

S5 Table. A list of amino acid sequences of DUF26 used for constructing phylogenetic tree

Single DUF26 sequences

| | |
|-------------|---|
| AT3G04370.1 | NYSNQNLFRAQALSSFLRKESESSRSKFLKTLVGNKHAVSGWFQCREDPSEICHKCVGDLREISSRSC GNATSARIHLRGCHLIYK |
| AT3G22030.1 | GNVNSFNKKTTEFLYKLGKADRLDVDGINFLYYAAGEMRLGKQTLFAMVQCAKDILSCKDCLEWSIKELS KCCDGKQGARVVGITICNLRYELY |
| AT4G20530.1 | KCSNTQGKYKQGSFAFEKLNLLVLTITSIGNFRDGFRTYEEGEDPNNVFMVQCRGDSYWSKCPPCISTA VSLRRRCPRNKGAIWYDQCLLKIS |
| AT4G20540.1 | KCSNTQGKYKQGSFAFEKLNLLVLTITSIGNFRDGFRTYEEGEDPNNVFMVQCRGDSYWSKCPPCISTA VSLRRRCPRNKGAIWYDQCLLKIS |
| AT4G20600.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDIFTKCFECLE GILRKFPQCCDGKRGGRVFGTSCNFR |
| AT4G20630.1 | KCSNTQGKYKQGSFAFEKLNLLVLTITSIGNFRDGFRTYEEGEDPNNVFMVQCRGDSYWSKCPPCISTA VSLRRRCPRNKGAIWYDQCLLKIS |
| AT4G20650.1 | KCSNTQGKYKQGSFAFEKLNLLVLTITSIGNFRDGFRTYEEGEDPNNVFMVQCRGDSYWSKCPPCISTA VSLRRRCPRNKGAIWYDQCLLKIS |
| AT5G41280.1 | CNDSSGNFTRNTTYNTNLNTLLSTLSNQSSFANYNLTGLGSDTVHGMFLCIGDVRNRTTCNACVKNATI EIAKNCTNHREAIYYFSCMVRYS |
| EFJ04200 | NVNSAMVVLSSHGSSTTVTSGDGKSRVFLRECRDMSAEQCNTCMAVATKNLHRETICARFDTFL |
| EFJ10327 | SFSPGSAFERNLDAALQSVISSRSPPSAALGASPDVAYARGECYNNLSPQDCVLCGLMANQTIRGQAPR TIGARLFSNSSDYSCYLRNY |
| EFJ12758 | NTSLGSPFQQNWLVDVYQVLLDHAPQAVSSEFSHGQSPNTVSGFALCIKGSNCKGCLQTIKANLDRAAPL SKGARLCMKTSTDVCYMRYEAY |
| EFJ12964 | ESSEDSPEKKNLASAYESLLSPSQESPRQAQAGDDPDTVYGYAACFEGNCECLATCKNYFTQVAPHAV GARLCLKSGSDACYLRNY |
| EFJ13641 | RTYARGSVYGSNLNLLFDRLITTTGYDHSVGSNRVYGFSECYGSPNCRSCLLAAVNSIRSAPRAIGARIC KALCYLRNY |
| EFJ13924 | NTSLGSPFQQNWLVDVYQVLLDHAPQAVSSEFSHGQSPNTVSGFALCIKGSNCKGCLQTIKANLDRAAPL SKGARLCMKTSTDVCYMRYEAY |
| EFJ15639 | STPYATNQNRLLDILKDTGSDSFIYTSVGDAPYIAYGRAECYGNCGNCLVEARNTIKNAVPPQAVGARLCT DDCYLRFENY |
| EFJ15855 | NTTEGSPFQKNVETVLNFFYEHNPPNGFATCLGYGDFPNTVYGHGTGCYNMSDQPSCEICKAYQGIQ QNAPYTLGGTYWINETEIRCLRYENY |
| EFJ16456 | NVNSAMVVLSSHGSSTTVTSGDGKSRVFLRECRDMSAEQCNTCMAVATKNLHRETICARFDTFL |
| EFJ18708 | KTTEGSPFQKNVETVLKFFYEHNPPNGFATCLGYGDFPNTVYGHGTGCYNMSDQPSCEICKRAYQGIQQ YALYALGGTYWINETESRCLRYENY |
| EFJ22561 | ESSEDSPEKKNLASAYESLLSPSQESPRQAQVGDGDDPDTVYGYATCFEGNCECLATCKNYFTQVAPHAVG ARLCLKSGSDACYLRNY |
| EFJ22969 | CSDESIPTGSTYWTSLNQLTLDLIQNTAYANNMTYSVKNGGDDVSAYGQAQCFNMVGNPVMCKSCVE DLVRRRAWRECGDAIAGMLMLKDKTIRYQD |
| EFJ28936 | RTYARGSVYGSNLNLLFDRLITTTGYDHSVGSNRVYGFSECYGSSNCRSCLLAAVNSIRSAPRAIGARIC KALCYLRNY |
| EFJ30128 | RKTTQGSQFQKNVETVIQFLYEHNPPNGFASCLGYGDFPDTAYGHGTGCYNMSDQTSASCISQIQQTYSEFQ QLAPLAVGGVLTWNTDSNRCRIRFENY |
| EFJ30567 | CSDESIPTGSTYWTSLNQLTLDLIQNTAYANNMTYSVKNGGDDVSAYGQAQCFNMVGNPVMCKSCVE DLVRRRAWRECGDAIAAMLMLKDKTIRYQD |
| EFJ32980 | NTTEGSPFQKNVETVLNFFYEHNPPNGFATCLGYGYFPNTVYGHGTGCYNMSDQPSCEICKAYQGIQQ NAPYTLGGTYWINETEIRCLRYENY |
| EFJ33692 | RNTQPGSAFQRNLSNVYRRIINGATFRQGSISYNAGVDPDRVYGFSAFCGGFTAPGDVCVQLVDIRANF DSVAPLAVGARMCSRNGERTCYLRNY |

| | |
|------------------|--|
| EFJ33923 | LYSFGDPFGKNLGLVLDLDDLLGTTGRDFKDYTAISPRPSRFVYGHAKCRHALSAGECGVCLKGVAAALAD QCGNAVGGGRAMFVDCFMRYEAY |
| EFJ37042 | RNTQPGSAFQRNLSNVYRRIINGATFRQGSISYNAGVDPDRVYGFSAFCGGFTAPGDCVQLVDIRANF DSVAPLAVGARMCSKNGERTCYMRYENY |
| EFJ37434 | LYSFGDPFGKNLGLVLDLDDLLGTTPRRDFKDYTAISPRPFRFVYGHAKCRHALSAGECGVCLKGVAAALAD QCGNAVGGGRAMFVDCFMRYEAY |
| Gnk2 | CNTQKIPSGSPFNRLRAMLADLKQNTAFSGYDYKTSRAGSGGAPTAYGRATCKQISQSDCTACLSNL VNRIFSICNNAIGARVQLVDCFIQYEQ |
| LOC_Os01g36500.1 | CGASNYTADSMYRLNLDGMSASLFPAGAGGGGGIFVRGSSGADPDKVYVAVALCRGDVDDAPACSSCF DAAFRRAMQLCPRSKDATIYYDECLLRFS |
| LOC_Os01g38910.1 | CSLSGGRYGQNTTYEDNLKALAARLVGVARVSNFASHTVGSAPDAAYGIALCRGDYTGDECANGLRKA ENAVENRFLCDRFRDATIYYDQYMLRFS |
| LOC_Os01g56720.1 | GRVVAQCAAGVAPADCVQCLEGAAREMPRCFREARREEQEGEVGIVVSDDCVLRFD |
| LOC_Os01g56840.1 | TGSNGTAFRANLLTLLASLPDQAAPTGFASMQAGAGGRAPGGDDDDRAFARGSLGDSTPSQCRDCL AAAVIDVAEGCGADTRRAGAWLSGCYLAYAD |
| LOC_Os03g19840.1 | NGKTRRRSINSVSDLVAKAASNGGFATSSAGKGNVYGLAQCRGDVSASDCKACLVEAANYTSLFCH YASDSRMWYDYCFMRYKN |
| LOC_Os07g35190.1 | YAANSTYEANLRYLAATLPKVMNGSSSSSDVLAGERPNIASASCNSSSSEYHDCGACVAEAFRCAR RLCPYSRHAVVHLGGGACSVRY |
| LOC_Os10g10540.1 | CTSTAAGNYTQDGAYAANLGRLLAMLPNETVSKNGGFFNGTVGNGTATVYGLAMCAADFSRADCMD CLVAAGISAGGVVKRCPGSTTVSAMFDQCLLRYS |
| LOC_Os12g41510.1 | CSTTGNYTVGNQFEKNLDQLLSTLATAATDDGWFTSSVGTGTAYQVFLIMCHADYNATECKKLAG APAGIKQVCPGSRVTKANYDACLLRYS |
| PTQ30062 | RNGTAYQHNVRVSLKLMKAVQSRPLFDVWDEASDAYDNSETAYGVAGCNTVTPPECRYCLQYIVTNL QQWCPKDPKSAKIVLKDCYLHYDRY |
| PTQ32071 | AVSACIDSLTEEPMDKKTASAIEVTPDKVVYCSMDCKQNLTLQEQACLQAKLLRENYCPRAVSASSVI GICSLMHET |

