYELPKDKDWAAQL
LAVSCLSLASKMEETDVPHIVDLQVEDPKFVFEAKTIKRMELLVVTTLNWRLQALTPFSFIDYFVDKISGHV

SENLIYRSSRFILNTTKAIEFLDFRPSEIAAAAVSVSISGETECIDEEKALSSLIYVKQERVKRCLNLMRS
LTGEENVRGTSLSQEQARVAVRAVPASPVGVLEATCLSYRSEERTVESCTNSSQSSPDNNNNNNSNKRRRK
Q*
>Arath;CYCD3;1 (AT4G34160)
MAIRKEEESREEQSNSFLLDALYCEEEKWDDEGEEVEENSSLSSSSSPFVVLQQDLFWEDEDLVTLFSKEEE
QGLSCLDDVYLSTDRKEAVGW**ILRVNAHY**GFSTLAAVLAITYLDKFICSYSLQRDKPWMLQLVSVACLSLAA
KVEETQVPLLLDFQVEETKYVFEAKTIQRMELLILSTLEWKMHLITPISFVDHIIRRLGLKNNAHWDFLNKC
HRLLLSVISDSRFVGYLPSVVAAATMMRIIEQVDPFDPLSYQTNLLGVLNLTKEKVKTCYDLILQLPVDRIG
LQIQIQSSKKRKSHDSSSSLNSPSCVIDANPFNSDESSNDSWSASSCNPPTSSSSPQQQPPLKKMRGAEENE
KKKPILHLPWAIVATP*
>Arath;CYCD3;2 (AT5G67260)
MALEKEEEASQNGAFCVLDGLYCEEETGFVEDDLDDDGDLDFLEKSDESVVKFQFLPLLDMFLWDDDEILSL
ISKENETNPCFGEQILDGFLVSCRKEALDW**VLRVKSHY**GFTSLTAILAVNYFDRFMTSIKLQTDKPWMSQLV
AVASLSLAAKVEEIQVPLLLDLQVEEARYLFEAKTIQRMELLILSTLQWRMHPVTPISFFDHIIRRFGSKWH
QQLDFCRKCERLLISVIADTRFMRYFPSVLATAIMILVFEELKPCDEVEYQSQITTLLKVNQEKVNECYELL
LEHNPSKKRMMNLVDQDSPSGVLDFDDSSNSSWNVSTTASVSSSSSSPEPLLKRRRVQEQQMRLPSINRMFL
DVLSSPR*

>Arath;CYCD3;3 (AT3G50070)
MALEEEEESQNAPFCVLDGLFCEEESEFHEQVDLCDESVEKFPFLNLGLSDHDMLWDDDELSTLISKQEPCL
YDEILDDEFLVLCREKALDW**IFKVKSHY**GFNSLTALLAVNYFDRFITSRKFQTDKPWMSQLTALACLSLAAK
VEEIRVPFLLDFQVEEARYVFEAKTIQRMELLVLSTLDWRMHPVTPISFFDHIIRRYSFKSHHQLEFLSRCE
SLLLSIIPDSRFLSFSPSVLATAIMVSVIRDLKMCDEAVYQSQLMTLLKVDSEKVNKCYELVLDHSPSKKRM
MNWMQQPASPIGVFDASFSSDSSNESWVVSASASVSSSPSSEPLLKRRRVQEQQMRLSSINRMFFDVLSSSP
R*

>Arath;CYCD4;1 (AT5G65420)
MAEENLELSLLCTESNVDDEGMIVDETPIEISIPQMGFSQSESEEIIMEMVEKEKQHLPSDDYIKRLRSGDL
DLNVGRRDALNW**IWKACEVH**QFGPLCFCLAMNYLDRFLSVHDLPSGKGWILQLLAVACLSLAAKIEETEVPM
LIDLQVGDPQFVFEAKSVQRMELLVLNKLKWRLRAITPCSYIRYFLRKMSKCDQEPSNTLISRSLQVIASTT
KGIDFLEFRPSEVAAAVALSVSGELQRVHFDNSSFSPLFSLLQKERVKKIGEMIESDGSDLCSQTPNGVLEV
SACCFSFKTHDSSSSYTHLS*

>Arath;CYCD4;2 (AT5G10440)
MAEFMEPNLVSNFDDEKSNSVDTRSIFQMGFPLESEEIVREMIEKERQHSPRDDYLKRLRNGDLDFNVRIQA
LGW**IWKACEEL**QFGPLCICLAMNYLDRFLSVHDLPSGKAWTVQLLAVACLSLAAKIEETNVPELMQLQVGAP
MFVFEAKSVQRMELLVLNVLRWRLRAVTPCSYVRYFLSKINGYDQEPHSRLVTRSLQVIASTTKGIDFLEFR
ASEIAAAVALSVSGEHFDKFSFSSSFSSLEKERVKKIGEMIERDGSSSSSQTPNNTVLQFKSRRYSHSLSTA
SVSSSLTSLS*

