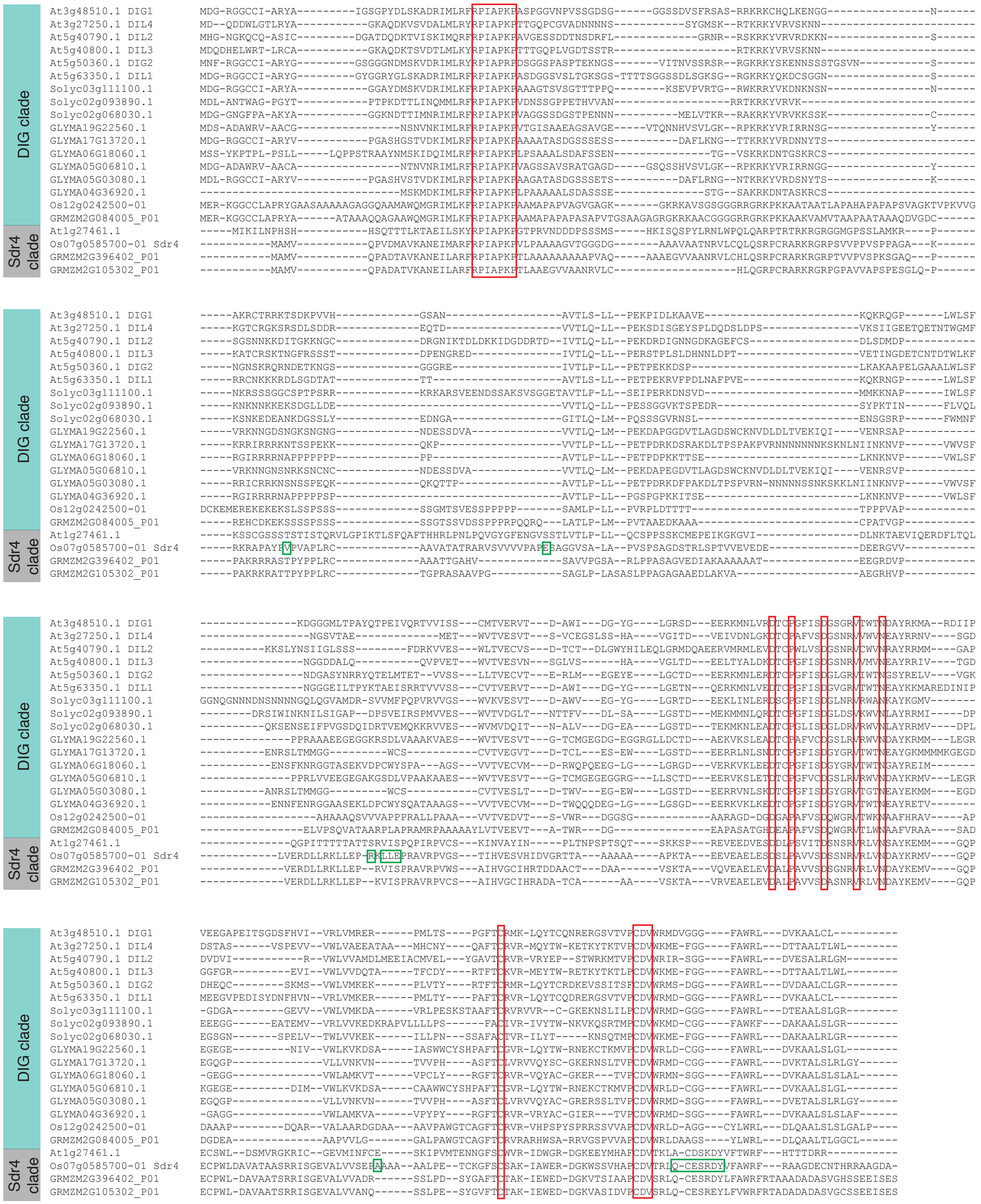

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At3g48510.1 DIG1       MDG-RGGCCI-ARYA---------IGSGPYDLSKADRIMLRFRPIAPKPASPGGVNPVSSGDSG------GGSSDVSFRSAS-RRKRKCHQLKENGG----------------N------
At3g27250.1 DIL4       MD--QDDWLGTLRYA-----------GKAQDKVSVDALMLRYRPIAPKPTTGQPCGVADNNNNS-----------SYGMSK--RTKRKYVRVSKNN------------------------
At5g40790.1 DIL2       MHG-NGKQCQ-ASIC---------DGATDQDKTVISKIMQRFRPIAPKPAVGESSDDTNSDRFL-------------GRNR--RSKRKYVRVRDKKN----------------S------
At5g40800.1 DIL3       MDQDHELWRT-LRCA-----------GKAQDKTSVDTLMLKYRPIAPKPTTTGQPLVGDTSSTR-------------------RTKRKYVRVSKNN------------------------
At5g50360.1 DIG2       MNF-RGGCCI-ARYG---------GSGGGNDMSKVDRIMLRYRPIAPRPDSGGSPASPTEKNGS-------VITNVSSRSR--RGKRKYSKENNSSSTGSVN-----------S------
At5g63350.1 DIL1       MDG-RGGCCI-ARYG---------GYGGRYGLSKADRIMLRFRPIAPKPASDGGSVSLTGKSGS-TTTTSGGSSDLSGKSG--RGKRKYQKDCSGGN----------------S------
Solyc03g111100.1       MDG-RGGCCI-ARYA-----------GGAYDMSKVDRIMLKFRPIAPKPAAAGTSVSGTTTPPQ--------KSEVPVRTG--RWKRRYVKDNKNSN----------------N------
Solyc02g093890.1       MDL-ANTWAG-PGYT-----------PTPKDTTLINQMMLRFRPIAPKPVDNSSGPPETHVVAN------------------RRTKRKYVRVK---------------------------