DUF26-A sequences

| | |
|-------------|---|
| AFP1 | CSGSSYAGSSKAVANINSLADLVASASSTGGYATSTAGKGNNSIYGLAQCRGDVSASDCASCLADA QLPSTCSYSSDARIWYDYCFMRYEN |
| AT1G04520.1 | QQFSDPSGLYSQALSAMFGSLVQSTKTRFYKTTTGTSTTTITGLFQCRGDLSNHDCYNCVSRPLVSDKL CGKTIASRVQLSGCYLLE |
| AT1G19090.1 | SSITDVSPPIYVFLQCRELDVSDCRHCFNESRLELERKCSGSGGRIHSDRCFLRFD |
| AT1G61750.1 | CYTSNGYTPNSSYKSNLDTLISVLDSQSSNKGFYASGSSPTTIVYGSYLRCRDISSTCETCISRASKNVFI WCPVQKEAIIWYEECFRYS |
| AT1G63550.1 | CNPTNFTQTSSYETNRDTLASLRESSSLGHYSNATEGLSPDTVHGMFLCRGDITASCVDCVQTATTEI ASNCTLNKRAVIYYDECMVRYSN |
| AT1G63570.1 | CSVDSFTQTSSYETNRNILLTTLSSLVHYLNATIGLSPDTVYGMFLCRGDINTTSCSDCVQTAIEIATN CTLNKRAFIYYDECMVRYSN |
| AT1G63580.1 | PDTYQSNRNTVLSTLRNHSSLSGYSYFNATAGLSPNTVYGMFLCIGNISKTSNCVHSATLEMDKSCESH DTSFMFSDECMVRYSD |
| AT1G63590.1 | CTQFDNVTRTSSYLSNRDVLSTLRNRSSIGSYSNATAGLSPNTIYGMFLCRGDLNRTSCSDCVNATTLEIY KSCFYRKSALVISNECIVRYSN |
| AT1G63600.1 | CNQFSDNFTQTSTYETNRETVLSSLRLRSSLGYSYFNATAGLSPNTVYGMFLCRGDISETSCSDCVQTATTEI SRNCTYQKEAFIFYEEMVRYSD |
| AT1G70520.1 | ETAYVPNFVATMEKISTQVQTSFGVVALTGTGPDANYGLAQCYGDLPLNDCVLCYAEARTMLPQCYPQ NGGRIFLDGCFMRAENY |

| | |
|-------------|---|
| AT1G70530.1 | CNNRRTTPQQRSLFVTNFLAAMDVAVSPLVEAKGYQVVTNGTGNLTVYAYGECIKDLDKDCDLCAFIK AKVPRCLPFQKGRGGQVFSQDGCYIRYDDY |
| AT1G70690.1 | CSPAKFSPSSGYETNLNLSLSSFTSTAQTRYANFTVPTGKPEPTVTVYGIYQCRGDLPTACSTCVSSAVA QVGALCSNSYSGLQMENCLIRYDN |
| AT2G01660.1 | CSQEKYFPGSPYESNVNLSLTSFVSSASLYTYNNFTTNGISGDSVVYGLYQCRGDLSSGSDCARCVARA VSRLGSLCAMAASGGALQLEGCFVKYDN |
| AT2G31620.1 | CINSEGKYKAKNSYESRLKDLHLSMSNILDYGFHGVGGADSSTYYIKAQCRGDASESKRCLFTAFSGIL RRCNNRGRRIIWDNCFLYIS |
| AT2G33330.1 | PSGLYSQALSAMYGLLVQSTKTRFYKTTTGTSQTSVTGLFQCRGDLNNDNCYNCVSRPVLVSGKLCGK TIAARVQLSGCYLLE |
| AT3G21960.1 | CINGEGTFKSGSPYEKEIKLIDFLSSFIKDYSFVHGVSGIGPDDINVKFQCRGDTLQAKRCLATAFSEIR SKCPNNKGRRIIWDNCHLDL |
| AT3G21970.1 | CNNTQGRYTHGSTFEKNLNQVLHNISNLDLRYGYAYVSNVVAYKVKDPNIVFVLLQCRGDSFGSKCHS CLSTAVSGLRERCPGNRGATIWDQCLEIS |
| AT3G21980.1 | KCNNTGKYSHGSAFEKYINLALRAIDSDNYLNGFAYIERGEDPNKVFVMYQCRGDSYSGKCKSCISAAS |
| AT3G21990.1 | KCSNTQGKYKQGSFAEKNLNLVSTITSIGNFRDGFYTEEEDPNNVFMFQCRGDSYWSKPPCISTA VSLRRRCPRNKGAIIWYDQCLLKIS |
| AT3G22040.1 | CRVGQKGYHPGSRYEKDFDSLTSFVAANKFIDGFFVHSSNSDGNSTIIFQCRGDSYKNCRTCYDTALA GFRKRCPRNKGGIWDQCFLDVS |
| AT3G22060.1 | CSDIEGSFTSKSLYESNLNLSQSLYKVPSTGFAASSTGNTPNNVNGLALCRGDASSDCRSCLETAIPEL RQRCNNKAGIVWYDNCLVKYSS |
| AT3G29040.1 | CNNTQGTYTRGSTFEKNLNQVIRNISHLHLYGYTYNSNVEAYEVSKDPNIVFVLLQCRGDSYSGKCHSCL HTAFSGLRERCRGNKGAIIWYDQCVLEIS |
| AT3G45860.1 | SSILTYSRNSTYFTNLKTLSSLSRNASYSTGFQTATAGQAPDRVTGLFLCRGDVSEQVCRNCVAFSVKET LYWCPYNKEVVLVYDECMLRYSH |
| AT3G60720.1 | CSPEKYTPNTPFESNRDTFLSSVVTSSSDASFNSFAVGNDSSSSSSSSAVFLYQCRDDLRSDDCKCIQTS VDQITLICPYSYGASLQLEGCFLYET |
| AT4G00970.1 | CLSQQSNFAKSSQFSKNLDSLVSSIPSLKSNNTYNYFSLVSGSISDQERVEAIGICNRVNRVDCLNICIAQAA VNLTMYCPQHRGAYVRATKCMFRYSD |
| AT4G04490.1 | EDFSPNTSYVENESLLPSLASNVIRERGFYVNSLDGVYALALCRKHVEVQACRRCVDRASRTLLTQCRGK TEAYHWSENDANVSCLVRYSN |
| AT4G04500.1 | NYGVSRTYLFSSLPNSVVSNGGFYNASFGGRDSKNNRVHVVALCRRGYEKQACKTCLEHVEDTKSKCPRQ KESFSWVTDEFDDVCSLRYTN |
| AT4G04510.1 | SFPTNSSYQKNRDSLFSTLSDKVTNGGFYNASLDGVHVVGLCRRDYDRQGCINCVEESIRQIKTSCSNRV QSFHCNSDDRERVSCLVRT |
| AT4G04540.1 | SFFNGNSSYAQNRRDLFSTLPNKVVTNGGFYNSSLGKSPNIVHAVALCGRGYEQQACIRCVDSAIQGILT TTSCLNRVDSFTWDKDEEDNVSLVSTS |
| AT4G04570.1 | FNGNSSTFAQNRQKLFPTLADKVIINDGFYNASLGQDPDKVYALVSCARGYDQACYNVQSLTQNTLT DCRSRRDSFIWGGNDVTCLVRSSN |
| AT4G05200.1 | CPNTTYSRNSSYLNLRTVLSSLSPPNAAAYASLFDNAAAGEENDSNRVYGVFLCRGDVSAEICRDCVAFA ANETLQRCPREKVAVIWYDECMLVRYSNQ |
| AT4G11460.1 | CSEKFGTFTPGGTFDKNRRILSSLPSEVTAQDGFYNASIGTDPDQLYAMGMGIPGAKQKLCRDCIMDVT RQLIQTCPNQTAIIHWSGGGKTVCMARYYN |
| AT4G11470.1 | VFFRPNGNYDTNRRLLVSTLASNVSSQNNRFYNVSVGEGAGRIYALGLCIPGSDPRVCSDCIQLASQGLL QTCPNQTDSEFYWTGDNADKTLCFVRYSN |
| AT4G11480.1 | FFRPNGTYDTNRHLILSNLASNVSSRDGYNGSVGEGPDRIYALGLCIPGTDPKVCCDCMQIASTGILQN CPNQTDSDWRSQKTLCFVRYSN |
| AT4G11490.1 | CNETGYFEPWKTYDTNRRQLTSLASKVVDHYGFYNSIGKVPDEVHVMGMGICIDGTEPTVCSDCCLKVAA DQLQENCPNQTEAYTWTPHKTLCFARYSN |