>Arath;CYCD5;1 (AT4G37630)
MGEPKDSLALFLCHESESSLNEDDDETIERSDKQEPHFTTTIDDEDYVADLVLKENLRFETLPSKTTSSSDR
LIAIDW**ILTTRTRF**GFQHQTAYIAISYFDLFLHKRFIGLQKDETWAMRLLSVACLSLAAKMEERIVPGLSQY
PQDHDFVFKPDVIRKTELLILSTLDWKMNLITPFHYFNYFLAKISQDNHSVSKDLVLLRSSDSLLALTKEIS
FTEYRQFVVAAVTTLLASSSTSSDIRLTREEIANKFGSISWWTSNENENVYLCYQRTLEIEERKHMTPPPEI
AVSREPPASGSGAKRRLSFDDSDQSSPPAKRMRRL*

>Arath;CYCD6;1 (AT4G03270)
MEFHLEHPLSHSSLHNNFNDDTDYETLPHSLFLVEFQHMPSSHYFHSLKSSAFLLSNRNQAISS**ITQYSRKF**
DDPSLTYLAVNYLDRFLSSEDMPQSKPWILKLISLSCVSLSAKMRKPDMSVSDLPVEGEFFDAQMIERMENV
ILGALKWRMRSVTPFSFLAFFISLFELKEEDPLLLKHSLKSQTSDLTFSLQHDISFLEFKPSVIAGAALLFA
SFELCPLQFPCFSNRINQCTYVNKDELMECYKAIQERDIIVGENEGSTETAVNVLDQQFSSCESDKSITITA
SSSPKRRKTSTRRY*

>Arath;CYCD7;1 (AT5G02110)
MDNLLCEESWPASPLTPEPLPNFRHRSHDNDVVKMYPEIDAATMEEAIAMDLEKELCFNNHGDKFVEFFVSK
KLTDYRFHAFQW**LIQTRSRL**NLSYETVFSAANCFDRFVYMTCCDEWTNWMVELVAVTSLSIASKFNEVTTPL

LEELEMEGLTHMFHVNTVAQMELIILKALEWRVNAVTSYTFSQTLVSKIGMVGDHMIMNRITNHLLDVICDL
KMLQYPPSVVATAAIWILMEDKVCRESIMNLFEQNHKEKIVKCVDGMKNRDIDHQSSRRRYSEGRSILSLLQ
RGDVMNMNGDYNVEDLSKIFQIFRYEKKKRDRGNHQDNIRPAKRMTIEMSNYI*

Rice CYCD

>Orysa;CYCD1;1 (Os09g21450)
MPADDDDASYLLCAEDAGAAVFDVAVDISTCTTEDDECCSVGGEELYSAASIAELIGGEAEYSPRSDYPDRL
RSRSIDPAARAESVSW**ILKVQEYN**GFLPLTAYLAVNYMDRFLSLRHLPEGQGWAMQLLAVACLSLAAKMEET
LVPSLLDLQVECSRYVFEPRTICRMEFLILTALNWRLRSVTPFTFIDFFACKVDPKGKHTRYLIARATEMVL
ATIHGKNTDVFAG*

>Orysa;CYCD1;2 (Os06g12980)
MMYKHVGDDARGSSAGVVCCVDVVDDDVDALLCGEDAGELEREGEPAQGSSPSSSLSCAAAAAAAADDDDED
EDEHGVHGEVVQVTPGGEEHCYDYDYDVDVPVGAELVMPACSPPRTAVHRPGWSESVSW**ILKVRSVH**GFQPA
TAYLAVSYMDRFMSSRSLPDHGWASQLLCVACLSLAAKMEESSAPPLLDLQIEGTRFIFEPRTIQRMELIVL
VELDWRLRSVTPFAFVDFFACKVGSSGRSSRILALRACQIILSAIHELEFLNHCASSMAAAAVLFAVNESPA
AMSHRSSVSSESAASWCIGLTEERISSCYQLLQRALNATARKRKRHPMILAACSSVTSSSSRSKRRKLDGHF
GED*

>Orysa;CYCD1;3 (Os08g32540)
MGAPATAASGGGDDDDRDVVFEYLLCTEEDAASAGSFFQQLQGPAPAVSSSPSTTTATAPAAAGSCDDGGEE
EEEEVWTVDVVAELIGGEAERSHSPRADYPGRLRSGRPADLAARADSVAW**ILKVRELY**GMLPVTAYLAVSYM
DRFLSLHRLPGNGWAMQLLAVTCLSLAAKMEETLVPSILDLQMEDARYIFEHRTIFRMELLVLDALDWRLRS
ITPFTFMYLFADKVDPNGKHIRELIHQATQVTLATIHDTEFLDHCPSSIAAAAVLCASSEIMQLVSIDHGTL
VSWRIIGLDEEAIIRCYRLMQQLISSNNVGRESTEITMATTTTTATTAVSSEEVVSSSPPSKRRKM*

>Orysa;CYCD2;1 (Os07g42860)
MGVLCFGASNILLCAEDSSSVLGLGGFGGGGGEVAAELGCGGGGGFDFFGFGGGAVFPIDSDEFVALLVEKE
MDHQPQRGYLEKLELGGLECSWRKDAIDW**ICKVHSYY**NFGPLSLYLAVNYLDRFLSSFNLPHDESWMQQLLS
VSCLSLATKMEETVVPLPMDLQVFDAEYVFEARHIKRMELIVMKTLKWRLQAVTPFSFIGYFLDKFNEGKPP
SYTLASWCSDLTVGTLKDSRFLSFRPSEIAAAVVLAVLAENQFLVFNSALGESEIPVNKEMVMRCYELMVEK
ALVKKIRNSNASSSVPHSPITVLDAACFSFRSDDTTLGSSQSNSNNKDYNSQDSAPASKRRRLNTTPI*

>Orysa;CYCD2;2 (Os06g11410)
MAPSFDFAASILLCAEDNTAILDLGEESEEISWVVGVDASLGDLSMDFPLQSDDCIEALLGREEQQHIPMEG
YLQRLLLQPDGLDLVAVRSDAIDW**IWKVHELY**KFGPLTAVLSVNYLDRFLSVFDLPQEEACMTQLLAVASLS
LAAKMEETVVPHPLDLQVCDAKYVFETRTIKRMELAVLNALKWRMQAVTACSFIDYYLHKFNDDDTPSTSAL
SRSVDLILSTCKVAEFLVFRPSEIAASVALVALEEHETSMFERVATCYKNLKKERVLRCYEMIQDKIIMRNI
MRQSAGSVFSIPKSPIGVLDAAACISQQSEDTFVGSPATNYESSASSKRRRICR*

>Orysa;CYCD2;3 (Os03g27420)
MGFLCRRRSSAAPAESFSLLCEEDSESVFGSDDDGVEETATMAPELGKMMSLGFSASHHLGDGGGGGEELVG
SFMEKEVEQMVETARGEYLTKLSNGGIELSCRIAAIDW**ICKVQAYY**SFGPLCAYLAVNYLDRFLSSVEFSVT
NDMPWMQQLLIVACLSLAAKMEETAAPGTLDLQVCNPEYVFDAETIHRMEIIVLTTLKWRMQAVTPFTYIGH
FLDKINEGNRITSELISRCTEIILSTMKATVFLRFRPSEIATAVALSVVADGGRVLDFGGVLESSKLPVDKD
NVGRCHQAMQEMALVMQNSTASPSDSLCYDMTNPVLDCHILRRRECVSLQSGPRDELEMGWAPFAITVSEKE
ESERRCDDGWRRGGEAAQYCEQADEQRRSTDGRAGVRLEEQAGGE*

>Orysa;CYCD3;1 (Os09g02360)
MAFATLFDSLYCPEEHLDLFHDTAADDDLHLDLHLHQPPPPPPLLDDDLPALFHALRGKEDPLRPAADDDGY
GGVSAREAAVGW**ALRAVARL**GFSALTAALAVAYLDRCFLGGALRLGDRPWMARLAAVACVALAAKVEETRVP
VLLDLQLCAAERADPNEAYVFEDKTVRRMELLVLSALGWRMHPVTPLSYLQPLLGTAHAARLHHCDTALLAL
MPDWRWPRHRPSAWAAAALLATAGWCGGGGGDDAELLALIDAPKDEMAECAKIISEEAAAAAAGGIVIGGEN
KRKGAAGLYSAPASPSGVIGASACFSCDSSSSSVDSLFAALEPPGRPIKRGAAAATTADPLPADEESRDAWP
PYAA*

>Orysa;CYCD4;1 (Os09g29100)
MAALTSYEMAASILLCAEDSSSVLGFGGEEEEEEEDVVAGKRARCAGPPPPPCVDVAGVDFAVPSEECVARL
VETEADHMPREDYAERLRAGGGDGDLDLRVRMDAIDW**IWKVHSYY**SFAPLTACLAVNYLDRFLSLYQLPDGK
DWMTQLLAVACLSLAAKMEETDVPQSLDLQVGEERYVFEAKTIQRMELLVLSTLKWRMQAVTPFSYVDYFLR
ELNGGDPPSGRSALLSSELILCIARGTECLGFRPSEIAAAVAAAVVGEEHAAFSHVNKERMSHCQEVIQAME
LIHPKPSSPSRVFVSSSIPRSPTGVLDAAGCLSYRSDDSAVASHYAASSWGYEHDSSPVSSKRRKISR*