| | |
|-------------|--|
| AT4G11521.1 | YFKPNGTYDLNRRRILSSLASKVTAHNGFYSSSTIGQPNQMFIISMCIPIGTKPERCSDCIKGSTDGLLRSCP NQTVGYVWPDCCMVRYSN |
| AT4G11530.1 | FFKPNSTYDLNRRQILSTLSSNVTSHGFFNSKFGQAPNRVINGMCIPGTPETCSDCIKGASDKISESCP NKTDAYTWPDCCMVRYSN |
| AT4G20550.1 | KCSNTQGKYKQGSFAFEKNLNLVLSTITSIGNFRDGFYRTEEGEDPNNVFVFMFQCRGDSYWSKPPCISTA VSGLRRCRPRNKGAIWYDQCLLKIS |
| AT4G20560.1 | KCSNTQGKYKQGSFAFEKNLNLVLSTITSIGNFRDGFYRTEEGEDPNNVFVFMFQCRGDSYWSKPPCISTA VSGLRRCRPRNKGAIWYDQCLLKIS |
| AT4G20570.1 | KCSNTQGKYKQGSFAFEKNLNLVLSTITSIGNFRDGFYRTEEGEDPNNVFVFMFQCRGDSYWSKPPCISTA VSGLRRCRPRNKGAIWYDQCLLKIS |
| AT4G20580.1 | KCSNTQGKYKQGSFAFEKNLNLVLSTITSIGNFRDGFYRTEEGEDPNNVFVFMFQCRGDSYWSKPPCISTA VSGLRRCRPRNKGAIWYDQCLLKIS |
| AT4G20590.1 | KCSNTQGKYKQGSFAFEKNLNLVLSTITSIGNFRDGFYRTEEGEDPNNVFVFMFQCRGDSYWSKPPCISTA VSGLRRCRPRNKGAIWYDQCLLKIS |
| AT4G20600.1 | KCSNTQGKYKQGSFAFEKNLNLVLSTITSIGNFRDGFYRTEEGEDPNNVFVFMFQCRGDSYWSKPPCISTA VSGLRRCRPRNKGAIWYDQCLLKIS |
| AT4G20610.1 | KCSNTQGKYKQGSFAFEKNLNLVLSTITSIGNFRDGFYRTEEGEDPNNVFVFMFQCRGDSYWSKPPCISTA VSGLRRCRPRNKGAIWYDQCLLKIS |
| AT4G20620.1 | KCSNTQGKYKQGSFAFEKNLNLVLSTITSIGNFRDGFYRTEEGEDPNNVFVFMFQCRGDSYWSKPPCISTA VSGLRRCRPRNKGAIWYDQCLLKIS |
| AT4G20640.1 | KCSNTQGKYKQGSFAFEKNLNLVLSTITSIGNFRDGFYRTEEGEDPNNVFVFMFQCRGDSYWSKPPCISTA VSGLRRCRPRNKGAIWYDQCLLKIS |
| AT4G20670.1 | KCSNTQGKYKQGSFAFEKNLNLVLSTITSIGNFRDGFYRTEEGEDPNNVFVFMFQCRGDSYWSKPPCISTA VSGLRRCRPRNKGAIWYDQCLLKIS |
| AT4G21230.1 | GNFTSNTSYSNLNRLISSLPDLTPTINGFYNISINGEVNAIALCRGDVKNQDCISCITTAQQLVESCPNII EANIWLEKCMFRYT |
| AT4G21400.1 | CVASGGNFTANSSFAGNLNGLVSSLSTSKPYGFYNLSSGDSSGERAYAIGLCRREVKRDDCLSCIQIAR NLIEQCPLTNQAVVWYTHCMFRYSN |
| AT4G21410.1 | CVDRGNFTANSTFAGNLNRLVSSLKQAYGFYNLSSGDSSGERAYAIGLCRREVKRDDCVSCIQTAAR NLTKQCPLTKQAVVWYTHCMFRYSN |
| AT4G23130.1 | CTNRISRNSIYFSNLQTLTSLSSNNAYFSLGSHSLTKGQNSDMVFGLYLCKGDLSPESCRECVIFAAKDTR SRCPPGKEFLIQYDECMLGYSD |
| AT4G23140.1 | CPNTTYSNSTYSTNLRTLSSLSRNASYSTGFQATAGKAPDRVTGLFLCRGDVSPEVCRNCVAFSVN QTLNLCPKVREAVFYEQCILRYSH |
| AT4G23150.1 | CPNATTYSSNSTYLTLNLKLLSSLSRNASYSTGFQATVQGALDRVTGLFLCRGDVSPEVCRNCVTFAVN NTFSRCPNQREAVFYEECILRYSH |
| AT4G23170.1 | CPNTTYSRSTYSTNLRTLSSFASRNASYSTGFQNVTVGQTPDLVTGLFLCRGDLSPEVCSNCVAFSVD EALTRCPSQREAVFYEECILRYSD |
| AT4G23180.1 | CQNTANYTSNSTYNNLKLTLASLSRNASYSTGFQATVQGAPDRVTGLFNCRGDVSTEVCRRCVSAFA VNDTLTRCPNQKEATLYYDECVLRYSNQ |
| AT4G23190.1 | CTTDKGTFRPNGTYDVNRRILSSLPNVTDQDGLYNGSIGQQPNRVYAIGMCIPGSTSEDCSDCIKES EFFLKNCPNQTEAYSWPGEPTLCYVRYSN |
| AT4G23200.1 | TYFIPNSTYDTNRRVILSLLPSNVTSHFHFFNGSIGQAPNRVYAVGMCLPGTEEESCIGCLLSASNTLLETCL TEENALIWIANRTICMIRYSN |
| AT4G23210.1 | CIENRKYFTPNGTYDSNRRILSSLPNNTASRDGFYYSIGEEQDRVYALGMCIPKSTPSDCSNCIKGAAG WLIQDCVNQTDAYYWALDPTLCLVRYSN |
| AT4G23260.1 | CDNTTGTFFIPNSPYDKNRRILSTLASNVTAQEGYFISIGIAPDQVFATGMCAPGSERDVCSLCIRSTSESL LQSCLDQADAFFWSGEETLCLVRYAN |
| AT4G23270.1 | CSVTTTSSNSTYSTNLKLLSSLSLNASSYSTGFQATAGQAPDRVTGLFLCRVDVSSEVCRSCVTFAVN ETLTRCPKDKGCVFYEQCLLRYSN |
| AT4G23280.1 | CSITTYSSNSTYSTNLKLLSSLSRNASYSTGFQATAGQAPDMVTGLFLCRGNVSSEVCRSCIALSVNE SLSRCPNEREAVFYEQCMLRYSN |

| | |
|------------------|---|
| AT4G23300.1 | C IENRKYFTPNGTYDSNRRLILSSLPNNTASQDGFYYSIGEEQDRVYALGMCIPRSTPSCDFNCIKGAAG WLIQDCVNQTDAYYWALDPTLCLVRYSN |
| AT4G28670.1 | CNNGTVSNEEAYRRSYQINLDAIRGDMRHVKFGTHEHGDPPERMYVLSQCVDLSSDECSLCWSRATD LLSQCFPATGGWFHLDGCFVRADNY |
| AT4G38830.1 | CSNVTGNFTVNTPYAVNLDRLISSLSLRRNVNGFYNISVGDSDSEKVNISISQCRGDVKLEVCINCIAMAGK RLVTLCPVQKEAIIWYDKCTFRYSN |
| AT5G37660.1 | CSQQKFPASAYESNLNLLTSLVNSATYSSYNFTIMGSSSDTARGLFQCRGDLSPDCATCVARAVS QVGPLCPFTCGGALQLAGCYIKYDN |
| AT5G40380.1 | TFVEDMHLSLKLTRRFATESLNSTTSIYALIQCHDDLSPSDCQLCYAIARTRIPRCLPSSSARIFLDGCFLR YETY |
| AT5G41290.1 | CMKSSRNNTSNTTYNKNLNTLLSTLSNQSSFANYNLTGLASDTVHGMFLCTGDVNRITTCNACVKNAT IEIAKNCTNHREAIINYDCMVRYSN |
| AT5G41300.1 | CIDSSRNNTGNTTYNKNLNTMLSTFRNQSSIVNNYNTGLASDTVYGMFLCTGDVNITTCNNCVKNATI EIVKNCTNHREAIINYDCMVRYSN |
| AT5G43980.1 | CANQKSPDPTGVFSQNLKLFSLVSQSSQSFASVTSQDNTTAVIGVFQCRGDLQNAQCYDCVSKIPK LVSKLCGGRRDDGNVVAARVHLAGCYIRYES |
| AT5G48540.1 | CNTNSNISASSQVSKNIDSLLATLVSKTPSKGFKTTTSSSYNNKEKVYGLAQCRGDISNTDCSTCIQDAAKK IREVCQNQSDSRILYDFCFLRYSQ |
| EFJ11427 | AQMGRNLLTVLATLQDQGAAGGYKSTSFSGMSDVTYGFQCRGDISAQECSSCARSAVQILNSTCVRN STKGGRIHPGNCFLRYED |
| EFJ16458 | CGEEKFTNGSSYSTALDNLLATLITNAPVTGFFQSSVQSAELTYGLLQCRQDMSRSDCDQCARDIGQAV KSRCSSSLGAKIQLYGCFLYEN |
| EFJ17937 | CGEEKFTNGSSYSTALDNLLATLITNAPVTGFFQSSVQSAELTYGLLQCRQDMSRSDCDQCARDIGQAV KSRCSSSLGAKIQLYGCFLYEN |
| LOC_Os01g23970.1 | CNATAGNHTAVGSAYLSNLRALGGALSRRALATGFASGSYGAAPDEVHGLVLCRGDFTGGNCTDGLAS AFRDAQAQFCPGAADATVYYDQYMIRYTN |
| LOC_Os01g26390.1 | CQDSRGKYTSNSTYQANIQLSSTLPKAAAPSTGLFATRIVAGNAPDTVYALAFRCRGDITNASACAGCVA SGFQDAQQLCPFNKAASLYDLCLLRFAD |
| LOC_Os01g36790.1 | MDDLNSNVSANGFGTSAVGTAGLNPNAVFLGQCYRDLSPVDCKLCFAEVRSLPKCYPASAGGRLYLD GCFGRYANY |
| LOC_Os01g38850.1 | CSLSGGKYEPNSTYEANLRALASLLAEARATAFASDSFGAAPDAVYGIACRGDYAGDACAGGLRKAFR DAIDHGVFCAGFRDVTVYDEHMFERS |
| LOC_Os02g43000.1 | CSPSKYEPNTAFQSNLNLSSIASTASSGAAYNSFTAGGGAGPDAAGTAAAGLYQCRGDLSPGDCVAC VRQTVARLGAVCANAYAASLQVDGCVVRYD |
| LOC_Os02g50200.1 | CSQGRYASGTQYASDVDSVLTSVANSAPYSPYANFTSPTSNSVVGYYQCRSDLPASVCTGCVRSAISRLSS LCAWATGGAVQLRACFVRYGN |
| LOC_Os03g16950.1 | AGNSKAVASINSVLTDLVAKGSTGGGFATSSAGKANNVIYGLAQCRGDVSTSDCQACLASAANQILTSC NYQSDSRIWYDYCFMRFEN |
| LOC_Os03g16960.1 | SKAVASINSVLTDLVTKGSTGVGFATSTAGKGNVVIYGLVQCRGDVSTSDCQACLASAANQILTSCNYQS DSRIWYDYCFMRFEN |
| LOC_Os03g36650.1 | CSATDSFAADSSFAGNLGRLVSLLEAKAPAIGFDIATVGVGGDGEDQRVHGLALCRGDVARATCAECIRA AGALARRVCPSKKDAVVWLDACMLRYS |
| LOC_Os04g09780.1 | CSPQNYTAGSAYGTSRLRGVLKDVVDAAVSGGGYAVANDAGGAAHGLAICYADAPPEVCRLCLAMAAG NLSLACPRAVGGAMLYNNCLLRYA |
| LOC_Os04g25060.1 | CDTSAGTYKAGSAYESNLRDLAAALRADAAASPSALFATGNRGGAPDAVYGLLLCRGDLVSDCFDCGT RVLADVGRVCGGRHGRAKDVALVYNQCYARFSN |
| LOC_Os04g25650.1 | CDTSAGTYKAGSAYESNLRDLAAALRAGAAASPSALFATGIRGGAPDAVYGLLLCRGDLVSDCFDCGTR VLADVGRVCGGRHGRAKDVALVYNQCYARFSN |