>Orysa;CYCD4;2 (Os08g37390)
MAPSSSSCHDAAASMLLCAEDNSSILWLEDEEGEVGERRSGGCRSMVGDLAAGGGGGSGGGGVEEEEDMFPR
QSEECVASLVEREQAHMPRADYGERLRGGGGDVDLRVRSEAIGW**IWEVYTYY**NFSSVTAYLAVNYLDRFLSQ
YELPEGRDWMTQLLSVACLSIAAKMEETVVPQCLDLQIGEPRFLFEVETIHRMELLVLTNLNWRMQAVTPFS
YIDYFLRKLNSGNAAPRSWLLRSSELILRIAAGTGFLEFRPSEIAAAVAATVAGEATGVVEEDIAEAFTHVD
KGRVLQCQEAIQDHHYSMATINTVQPKPASTRRGSASASSSSVPESPVAVLDAGCLSYKSDDTDAATIASHG
GGRRKSCFDSSPVTSKKRRKLSR*

>Orysa;CYCD5;1 (Os12g39830)
MSMEEAEECSAACGFSLTCQEDGADLGDGVVDDDDDGDVFLFYNAVAAADDEEEEEEYVEQMVSKEASFCCS
SSSSLFDAAAGDGYGDGDGDGDWFRQARLAAVKW**ILETRGYF**GFGHRTAYLAIAYFDRFCLRRRVDREAMPW
AARLLSIACVSVAAKMEEYQSPALSEFDAGGGRVFCSDSIRRMELLVLSTLGWRMGAVTPFDFLPCFSSRLH
RHHHGGAGAAGHGAAAAARVALNAVGFIFATAEAGSVLDYRPSTVAAAAILAASYGAPLTKEALESKMSNLS
PSCLIDKENVHACYSMMVGDMNNNRRSSKRPLQCSDSNEITTTSTYDSVLVDDVTDTAAFAATAMNKRLRPE
PPRIR*

>Orysa;CYCD5;2 (Os03g42070)
MEAEDEYSAGCSFSLMCQEDSTDLDDDGGGGGCFAGDGRADLLLVYNAAAAADDEDEEEVEEYMDHLVSKES
SFCSSSSSTSSSSCCFSDAGGESAAAAAPMDWFALARRATVKW**ILETRGCF**GFCHRTAYLAIAYFDRFCLRR
CIDRSVMPWAARLLAVACVSLAAKMEEYRAPALSEFRAGVGDDGYEFSCVCIRRMELLVLSTLDWRMAAVTP
FDYLPCLSSRLRRHVGGGGGAGASAALIFSAAEAASVLDHRPSTVAAAAVLAATHGALTREALESKMSGLSP
SFLLDKEDVFACYSAMLSQPTSPASKSTTTTTGKRSSSSSCSESTDAASSYDATAASFPAAASCGSKRMRLE
LPGGILR*

>Orysa;CYCD5;3 (Os03g10650)
MGDASASTSAPATPTSTLICREDGNDLFSADPADDDGGGGSGGDWELSIADDDHVLLMDRDDEYLALMLSKE
RCAGGGGGGERGDEEEEEMVEEWMKNARAWCVGW**IVKTNAGF**RFSLKTAYVAVTYLDRFLARRCVDRDKEWA
LQLLSVACLSLAAKVEERRPPRLPEFKLDMYDCASLMRMELLVLTTLKWQMITETPFSYLNCFTAKFRHDER
KAIVLRAIECIFASIKVISSVGYQPSTIALAAILIARNKETAPNLDELKSVVGSLWQQLDTGHVYSCYNKMM
IQEDRSMQSTTEVASSGVSVAHIGGSEDSAMGGANNATTLEATPDKKRKRLHSPQRQ*

>Orysa;CYCD6;1 (Os07g37010)
MDMATGAKEVVVVEAYEYEFDLENPFTSPADEPIASLLDAEGHHSPSVSAAASAARREAAGF**ISKVRYDG**EL
DVHPRVAYLALNYVDRYLSKRQLACERNPWAPRLLAISCLTLAAKMQRAAAISAADIQRGEEFMFDEAKIQR
MEQMVLNALEWRTRSVTPLAFLGFFLSACFPQPRHPALLDAIKARAVDLLLRVQPEVKMAEFSPSVAAAAAL
LAAAGEVAGAHLLGFEAGVAACPFVNSEKLRECGEVMAAACGVGPSWAAAATSAETPVTVLGHHRSASSESE
RTTTVGSAANSADAKRRCMGPPRQWGVGGPDE*