| | |
|------------------|--|
| LOC_Os04g45460.1 | CSPSKYQPGTPFEGNLNLSLLASIANAAPNGGYNSTAGSNGTGDGAAAYGLYQCRGDLGNADCAACVR DAVGQLNEVCAAAYAASLQLEGCVRYDS |
| LOC_Os04g56430.1 | CGDGTYEQGSAYENLLNLALTLRDGASSQEILFSTGSNGAAPNTVYGLLLCRGDISRAACYDCGTSVWR DAGSACRRAKDVALVYNECYARLSD |
| LOC_Os05g02200.1 | QASVAQVLSLVPRASAGYYATATAGRGGDGSIAIWGLAQCRGDIPAPDCALCASAAARQLAGACRGR ADARVWYDYCFARYDD |
| LOC_Os05g03920.1 | ADQEGFDVSVNTLELIYQNVTRSGFGAAASGEGADTVYGLGQCMGYLSPTDCQLCYAQRSVKLPHCLP ATGGRIYLDGCFLYG |
| LOC_Os05g41370.1 | CPTTSSTNSSHVDDGAFGANLRALLSSLSAAAAASSSGFAENATGAAPDTAYGLAQCRGGIVGGGNGTS CRSCLDDSVRDAKACPGEKSAVIISDYCLVRYSN |
| LOC_Os06g14280.1 | CSQARYDAGTQYAADVDTALSALTNSAGYTAYANYTSPSAASGTGLVGVYQCRSDLPAAICGGCVRSAA TKLASLCNSAAGAGVQLRACFVRYGN |
| LOC_Os07g30410.1 | CGSSGNYTAGSKYQANLQALAATLPSTASSSSPALFAKDAAGGGDAEPDRVFALTLCRGDTASANASSSS CADCASRAFRDAQSVCPSYKEVAVYYDPCLLYFS |
| LOC_Os07g30510.1 | CGSSGNYTAGSKYQANLQALAATLPSTASSSSPALFAKDAAGGGDAEPDRVFALTLCRGDTASANASSSS CADCASRAFRDAQSVCPSYKEVAVYYDPCLLYFS |
| LOC_Os07g34980.1 | CSNANTITHMEPTYKTNLLQLAKNLITNVNQTLHSANGTAGAAGPDTVYGAVLCRGDSSAESCATRL QRVLDTAS |
| LOC_Os07g35004.1 | CNTTAARRTYLPNSTFEANLNGLFAVLSRNASASGYAAGAFGAAPDTAYGLLLCRGDFGTNDCSAARLA SSFQQAASSCLYSKDVAVYYDQYQLRYSQD |
| LOC_Os07g35140.1 | CNGTRGNFTEGSFGLNLELLAAELPANASSSRSLFASAAVGAAPEDRVFGLALCRGDMRDAACA GCVSGAFQRLRALCGRDRDATYHDLCCVRYNS |
| LOC_Os07g35280.1 | SGDVFAPRSTYQSNLALLSAGLAKNASASPALFAAGGVGDPPDTVYGLALCRGDTTATACGACVAAAF QDGGQLCAYAREATVFYDPCYLRFNS |
| LOC_Os07g35290.1 | CGQSGNFSANSAYQSNLRQLSATLPKNASAALFAAGSLGTVPDIVYALALCRGDANASACESCVDNAFQ GGQQLCPYNKDFIVYDLCYLRFTN |
| LOC_Os07g35300.1 | CGQGGNYSANGTYQSNLAGLSATLPKNASASRTLFAKDSLGAVPDIVYALALCRGDVANATACESCVAT AFQDAQQLCPYDKDAFIVYDLCYLAFSN |
| LOC_Os07g35310.1 | CGTTGNFTANSTYQANLDAVAAALPRNISSSPDLFATAMVGAVPEQVSALALCRGDANATECSGLATA FQDVQNMCAYDKDAAIYYDPCILYYSN |
| LOC_Os07g35330.1 | CASGAYAANSTYEANLAVLAAALPGNASTAAAAGYATATVGAVPDQVSALALCRGDANATACRACVA ASFRVARRDCPSSKDATTYQDGCIVRFSD |
| LOC_Os07g35340.1 | NTYVGNSTFEANLNHLAAELPGNVSTAHTGGFAVATVGADPDQVFALALCRGDVNATACRACVAAAF VDGKNACPGINGVTVYEDACVVRFS |
| LOC_Os07g35380.1 | CDEGVGNTYVANSTFEANLNVLAAALSPNVSVAPAGFAVATVGADPKVFAMALCRGDVNASACSAC VAAAFVDGKKDCPGNSGVAMYEDACVARFSRY |
| LOC_Os07g35390.1 | CNDTAGEFPARRSSYLASINLIAATLPGNASAPDLFATAEGVGAPPDQVSALALCRGDANASTCLAHLT QAFLDLPNACAYHKVAAIFYDSCLLAYSN |
| LOC_Os07g35410.1 | CDMGVATYAANSTFEANLDRLGAELPANVSAARATGGYAVATVGAAPDLVYALALCRGDVNASACGA CVAAAFADGKRSCPGIKGATVSGPGDGCVLRYNS |
| LOC_Os07g35540.1 | TNVTGNSAFDRNLGLLAAALANASAAGAPGFAVRTAGAAPPDQVYALALCRGDVNASACRACVAAAF VDAKGVCPGGISLYEDAQLRFT |
| LOC_Os07g35580.1 | CGENGNYTANSTYQANLQLAALHKNVSSGTGGGRLFASGAVGAVPDAVYALALCRGDINASACADC VGTIFQDAQQLCPYRKEVSIVYDSCYLRFSN |
| LOC_Os07g35640.1 | CNATAGNYTEGSAYQANVRALASALPANASSSRALFAEGAAGTAPDKVYAIALCRGDTNASSCAACLA AFDTAQQQLCAFNRRTLFNDPCILRYSQD |