>Orysa;CYCD7;1 (Os11g47950)
MDDDDDTSFNNSLDLYCDEDPFDSTPPPPPPPPEQQQQAGTTTPDDIDDEVMEYYKAKQRCYALQIRDYCCY
LQCHHLLLQQQQHGVAAAR**LKAAMGRL**GLEAATAFNAANYLDRFLSINCHLKWEEWMVEVVSVGCLSLACKL
DEVTIPSLHDLQMEEAMGHSFRASTIRDMELTLLKALRWRLACVTPFSFLPVTTTTTTTRALLLRSLLDPSF
LRFDASLLAASALTLSSTTPQHPNHLLLNRLIHPFSQTDHEVKECFNMMKALHLDMSKNPGRSSDHPCWSPI
SVVIPFHTDGTVKRSAISRCLFGSGRLKARSI*

Poplar CYCD

>Poptr;CYCD1;1 (AM746109)
MSYSDCLSDLLCGEDSSDIFSGESPECSSDLESHDFVEESSIAGFIEDERNFVPGYDYFSRFQSQSLDASAR
EQSVAW**ILKVQACY**GFQPLTAYLSVNYLDRFLYSRRLPQTDGWPLQLLSVACLSLAAKMEEPLVPSLLDLQV
EGAKYIFEPRTIRRMELLVLGVLDWRLRSITPFSFTGFFACKLDPAGAYTGFLISRATEIILSNIKEASFLE
YRPSSIAAAAILCAANDIPNLSLVNPEHAESWCDGLSKDKIISCYRLMQDLVLDDSRRKSTKVLLPRLRVTI
RARMRSSGSDSSSSSSSSSYKKRKLNNCLWVVDDDKGNSE*

>Poptr;CYCD1;2 (AM746110)
MSYSDCLSDLLCGEESSDIFSGESPGCSTGLESHDFVEESSIASFIEDERNFVPGFDYLSRFQSQSLDASAR
EESVAW**ILKVQAYH**GFQPLTAYLSVNYLDRFFYSRRLPQTDGWPWQLLSVACLSLAAKMEEPLVPSLLDLQV
EGAKYIFEPRTIRRMELLVLSVLDWRLRSITPFSFTGFFACKLDPTGAYIGFLISRATEIILSNIKEASFLE
YWPSSIAAAAILCAANDIPNLPLFNPEHAESWCDGLSKDKIISCYRLMQDLVLDNSRRKSTKVLLPQLRVTI
RARMRSSGSDSSSSSSTSSYKRRKLNNCFWVHDDKGNSE*

>Poptr;CYCD1;3 (AM746111)
MSHPHSPDHCASAVNSLYCGEDASENTITKFIDSESQFMPLSDYLHRCRHRSIDTTARQDSINW**ILKVHAHY**
AFRPLTALLSVNYFDRFLSSYSLPENGWPYQILSVACLSLAAKMEEPDVPLLLDLQVLEPGFIFEPKNIQKM
ELRVMAYLNWRLRSVTPFDYLDYFISKLPSCSSTNPDNFSRLLKDSSDLILNTTRVIDFLGFTPSTVAAAAA
ISAAGKSYDTIPWEAGDGQFFHERVNKEMVRSCHQLMEEYLIDTCPLSRHKIDHYPAPPDTLSNFYYLY*

>Poptr;CYCD1;4 (AM746112)
MQVYAHYEFRPLTALLSVNYFDRFLSSYSLPENGWPFQLLSVACLSLAAKMEEPDVPLLLDLQILEPGFIFE
PKNIQKMELRVMANLNWRLRSTTPFDYLDYFISKLPSCSSTKPENFDRVLKKSADLILNTTRVIDFLGFAPS
TVAAAAVISAAGKNFDTIPLKAGVGQFFHERVNREMVRSCHQLIEEYLIDTCPTARLKDLSDDALVDPASPA
GVLDAAAACGSCSTRSENPISASSQAPETEPIIKRLRSTATDVQEP*

>Poptr;CYCD1;5 (AM746113)
MSVSADVSTPSVNLYCNETAGDALCSNNADGISEINSAYFPVDIDESYIDNILVSELHQMPETELIARFPDI
PESGSAHQDTLNW**MLKVHAYC**RFRPETAYLSANYFHCFILSHTLQKGKGWPLQLLAVACLSVAAKLEETRVP
SLLDIQTLEPRFLFKPSTVRRMELLVMGSLKWRLHIITPFSFLHYFIAKLSHLSPRSKNLILAHSSDLIIST
CRVMNILAYTPSTIAAAAVLWVTDQSIGCPKLECFHNRMSKEMVRGCYNLIKQNTPQLSRGKALDATIPGKC
LAKKCCSKDFKSSQDMSPSKC*