| | |
|------------------|---|
| LOC_Os07g35650.1 | CDPYSASGRYSENSTFQANVNRLSATLPRNTSSSPAMYATGAAGDVPDKVYGYALCRGDVADAHACER CVAAALRDAPRVCPLVKDALVFHDLCLQLRYSN |
| LOC_Os07g35660.1 | CDTAGGNYTEGSTYQANVRALASALPVNASSSRALFAKGAAGAAPDVVYAIALCRGDTNASSCAACVAT AFQDAQQLCAFNRRTMFDDPCILRYSQ |
| LOC_Os07g35690.1 | GNYSKNGTYQVNLDLLSTLTPKNTSSSPAMYATGTVGDVDPDKVYGLALCRGDANASACERCVAAALRD APRRCPVKDVLVFDLCLQLRYSN |
| LOC_Os07g35700.1 | CGDSGNYTEHGTYHANIQLATSLPSYASSPSLAFASGSSGTVPAIYALALCRGDTNSSSCATCVAAAIQS AQELCPLVKTIVYDDTCILRFAN |
| LOC_Os07g35740.1 | GTYTANSTYDTNLQSLIAALQONASTSPTLFAAGALGAAPDAVYGLILCRGDVSSSDCYDCGTRAGQDV APACNRTRDAILVYNQCYTRFS |
| LOC_Os07g35750.1 | CGTGGTYAANSTYETNLLDLISALQGNASSSPTLYASGAVGSGGRDAVYGVMLCRGDLSTSDCNDGTR AGQDVGRVCNRTRDAALVYNQCYVRVSD |
| LOC_Os07g35790.1 | CGTSGGNYTAGSTYESNLLRLASTLRANASASPTLAFASGVRGAGPDAVYGLLLCRGDMNPSCDFDCGTR VGDDVAQACNRTKDAILVYNQCYAQFSD |
| LOC_Os07g35810.1 | CGTSGGNYTAGSTYESNLLRLASTLRANASASPTLAFASGVRGVGPDAVYGLLLCRGDMNPSCDFDCGTN VWRDAGPTCNRTKDAILVYNQCYAQFSD |
| LOC_Os07g43560.1 | CNGSSNYTANSAFQRNLGVLAAALPGNASTSPDLLANATVGGAPDTVYALAFCPPIDNQNASGCRACV ASAFADARSLCPNNRGAHIIYDGCVLTF5 |
| LOC_Os07g43570.1 | CSGRRYAANSSFDASLQQVARTLPGNASSPFLFATLAVAGEAYALALCQGGTSAGSCNYCVAQTMRD GEHACAGDADVAMYDDICTVRFSD |
| LOC_Os07g47230.1 | CPSTADGTYAPNSTYQSNLAALAEELIENSTEYGAAGSFGAAPDAVYGVALCRGDSKGPLCAGYLREAF DAAMNRTSSRPLCELRRNVTLFYDRFQLRFA |
| LOC_Os08g04210.1 | INFVSDLVAKARTGGGFATSKAGRGYDAFYGLAQCRGDVSGGDCACLAQAAKQMVSYCNYSDSRL WYEYCFMRYDNY |
| LOC_Os08g04230.1 | RSINSVSDLAAKARAGGFATSSAGRGIDAFYGLAQCRGDVSGGDCACLAQAAKQMVTCNNTLDS RIWYEYCFMRY |
| LOC_Os08g04240.1 | RSVNFVSDLVAKARTGGGFATSRAGRGYDAFYGLAQCRGDVSGGDCACLAQAAKQIVSNCNYSDS RIWYEYCFMRYNY |
| LOC_Os08g04250.1 | RAVNFVSDLVAKARTGGGFATSKAGRGSEVFYGLAQCRGDVSGGDCACLAQAAKQMVSNCNYS DSRIWYEYCFMRY |
| LOC_Os10g04720.1 | CGNGGNYTANGTYQSNLARLAAALPSNASSSPDHFATATAGQAPDAAYALALCRGDVANATACGDCV AASFQDARRTCPDKSATIYYDDCLLRF |
| LOC_Os10g04730.1 | GVFCDNLKFVSATLPNKTSPPHYATAAAGQAPDVVYVVALCRGDLNDTACGESVAYTFARLINESCVA NYTAGAYYGDCTGVYS |
| LOC_Os10g17950.1 | CNNGSAYAANTTYDTNVHSILATLTARTPNTTGFATATTGRGTDTEAWGLALCRGDTDRVGCASCLAA VPAVAFNECRGDMDVTFYDRCLARFS |
| LOC_Os10g17960.1 | CNNGSSYAANTTYHSNVRAVLTALSAITPNSTARFATASAGRGADAVWGLALCRGDTDRAGCASCLA AVPAVAFGECRDRDVAVFYDRCLARFS |
| LOC_Os11g28104.1 | CSQYNATPAAAFALANATFAVLRANLSSAGGGGFATAAEPRAAAPAFAMAQCRPYVAGAGSCAAC FDAAASRLRARGAANGGRAILDGCVVRYES |
| LOC_Os11g38850.1 | CGATNYTARSAYESNLERLIAGLAKNASTPSLFGKAAGAAPDTVYGVALCRGDLPNASACGDCVAGAS RVARRACPLAEDVVVADDAGCQLRFS |
| LOC_Os11g45540.1 | CGSSKYTANSIYQSNLDSLLSSFLVVSVDSSSALFAKGSRGAAPDTVYAVALCRGDANASACSGCVDA AYAAATARLCLPSKDAAVFYDECALRFSD |
| LOC_Os12g41270.1 | CSSWNNFVSGSYQVNLFKLLGNLAAGGAAAGSGGFYSYSGALSMDMFGVAMCYVDRHWTKCRRRC LDAATSGAAAFCPYSRRVDVVMYDECVLRYSD |
| LOC_Os12g41410.1 | CSTTGNYSGDSQYKKNLDQLLSTLATAATDDGWFNNTSSVGTGGDDQVFLIMCYADRNPTQCKECLAG APAGITQVCPGSRTVNANYDACLLRYSD |

| | |
|------------------|--|
| LOC_Os12g41490.1 | CSTAGNYTGDSQYKKNLDQLFTTSLAGAIAGDWFNTSSVGTGADQVFLGIMCYADRNSTQCQECLAGA PAGIVQVCPGSRADANYDACLLRYS |
| LOC_Os12g41530.1 | CSTTGNYTGDSQYKKNLDQLFTSLSGGAIAGDWFNTSSVGTGADQVFLGIMCYADSNATECQKCLAMA PAVVQHPCRGSRSVNANYDACLLRYS |
| SiCBMIP | GAQTQASISQVLAALVPRASAAYATATAGSGSSAIWGLAQCRGDIPASDCALCISAAAKQAASSCRGQ ADVRLWYDYCFRLRYTD |

DUF26-B sequences

| | |
|--------------|---|
| AFP1_DUF26-B | DNPKAFEKAVGKVMGKATAQASAAAGSAGLGRDKEQYTPFVSIYGLAQCTRD LAPLTC AQC LSTALSRFG DYCGAQQGCQINYSSCRVRYEI |
| AT1G04520.1 | AGTGFEERRDTAFGVMQNGVVS GHGFYATTYESVYVLGQCEGDVGD TDCSGCVKNALEKAQVECGSS ISGQIYLHKCFIAYS |
| AT1G19090.1 | GEFWRFLDEALVNVTLKAVKNGGF GAASVIKTEAVYALAQCWQTL DENTCRECLVNARSSLRACDGHE ARAFFTG CYLKYST |
| AT1G61750.1 | FINTVEYRMDRLIQEAYSSSYFAEETYHVSYLGEVYDLNGLVQCTPD LNQYDCYRCLKSAYNETKDCCYG KRFALVYSSNCMLTYK |
| AT1G63550.1 | NPTRFNQTLTEKFSELIFNVSSSLVPYFVEDQERV TQSEGSYDLDTMVQCSPDL DIFNCTVCLRVAFFRIS TCCGLPSYAKIFTPKCLLRFQT |
| AT1G63570.1 | NSNRFNQTLSNKLDQLIPNVSPSTLIPYFVEDQERV TQLEGSYDLVSMIQCSPLDPSNCTICLRFAYATVS TCCGVPSSALIFTPKCILRYR |
| AT1G63580.1 | YNQTLPGKLELILKAPSSFSPPYFVEDKEHVTQVEGSYDLEAMAQCSPDL DPSSCTVCLGLVVEKFSE CCSQSRWARIHF PKCLLRYD |
| AT1G63590.1 | FSQTLLEKLDALILRASLSSLPVPYFVDDQQHVTQLEGSYDLHAMVQCSPDL DPNCTVCLRLAVQRLS GCCSHAQFARIFYTKCLITYE |
| AT1G63600.1 | PNLDRFPQTLSDKMDELIINATSSPSLSTPYFVEDQERV KQFEGSFDIDSMAQCSPDL DPNCTTCLKLA VQEMLECCNQSRWAQIFTPKCLLRYEA |
| AT1G70520.1 | CGNTRNKNTFGDAVRQGLRNAVTEASGTGGYARASAKAGESESESAFVLANCWRTLSPD SCKQCLEN ASASVVKGLPWSEGRALHTGCF LRYSDQ |
| AT1G70530.1 | NRTVFRDNAAELVKNMSVEAVRNGGFYAGFVDRHNVTVHGLAQCWETLNRSGC VECLSKASVRIGSC LVNEEGRVLSAGCYMRFST |
| AT1G70690.1 | RTGGNGNVQGV AQCSGDLSTSQCQDCLSDAIGRLKSDCGMAQGGYVYLSKCYARFS |
| AT2G01660.1 | YRVGVS GELQGVAQCTGDL SATECQDCLME AIGRLRTDCGGAAWGDVYLAKCYARYSA |
| AT2G31620.1 | NKCLFNKNTKALLDKLKEAIRKEQEPYTRDYMYAAGEESL GTTKLYGMMQCTQDLSVKNCVCLDSIIA KLPRCCNGKQGGRV LNPSCTFRYELY |
| AT2G33330.1 | NVAGTGFEQRRDTAFGVMQNGV VQGHGFYATTYESVYVLGQCEGDIGSDSCSGCIKNALQRAQVEC GSSISGQIYLHKCFVGYSF |
| AT3G21960.1 | DKKSFYKNMKAF LHLKAKASSKENKPYVKDYMYAAGRESLGT VKLYAMVQCTQDLSLKNCTVCLDWI MTKLPECCNGKQGGRV LSPSCNF |
| AT3G21970.1 | NVTNDPKRFEDKRRDLLHKLML EATKDSKENGAKGLLYAVGEMRIGRNKMYAMVQCTQDLWQTGCH VCLEWITQMKYGEFFYRKP GGRVCGRSCSFRYELY |
| AT3G21980.1 | NDKELFNKETSALLEELTNKATDKNNMIGNKFVLYAAGDKRIGTKNVYAMVQCTKDLVTTTSAACFEWI FKMFSKCEGKQGGRV LGTSCNFRYELY |
| AT3G21990.1 | KNMSDREL FNKETSALLEKLANKASDRNNLDGKQLVLYAAGEKRIGTKKVSAMVQCTKDLIFTKCFECLE GILRKFP ECCDGKQGGRV LGTSCNFRYELY |
| AT3G22040.1 | GDTKMFSKKTNDFLQQLIVKADKPDMDGVELLYYAAGEMRIGREKLHAMVQCAKDLADCKSCLEWSF KELSKCCDGKRGARFLGTSCNLRYELY |