>Poptr;CYCD2;1 (AM746114)
MAPSFDCAVSNLLCAEDNNSIFDDNDHYDATVEEFEATWHHGNHQICNQNGGGDGGCLPMQSDECLVLMVEK
ECQHLPNGDYLKRLRNGDLDMGARKEAVDW**IAKAGSFF**FLFFFTIVHAHFGFGPLCAYLSINYLDRFLSAYE
LPNGKPWMMQLLAVACLSLAAKMEETEVPLSLDLQVGESRFVFEARTIQRMELLVLSTLSWRMQAITPFSFI
DYFLSKINNDQTPPPKSLILQSIHLILSTIRGIYFLEFRPSEIAAAVAIAVVGETKTVDAEQAISVLAQPVQ
KERVLKCLQLIHDLSLFGGSVKGTSASLLSVPQSPIGVLDAACLSYSSNHTTVEPCANSSHNTPDAKRRKLD
K*

>Poptr;CYCD2;2 (AM746115)
MAPSFDCTVSSLLCAEDNNSIFDDNDCYDATVEEFEATWHHGNHQIQNQNSGWWLPMQSEECLVLMVEKECQ
HLPSGDYLKRLRNGDLGLGARKEAVDW**IAKVNAHF**GFGPLCAYLSVNYLDRFLSAYELPKGNAWMMQLLGVA
CLSLAAKMEETEVPLSLDLQVGESRFVFEARTIQRMELLVLSTLDWRMHAITPFSFIDYFLGKIINDQTPPR
SLILQSILLILSTIKGIYFMEFRPSEIAAAVSIAVVGETKTVDVEQAISVLAQPVQKERVLKCFQLIHDLSL
FGESXSSKGPSASLLSAPQSPIGVLDAACLSYNSDVGPCANSSHNTPDAKRRKPAKPC*

>Poptr;CYCD3;1 (AM746116)
MASMYNPETSAVQDQQQYQQNPTLLYDALYCSEENWVEEVREDCFQDELEGESYCSNNSNKLNTFPIFLEQD
LSWEDEELSSLFAKEEQNQLCKDLETNPSLARARCEAVEW**ILKVNEHY**SFTALTAVLAVNYLDRFLFSVHLQ
KEKPWMAQLAAVSCLSLAAKVEETQVPLLLDFQVEDSKYVFEAKTIQRMEILVLSTLKWKMNPVTPISFLDY
ITRRLGLEHYLCLEFLKRCERMVLSILADSRSMPYVPSVMAAATMLYVIDNIEPSLAAEYQSQLLSILGIDK
DKVEDCSKFLMEFALRYHFKLLSNKRKFCSLPGSPSGVVDVSFSSDSSNDSWSVASSVSSSPKPLSKKSRAL
QSLNNATTSDFSQHSSLVP*

>Poptr;CYCD3;2 (AM746117)
QYQQNPTFLYDGLYCSEENWEKEVREDYFQDEVKGEYFYSIDSNKRNTFPVFVQQDLSWEEEELSSLFAKEE
QNQLYKILEINPSLARARCEAVEW**ILKVNVHY**SFSAVTAVLAVNYLDRFLLSVHLEKDKPWMAQLAAVACLS
LAAKVEETQVPLLLDFQVEDSKYVFEAKTIQRMEILVLSTLKWKMNPITPISFLDYIIRRLGLKDYLCLEFL
KRCERIVLSVVPGKLSMLYVPSVMATAVMLYIIDGVEPSLAAEYQSQLLGILGIDKDMVEDCSKLVMELAPR
DHFKFSSKRKYSSIPGSPNGVIDVSFSSDSSNYSWSVVSSVSSSPEPLSKKTR*

>Poptr;CYCD3;3 (AM746118)
ELNSQQEQNASFLLDALYCEEGRWEDESEEEVLQESTFVNDLFPLSLLEQDLFWEDEELLSLFSKEQEQQAS
VSVNNVADDPFLSRARQEAVEW**MLKVIAHY**GFSALTSILAFNYLDRFLSGPCYQRDSRPWMIQLVAVTCLSL
AAKVEETHVPFLLDLQVEDTKYVFEAKTIQRMELLVLSTLKWKMHPVTPLSFLDHIIRRLGLKTHVHWEFLR
RCEHLLLSVVSDSRSVSYLPSVLATATMMHVIDQVETFNPIDYQNQLLDVLKITKEKVNGCYGLILELSRNR
TIANNKSQKRKFEPMPSSPSGVIGAVFSSDSSNDSWAVQGSSVSSSPEPLFKKSRTQDK*