| | |
|-------------|---|
| AT3G22060.1 | NVSDPSTFNSQTKALLTELTKKATTRDNQKLFATGEKNIGKNKLYGLVQCTRDLKSITCKACLNGIIGELPN CCDGKEGGRVVGSCNFRYEI |
| AT3G29040.1 | KNVSSNAEQFKNKRKDLFHKLLGATKDVSDSNDAYAVGETRIGRNKMYAMMQCALDLTTNGCYVCLE WIIIGRYDSFYFDRRQGTRVLSRSCSLRYELY |
| AT3G45860.1 | NQNQVDEFRLVSSSTLNLAAVEAANSSKKFYTRKVVITPQPLYLLVQCTPDLTRQDCLRCLQKSIKMSLYR IGGRFFYPSCNSRYENY |
| AT3G60720.1 | CSSKSVENDYDFFKRRDDVLSDESTQLGYKVSRSGLVEGYAQCVDLSPSDCTACLAESVGLKLNLCGS AVAAEVYLAQCYARY |
| AT4G00970.1 | DRNEFIRLQSELLNRLRSMAASGGSKRKYAQGTDPGSPPYTTFFGAVQCTPDLSEKDCNDCLSYGFSNAT KGRVGIRWFPCSCNFQIE |
| AT4G04490.1 | QEFAARANRTVEVASTADESSVLKYYGVSSAEFTDTPEVNMLMQCTPDLSDDCNHCLRENVRYNQEHE NWDVGGTVARPCYFRWDDY |
| AT4G04500.1 | NMAMFSQEWIAMVNRTLEAASTAENSSVLKYYSATRTEFTQISDVYALMQCVPDLSPGNCKRCLRECV NDFQKQFWGRQGGVSRPCYFRWDL |
| AT4G04510.1 | TLFRQEWEMVDRTLEAVTIDNSTTVLKYYGALKSEFSEFPNVMMMQCTPDINSACKRCLQASVTY FRDQNWGRQGGGICRPSVFRWEF |
| AT4G04540.1 | KNMTLFEQEWNAMANRTVESATEAETSSVLKYSAEKAETEFPNVYMLMQCTPDITSQDCKTCLGEC VTLFKEQVWGRQGGVYRPSCFRWDL |
| AT4G04570.1 | TLFKQQWEEMVNRTLEAATKAEGSSVLKYYKAEKAGFTEFPDVYMLMQCTPDLSRDCKQCLGDCVM YFRKDYMGKGGMASLPSCYFRWDL |
| AT4G05200.1 | NITENQVSRFNESLPALLIDVAVKAALSSRFATEKANFTVFQTIYSLVQCTPDLTNQDCESLRQVINYL RCCDRSVGGRVIAPSCSFRYELY |
| AT4G11460.1 | NLTDFDRLWERLIAHMVTKASSASIKYLSFNSRFYAADETNLNSQMVMYALMQCTPDVSPSNCNTCLK QSVDDYVGCCHGKQGGYVYRPSCIFRWDL |
| AT4G11470.1 | AYTRTWDAFMNMFTRVGGQTRYLADISPRINQEPLSPDLIYALMQCIPGISEDCECTCLGKCVDDYQSCC NGFIGGVVNKPVCYFRWD |
| AT4G11480.1 | AYTRTWEFMNSMITRVRTRYLADISPRIGSARIYALMQCIRGISSMECETCIRDNVRMVYQSCCNGFIG GTIRKPVCFRWD |
| AT4G11490.1 | IWEALTDRLMSDASSDYNASLSSRRYYAANVTNLTFQNIYALMLCTPDLEKGACHNCLEKAVSEYGNL RMQRGIVAWPSCCFRWDL |
| AT4G11521.1 | FDRIWDELMSRTITTASRTHGSLSGHKYAAADVSLTTFQTIYTMVQCTPDVSSGDCEFLKRTVLDYKK CCRGHIGGAFVRPFVCFRWDL |
| AT4G11530.1 | TVFDRIWEELMLRTITAASLSSNGSSFGQKYFAAEVASLTFQTMVYAMMQCTPDVSSKDCFLKTSV GDYESCRCRGKQGGAVIRPSCVFRWDL |
| AT4G20550.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDILFTKCFECLE GILRKFPQCCDGKRGGRVFGTSCNFR |
| AT4G20560.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDILFTKCFECLE GILRKFPQCCDGKRGGRVFGTSCNFR |
| AT4G20570.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDILFTKCFECLE GILRKFPQCCDGKRGGRVFGTSCNFR |
| AT4G20580.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDILFTKCFECLE GILRKFPQCCDGKRGGRVFGTSCNFR |
| AT4G20590.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDILFTKCFECLE GILRKFPQCCDGKRGGRVFGTSCNFR |
| AT4G20600.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDILFTKCFECLE GILRKFPQCCDGKRGGRVFGTSCNFR |
| AT4G20610.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDILFTKCFECLE GILRKFPQCCDGKRGGRVFGTSCNFR |
| AT4G20620.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDILFTKCFECLE GILRKFPQCCDGKRGGRVFGTSCNFR |
| AT4G20640.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDILFTKCFECLE GILRKFPQCCDGKRGGRVFGTSCNFR |