>Poptr;CYCD3;4 (AM746119)
MAIPKQQELGQNELSTQQEQNTSFLLDALYCEEGKWEDDSEEEVLQESPSVNNPSGDLFSISLLEQDLFWED
EELLSLFSKEQEQQASVSVNNVASDPFLSRARQEAVEW**MLKVIAHH**GFSALTSILAINYLDRFLVSPCYQRD
NRSWMIQLVAVTCLSLAAKVEETHVPLLLDLQVEDTKYLFEAKTIQRMELLVLSTLKWKMHPVTPLSFLDHI
IRRLGLKTNVHWEFLRRCEHLLLYVVSDSRSGCYLPSVLATATMMHVIDQVETFNPIDYQTQLLDVLKITKE
KVNGCYGLILELSRTRAIANNKPKKRKFEPTPLQGSSVSSSLETLFKKGRTQDQWVFVDIIGSPR*

>Poptr;CYCD3;5 (AM746120)
MSFLQEQDTHRQSPALVLDGLYCEEEGFGEDYSCGFDDEIGDQNIKKEQTLSSVLLQQDLFWEDNELLSLIS
KEKETHVRFDGGGSIDGSLMVARREAVEW**FLRVKAHY**GFSALTGVLAVNYFDRFISSSRFQRDKSWMGQLAA
VACLSLAAKVEETHVPLLLDLQVEDAKYIFEAKTIKRMELLVLSTLQWRMNPVTSISFFDHIIRRLGLKTHL
HWEFLWRCERLLLSVISDSRFMSYLPSILATVTMLHVIKEGDPRNQLEYQNQLMAVLKTNEDEVNECYKLII
EPSGSQNQRHKRKYLSTPSSPNGVIDASFSSDISNNSWAVASSVSSSSVPQFKRSRAQVQQMRLPSLNCMCV
DVLSSPR*

>Poptr;CYCD3;6 (AM746121)
MSFFQQQETHNQSPALALDGLYCEEDGFGEDYSCSLDDETSQVYEQNVKKEQNLSPVLLEQDLFWEDNELLS
LISKEKETHFVFDSVGSRDGSLMVVRREAVEW**FLRVKAHY**GFSALTGVLAVNYFDRFISSSRFRRDKPWMGQ
LAAVACLSLAAKVEETQVPLLLDLQVEDAKYVFEAKTIKRMELWVLSTLHWRMNPVTSISFFDHIIRRLGLK
THMHWEFLWRCERLLLSVISDSRFMSYLPSILATATMLHVIKEVEPRNQLQYQTQLMAVLKTNEDEVNECYK
LILEQQGSQNQRHKRKYLSTPSSPNGVIDATFSSDSSNDSWAVASSISSSSSVPQFKRSRSHVQQMRLPSLN
RMCVDVLSSPH*

>Poptr;CYCD5;1 (AM746122)
MGDFDNSLSLSSLLCHENESCFFNDSISDHSNIKHDRSRFGLETEVDVEYVEKLVERETITFGYRCHASFDD
CLITSHNWLKFARLDAIEW**ILNTRAIY**GFRFHTAYLSVTYFDRFVSKRSIDEGKLWAIRLLSVACLSLAAKM
EERKVPPLSEFPVEDYCFGNKVIQRMELLVLNTLEWRMNSITPFAYLHYFIHKTCGESTPKETVSRAVELIV
AMIKEIDLLDHRPSIIAAAAVLAASNRQLTRKELELKMDMISSWGSLENENVFSCYIAMQEIEMGKAKTPRL
VFYPNSSAIHSGSFDVLENSSLVSGAGIKRSLTFNECDQTCPAKKICRP*

>Poptr;CYCD5;2 (AM746123)
MADESLSPGDLFCYEDFLGELAVADEDDTYIDITRTYVGDPDTEDEYLTLLANREPHQGFNANETLVLDASF
RTARLEAITW**ILRTRKNF**GFHFHTAYLSMIYFDRFLSSRFIDRNYTRVVSLISVGCISLAAKMEEVRVPSLP
QLQTEGVTFESTNVERVELGILSTLQWRMNYATPFAFLRYFIIKFSRQDSPPRETVSRTVQSILALMREIHL
MSHRPSVIAAAATLVVLNNSLTRTTLETQMNSIAYPGFLNIVSD*

>Poptr;CYCD5;3 (AM746124)
MAGESLSPNDLLRQEDFRAELSVADEDDTYIDISRTYVGDPDTEEEEYLALLANQEPHRGFSANDTLVIDSW
FRNARLEAITW**ILRTRKTF**GFHFHTAYLSMIYFDRFISSRSIDRRYSWVVKLISVACISLASKMEEVQVPSS
PEFQTDGVIFESKSVKRVELGILSTLQWRMNYTTPFAFLRYFIMRFSRQDSPPRETISRTVRYILALMKEIH
LMSHRPSVIAASSLVVINNSLTRTTLETQMNSVAYPGFLNIEDVFRCYNLLQQLDVENLRSTANGLPLKAR
PALFLFEALLAVFKFERGHETQDIVYGNQKEFLCLIIL*

>Poptr;CYCD6;1 (AM746125)
MKLDLENPLTSSEEHQSDTITYLFASEFDHMPSRNLLNFLETCDHFYVSFRHEAISL**ILQAQYSC**NCGPFIP
YLAVNFMDRFISRMEIPQGKPWILRLVVVSCLSLAAKMENTDFSISNFQGDEAGFIFDNKTINRMELLILDT
LDWRMRSITPFSFVHFFISLSQLKDPALTQTLKDRATEIIFKAQNEIKLLKFKPSIIAASALLVASKELLPL
QFPSFKFSISAFECVKEFNVGVRASLRAPRLIPWALKLTTM*

>Poptr;CYCD6;2 (AM746126)
MEFDLENSLTSLEEHQSDTVPNLFASESDHMPSRNFLHCLKTSGFYVSFRQEAISL**ILQAQYSC**NYDAFIPY
LAVNYMDRFISKQEIPQGKPWILRLVVISCLSLAAKMKNAHFSVSDFQGEEAGFIFDTQTINRMELLILDAL
NWRMRSITPFSFVHFFISVLELKDPSSSQPLKDRATEIIFKAQNEIKFLEFKPSIVAASALLVASNELLPLQ
FPLFKCSISSCAFVNKEKLLSCFNAVQEMVEMEWYESMLDTMSCTRTPLSVLDRQCTKSESETTSTTSINNG
STVPEIKRRRLNGHSSK*

>Poptr;CYCD6;3 (AM746127)
MEFDLENPLTSLKEYVSDTIPDLFVSESDHMPSRNFLHCLKTSDFYVSFREEAISR**ILQAQYSC**NYDLFIPY
LAVNYMDRFISRQEIPQGKPWILRLLVISCLSLAAKMKNKHFSISNSQEAEAGFIFDTQTINRMELLVLDAL
NWRMRSITPFSFVHFFVSLFELKDPSSSQPLKDRATEIIFKAQNEIKFLEFKPSIIAASALLVASNERFPLQ
FPCFKCSIYSCEFVNEEKLLECFNALQEMVEMEWYESMLDTMSWTRTPLSVLDRHFTKSENETTSIITSTTT
ITNGSTVPEIKRRKLNGYSGK*

>Poptr;CYCD6;4 (AM746128)
MDFNLENPLTNSHELHFDTTPSLFLIESDHMPSKNYLKTLKEIDFDVSFRREAISS**VLRVSCNF**DPSLSYLA
VNYLDRFLSSQGIPQPKPWVFKLLAVACVSLAAKMKEAEFYVTDIQGDGGFVFDPQTIQKMEVLILGALNWR
MRSITPFSFISFFISLFKPKDPPLRQALKARACEIIFKAQNDINLLEFRPSLTAASALLYACHELFPMQFLC
FRKAISICSYVNKENLLQCYNAMQETAMDGYKSQFDMVSSSDTPVNVLDRHFSSSESENTNGTVVMISSNGS
NKTWPEKGIKRRKISALCNNQTVQFSAFSDATTMLM*

>Poptr;CYCD6;5 (AM746129)
MDFNLENPLANSHDFHFDTIPSDLFLIESDHMPSNNYLNTLKEMDFDGSFRREAISS**VLRVSCNF**DPSLSYL
AVNYLDRLLSSQGIPQPKPWLFRLLAVACVSLAAKMKEAEFCISDTQARXDGGFVFDTQTIQKMEVLILGAL
NWRMRSITPFSFISFFISLFKPKDPPLRQALKARASEIIFKAQNDINLLEFKPSLIAASALLYASHELFPMQ
FLCFRKAISNCSHVNKENLLQCYNAMQEIAMDGYRSQFDMVSSSDTPVNVLDQHFSSSESEKT*

>Poptr;CYCD7;1 (AM746130)
MDSLLCDEVWLSSPATPDHHNQPRYSHGENYAAASSFYTTKEDCEKAVSIYLEKEFTCMPEPGYVEHLRTKN
LLFARLRAIQW**LIKSRERL**SLSFETVFNAANYLDRFMSMNQCHGWKCWMVELLCVACLSVASKFTETRTPCL
HDIQMEDLDHSFQPITIQRMELVLLRALGWRLGSTTAYSYVELLMMEIDFLKSYSYLQKDLVACRITELLLG
AMQDCSMVGFRPSITAISALWCSLEEFVPSKSDAHLAHIKGLLNALDHKDDVVIKCHGIMEAQLINPVYNLL
ACGKKHSYCCPSSPVTVLPTERIGIYDCDVDLSFFNDSGSNNKQETSKKKRKWHEKSIKDDGFQKRIK*