| | |
|-------------|---|
| AT4G20670.1 | NNMSDRGLFNKETSALLEKLAYKASDRNLDGKQLVLYAAGEKRIGTKKVYAMVQCTKDIFTKCFECL GILRKFQCCDGKRGGRVFGTSCNFR |
| AT4G21230.1 | SVTDKEGFSKGLGDLDSLAKIDAANETKEVKFAAGVKGTIYALAQCTPDLESDCRICLAQIFAGVPTCC DGKTGGWWTNPSCYFRFEV |
| AT4G21400.1 | ISANRDEFDRLQIELLDRLKGIAAAGGPNRKYAQGSGSVAGYPQFYGSAHCTPDLSEQDCNDCLVFGF EKIPGCCAGQVGLRWFFPSCSYRFET |
| AT4G21410.1 | NRDDFERLQRGLLDRLKGIAAAGGPNRKYAQNGSASAGYRRFYGTQCTPDLSEQDCNDCLVGFEN IPSCDAEIGLRWFSPSCNFRFET |
| AT4G23130.1 | TADQSDRFNDAVLSLMKKSAAEAA NSTSKKFAVKKSD FSSSQSLYASVQCIPDLTSEDVCMCLQQSIKELY FNKVGGRFLVPSCNSRYEV |
| AT4G23140.1 | KQIDGFTSFVSSTMSEAAGKAANSSRKLTVNTELTAYQNLYGLLQCTPDLTRADCLSLQSSINGMALS RIGARLYWPSTARYELY |
| AT4G23150.1 | QFTNLVLSNMNQIAIEAADNPRKFSTIKTELTAQTFFYGLVQCTPDLSRQNCMNCLTSSINRMPFSRIGA RQFWPSCNSRYELY |
| AT4G23170.1 | SQINQFIVLVQSNMNQAAMEAANSSRKFSTIKTELQTLYGLVQCTPDLSQDCLRCLTRSINRMPLS RIGARQFWPSCNSRYELY |
| AT4G23180.1 | DLLSDLVLP TLNQ AATVALNSSKFGTRKNNFTALQSFYGLVQCTPDLTRQDCSRCLQLVINQIPTDRIGA RIINPSCTSRYEI |
| AT4G23190.1 | TEFTKIWEGLMGRMISAASTAKSTPSSSDNHYSADSAVLTPLLNIYALMQCTPDLSGGDCENCLRQSAID YQSCCSQKRGGVVMPSCFLRWDL |
| AT4G23200.1 | YKTNETEFNTVWSRLTQRMVQEASSTDATWSGAKYYTADVAALPDSQTLYAMMQCTPDLSPAECNL CLTESVVNYQSCCLGRQGSIVRLSACFRAEL |
| AT4G23210.1 | LTEFTKIWEDLTSRTITAASAARSTPSSSDNHRYVDFANLTKFQNIYALMQCTPDISSDECNNCLQRGVLE YQSCCGNNTGGYVMRPICFRWFQ |
| AT4G23260.1 | NTNQTVFDIEWNNLTSSMIAGITSSSSGGNNSKYSDIALVPDFKNISALMQCTPDVSSDECNTCLRQ NVVDYDNCCRGHQGGVMSRPNCFRWEV |
| AT4G23270.1 | IDLNASQSLYGMVRCTPDLREQDCLDCLKIGINQVTDYDKIGGRILLPSCASRYDNY |
| AT4G23280.1 | KRFAVTKFDLNLQSLYGMVQCTPDLTEQDCLDCLQQSINQVTDYDKIGGRIFLPSCTSRDYDNY |
| AT4G23300.1 | TDFKNIWEDLTSRTITAASAARSTPSSSDNHRYVDFANLTKFQNIYALMQCTPDISSDECNNCLQRGVLE YQSCCGNNTGGYVMRPICFRWFQ |
| AT4G28670.1 | KEKSAEFKGLVKEVTKSIVEAAPYSRGSFVAKMGIRDLTVYGLGVCWRTLNDELCKLCLADGALSVTSCLP SKEGFALNAGCYLRSNY |
| AT4G38830.1 | NFTGDRDSWEKSLRGLLEGLKNRASVIGRSKKNFVGETSGPSFQTLFGLVQCTPDISEEDCSYCLSQGIA KIPSCCDMKMGSYVMSPSCMLAY |
| AT5G37660.1 | YFRAGGSGDVQGMGQCVGDLTVSECQDCLGTAIGRLKNDCGTAVFGDMFLAKCYARYST |
| AT5G40380.1 | FGVAGENGVHALAQCWESLGKEDCRVCLEKAVKEVKRCVSRREGRAMNTGCYLYSD |
| AT5G41290.1 | LESIVQCTPDLDPRNCTCLKLALQELTECCGNQVWAFIYTPNCMVSFDTY |
| AT5G41300.1 | SYDLDSLQVQSPHLNPENCTICLEYALQEIIDCCSKFVAMIFTPNCFVNY |
| AT5G43980.1 | QYESVYVLGQCEGLNSDCGECVKDGFKAKEGSESGVYVYQKCFVSYSY |
| AT5G48540.1 | PKKFDNELGALFDKIRSEAVLPKNKGLGKGTCLTPFVTLNGLVQCTRDLSLDCAQCFATAVGSFMTTC HNKKGCRVLYSSCYVRYEF |
| EFJ11427 | LAIFQNSRTALEFLKAKVPRNARKFVA AVAGIGSAVPAYALGQCIPDLASAADCASCLAAENAIASTCRG GGGGVCYSSCTLFFQ |
| EFJ16458 | IASSPGYDDNLKSALATLSRRGSSFTATVSGSGSQVFLGECRGLDSSQQCDSCVRVAMRNMTDRICGN TSGSILLNSCYTRF |

| | |
|------------------|---|
| EFJ17937 | IASSPGYDDNLKSALATLSRRGSSFTATVSGSGKSQVFLGECRGLDSSQQCDSCVRVAMRNMTDRICIGN TSGSILLNSCYTRF |
| LOC_Os01g23970.1 | AAARFMAKATELMNRTADLAAFSSSSPSRYATGETWFDEQGVSVVYGLVQCTPDLTGEQCRSCLAGII AQMPKLFGDASSRPVGGRIILGVRNRLRYEK |
| LOC_Os01g26390.1 | LLLFTLLNATAESAASSRRFTTSRLDVSSLPTLYCLMQCTPDLTAGECAACFEDFPRLTLQYLDGARGGRI LATRCTMRYEI |
| LOC_Os01g36790.1 | NYTGANPRGFADAVRAALANVTGVAASAAPVGGGDGYAVGSASAGGATAFALAQCWGSNLNATACG QCLRAAAAAAARCAPAAAEGRALYTGCYLRYST |
| LOC_Os01g38850.1 | FGDRVMELINTTAEFAAWNSSKRGYATGEAGFGELDVGATRLGLVEQQCRSSPDLVIFALVQCTPDLSP AGCLSCLSGIASQMPRWFTGAADYRLGGRILGVRNRLRYE |
| LOC_Os02g43000.1 | CSSSTRDGAFLSSRDGVLGELQAAAGYKLTSGTVQGVAQCLGDVPANDCTACLAEEAVGQLKGCAGT ALAADVLAQCYVRY |
| LOC_Os02g50200.1 | GSGGVQAMSQCVDLGAACSDCVSAAAGQLKAGCGYATAGEVYLGKCYARF |
| LOC_Os03g16950.1 | DNGKAFQKAVGKVMGKATSQASQAGSGGLGRTKDQYTPFINIYGLAQCTQDLSPLACAQCLSTAVSRF GQYCGAQQGCQINYSSCRVRYEI |
| LOC_Os03g16960.1 | DNAKAFQKAVGKVMKATAQVSQAGSGGLGRVKDQYTPFINIYGFAQCTRDLSPITCAQCLSTAVSRF DQYCGAQQGCRILYSSCMVRYEI |
| LOC_Os03g36650.1 | REVSRLMKRLTRTAYLSPLLFAAGEAVAVGGAQRLHGMAQCTKDLSGGDKMCLSAIDQLLARGCAK EGGKVLGGSCSLRYDF |
| LOC_Os04g09780.1 | GDAAQFGAALSRLMDRLALAAASSSSSRGRRFAFGQTNITGDGGDSLYAFVQCVDLSPDDCRRCLQ SIAASLPMTRGGRAVSLTCYTRFE |
| LOC_Os04g25060.1 | AAYDRAVTELLAATVRYAVEENPARLFATGQVRVGGDARDPGRNIYSMAQCSPDLPPASCRRCLDGLV ARWWQVFLNNEGARVAGARCYLRSE |
| LOC_Os04g25650.1 | AAYDRAVTELLAATVRYAVEENPARLFATGQVRVGGDARDPGRNIYSMAQCSPDLPPASCRRCLDGLV ARWWQVFLNNEGARVAGARCYLRSE |
| LOC_Os04g45460.1 | CSTSTSGDGFKNRDAVLAALQGGLANGYKVSSSGNVQGVQSCLGDLAAGDCTTCLAQAVGQLKGT CGTSLAADVLAQCYVRY |
| LOC_Os04g56430.1 | ADVAAYDRAVTRLLAATAEYAAGDIARKLFATGQVRVGGDARDPGRNLYATAQCAFDTLEACRGCLEGLVA RWWDTFPANVDGARIAGPRCLLRE |
| LOC_Os05g02200.1 | QNATDPEAFEKAQRKVMARVAADAGDAGGGGLARETARFKDGVTIYGLGWCTRDIITAADCGLCVAQ AVAEMPNYCRFRRGCRVLYSSCMARYETY |
| LOC_Os05g03920.1 | CSNATVSSPASFAATSALLRNVTAAAPGARDYYYYYASSSSASALPSVSPRVYAAAQCWRSLNATACA ACVATARDRVVGRCLPRAAEGYGLNAGCVVRYSTQ |
| LOC_Os05g41370.1 | DNATQPERFKSLLGTLMGNLTDAAARASSPLMFAAGETDLPPFTKIYGMAQCTRDLAAGDCYRCLVGA VNNIPKCCDGKQGGQVITRSCSIRFEV |
| LOC_Os06g14280.1 | GAAGYVQAMSQCVDLGAACSDCVSAAAGQLKAGCGYASAGEVYLGKCYARF |
| LOC_Os07g30410.1 | YTTVRMDVVTPLFSLMQCTPDMSSGDCRQCLQDLVGNTTFNGSVSGVRNIGARCGRYDYTY |
| LOC_Os07g30510.1 | YTTVRMDVVTPLFSLMQCTPDMSSGDCRQCLQDLVGNTTFNGSVSGVRNIGARCGRYDYTY |
| LOC_Os07g34980.1 | RAQFSQLFSELMEKIAAAVSRPVNYLTGRGWFDLKSQTVYALAQCTDGMPPENCRCSDGIIDEGKK MVGGGTLGGAVLGMRCSLWYQT |
| LOC_Os07g35004.1 | VAAFDAALVAELVNAVADRASNATRRYAAGKAGFAPEAMTVYIAIQCTPDLSPQCRGCLAGIIDQMPK WFSGRVGGRIILGVRCDFRYEK |
| LOC_Os07g35140.1 | TTRSFFLSLVGTLFGEMAMYGSYNSSARRYASAVMYVNPQLPTVYGLAQCTPDLSPAQCWHCFQGLQE QNRQWYDGRQGGRIILGVRNCFRYEY |
| LOC_Os07g35280.1 | APAEVFDAAVVALLNATADHAAASSPRRFATGVEAFRGWGVDRDIYALVQCTPDMSPAGCRSCLAGIIS WVNDPDYFSGSPTGRVLGVRNRYWYD |

| | |
|------------------|---|
| LOC_Os07g35290.1 | NASATAEVFDAAAATLLNATSGYAAANSSRRFATGEEAFDAADPTIYGLSQCTPDMSPDDCRSCLGGIIA LIPQYFGRKRGRARVIGTRCNRYREV |
| LOC_Os07g35300.1 | NASAPAEVFDAAVATLLNATSSYAAENSSRRFATGEEAFDAAAATPTIYGLSQCTPDMSPDDCRSCLGRII ALIPRYLSRRKGGRAIGMRCNFRYE |
| LOC_Os07g35310.1 | SDPGRFNGMVAALVNATADYAAHNSTRRYASGEAVLDRESEFPKVYSWAQCTPDLTPAQCGDCLAII AKLPRLFTNRIGGRVLGVRCSYRYE |
| LOC_Os07g35330.1 | FNAAVVALMNATVDTAVAAGSGSNNTKKYFATAVEDFDPKHYPKIYGMAQCAPVMTAAQCRSCLGG FVSSIPWFLNGKPGGRVLGIWCNLRYE |
| LOC_Os07g35340.1 | VGWFNAAIKILAALVDHAVATATGNNSTTKKYFATGEEDFDPNYGFACQVDPDLTQEQCCECLNTFLF QAKQVYFGKSLSWVGMNSVWCRLMYS |
| LOC_Os07g35380.1 | FNAAVTKILAAMVDHAVTSTTGNSTTKKYFVTGEEFDPNIYGFACQVDPDLTPAQCNCLDKLLFYAKQ AYLGKSLSWVRVNSVWCRLMYS |
| LOC_Os07g35390.1 | ATTEQARFNRLVAALVNATADYAAARNSTRRRYASGEADFNAEFPKVYSWAQCTPDLTPASCRSCLAQII GTIYIGFFENRVGGFVRAVWCSEFQYST |
| LOC_Os07g35410.1 | WFNAAVAKILAALVEHTWATTTSNATAKKYFSTGEEFNPKIYGFVQVDPDLSPEQCCECVRTLHDQAKI HYMGNSLPWASTYSVWCRLMYS |
| LOC_Os07g35540.1 | WFNAAVAKILAALVEHAWATTTTTTGNSTTTIKYFATGEEFNPKIYGFACQVDPDLTPEQCCECLRSLH DNAKTVYMGNSLRVWGIYSVWCRLMYS |
| LOC_Os07g35580.1 | GRYDRAVTGLLNATARYAAGNTNASSRLFATGVMVGFDAQFPKIYAMAQCSPDLSPAQCGLCLGAMV ARWWQTFEPNTQGARSVGARCNMRVEL |
| LOC_Os07g35640.1 | DYASAVYDAFSGMLVNATADYAAKDSVRRFGTGEMGFNVFDSPHYNIFSLAQCTPDMSEADCRSCLG DIIRMMMPKYFVGKPGGRVFGVRCNFRFEAY |
| LOC_Os07g35650.1 | AAFDAAVAMLANATAEYAAAANTSRRYGTAEEEGVDGDGDSGRPRMYALAQCTPDKAADVCRACLT TLTTVQLPKLYSGGRTGGGVFGVWCNLRYE |
| LOC_Os07g35660.1 | AAAFDAASGRLVNATAGYAAADPVRRFGTGEVGFDDATYPRIFSLAQCTPDSEADCRSCLGRIIRWVP QYFAGKPGGRVFGVRCNFRFESY |
| LOC_Os07g35690.1 | AAAFDAAVAVLVNATADYAAADSSRRYGTGEEGVDGDSDRPKIYALAQCTPDKTPEVCRTCLSTVIG QLPKEFSGRTGGGMFGVWCNFRYE |
| LOC_Os07g35700.1 | PAFEAAVRLINTADYAATDSVRRFGTGEEAFDETTFPKIYSLAQCTPDMAATACRSCLDIVGRMVSG NLIGRMGGRVLGVRCNLWFEV |
| LOC_Os07g35740.1 | DVAGYDRAVTELLSATLMYAVVNTTRLFATGQRVQADPGFPNIYSAQAQCTPDLSPALCRSCLDLVARW WKTFRPTTVGARIVGTRCSLRSE |
| LOC_Os07g35750.1 | ADVRAVDAAVSVLLNATVRYAVENSTRMFATGQRVGSDPGFSDIYSMAQCSPALSRPLCRSCLDGLVG QWWDTFPVNVEGARIAGTRCNLRSE |
| LOC_Os07g35790.1 | VAGYDRAVTELLNATVRYAVENSTRLFATGQRVGADPGFRNIYSMAQCSPDLSPAQCRSCLDGLVGQW WTGFLFPRNGEGARVAGPRCYLRSE |
| LOC_Os07g35810.1 | TDVAGYDRAVTELLNATVRYAVENSTKLFATGQRVGNDTGFNSIYSMAQCSPDLSPAQCRSCLDGLVG QWWKTFPLNGKGARVAGPRCYLRSE |
| LOC_Os07g43560.1 | SDVGEFNGAIYEVLNATADYAAAARRFGTGEISFDPTYPIYISMAWCTPDMAPGRCRACLADTIAQM HAYFNPNAQGARLVGVRCAARYEI |
| LOC_Os07g43570.1 | AAGRFRYLVEGELLDATADYAVANSTARFATGDVGVGGYFDGEPFSKIYALAQCTPDLTPAQCRACLASA MEEMTRQVFAASSPGGKVIIGERCGLRFE |
| LOC_Os07g47230.1 | AGRFREHVAALLNATARDAAAQPDYGTGDSWFQEGGSMVYALVQCTRDMDPGRGACLQRIISEM PRMLDASQIGGRVLGVRCLLRYE |
| LOC_Os08g04210.1 | KAFQKAAGKAMGKATAQAVAVGSSGLGRAKEQYTPFVSVYALAQCTRDLSPSCAQCLSAAVSKFDKA CGSGPGCQIDYSSCWARYEI |
| LOC_Os08g04230.1 | FVNVYALAQCTRDLAPPLCAQCLSTTVSKFAEACGSGQGQCQIDYSSCWVRYEI |
| LOC_Os08g04240.1 | DNPKAFQKAAGKAMGKATAQAVAVGRSGLGRAKEQYTPFVSVYALAQCTRDLAPPACARCLSEIVSKF DKTCNSAQGCQIDYSSCWARYEI |
| LOC_Os08g04250.1 | KAFQKVVGKAMVKATTQAVSVGGNGLGRAKEQYTPFVSVYALAQCTRDLAPPACAQCLSSTVSKFDKA CGAAQGCQIDYSSCWARYEI |

| | |
|------------------|---|
| LOC_Os10g04720.1 | ANVRELLTVTARTAAAAARRFATGFMDSSESQTLYSLAQCTPDLAAGDCLACLQRLIAMVNSTTSVR LGGRVLLLRNLFE |
| LOC_Os10g04730.1 | QQLLSEVERAAGAAGRFATGVVDTGRTFPLVYSLAQCTPDLASAGDCLACLRLTGMINSTMAVRMGA QHVTRCYFRYEAY |
| LOC_Os10g17950.1 | AGHFDALVADLAGALADWAAYNSTLRYAAGVMTSGDGMSTTEDMVHNIYGVVQCTPDQAAAACR ACLEALRVDMPKVFAGKMGGRFNAVWCNLRYET |
| LOC_Os10g17960.1 | AGRFDALVARLAGALADWAAYNSTRRYAAGLMSGDGFTSTTEDMVHNIHGVVQCTPDQAAAACRA CLETLRVDMPKVFAGRIGGRFNAVWCNLRYET |
| LOC_Os11g28104.1 | ADGSFAGAARGLVGDIAAAAPRAGLAAAAARGGVYAAAQCVETVGECCGCAQCLAVPARNIDGCPP DSDGRAVDAGCFMRYSD |
| LOC_Os11g38850.1 | LVQETARTAAYNSSPPPPATTTYATGRMDVSATFPTLYSMAQCTPDLRPGGCWRCLQSINDMTTRYF AGRRGGRILGLWCNFRYET |
| LOC_Os11g45540.1 | FTQFFIKTMNYIVAQALSTTKHYAIRVDMDDADASNTVTLPRRLFCLAQCAPDLVEDICYNCLQNFSDL ATANFAGRQGGRILALRCNLRYDT |
| LOC_Os12g41270.1 | YTDSRGESLTVYGMVQCGRGLLPEECSKCLRHLGELTTGLPNTAGIIRGYSCYSRYD |
| LOC_Os12g41410.1 | ETRWQLMSQLAETAGQTKLRDLTGSTRLGSTSMYGLAQCTRD LAVSECSTCLSDYIVQLSKIFPNNSW AAIKGYSCYLRYD |
| LOC_Os12g41490.1 | TMNDTRRRRLMSQLAERAGDTKLRDLNGLSPYADSKLGTSAALYGLAQCTRD LAASECRRCLSGYVDDLSN TFPNSGGAIKGYSCYLRYH |
| LOC_Os12g41530.1 | RWQLMSQLAERAGDTKLRDLNGLSPYVDSKLGTSALYGLAQCTRD LAASECRRCLSGYVNDLSNTFPNN SGGAIKGYSCYLRYQ |
| SiCBMIP | NASDPAAFDRERKLMARVAAEAGDAASGGLVRETARFGSATTIYGLGWCTRDITAADCGLCVAQAVA ELPNYCQFRRGCRVLYSSCMARYETY |