Solyc02g068030.1       MDG-GNGFPA-AKYA-----------GGKNDTTIMNRIMLRFRPIAPKPVAGGSSDGSTPENNN----------MELVTKR--RAKRKYVRVKKSSK----------------C------
GLYMA19G22560.1        MDS-ADAWRV-AACG----------------NSNVNKIMLRFRPIAPKPVTGISAAEAGSAVGE-----VTQNNHVSVLGK--RPKRKYVRIRRNSG----------------Y------
GLYMA17G13720.1        MDG-RGGCCI-ARYV-----------PGASHGSTVDKIMLRFRPIAPKPAAAATASDGSSSESS----------DAFLKNG--TTKRKYVRDNNYTS-----------------------
GLYMA06G18060.1        MSS-YKPTPL-PSLL-----LQPPSTRAAYNMSKIDQIMLRFRPIAPKPLPSAAALSDAFSSEN---------------TG--VSKRKDNTGSKRCS-----------------------
GLYMA05G06810.1        MDG-ADAWRV-AACA----------------NTNVNRIMLRFRPIAPKPVAGSSAVSRATGAGD-----GSQSSHVSVLGK--RPKRKYVRIRRNGG----------------Y------
GLYMA05G03080.1        MDL-RGGCCI-ARYV-----------PGASHVSTVDKIMLRFRPIAPKPAAGATASDGSSSETS----------DAFLRNG--NTKRKYVRDSNYTS----------------K------
GLYMA04G36920.1        -------------------------------MSKMDKIMLRFRPIAPKPLPAAAAALSDASSSE--------------STG--SAKRKDNTASKRCS-----------------------
Os12g0242500-01        MER-KGGCCLAPRYGAASAAAAAGAGGQAAMAWQMGRIMLKFRPIAPKPAAMAPAPVAGVGAGK-------GKRKAVSGSGGGRRGRKPKKAATAATLAPAHAPAPAPSVAGKTVPKVVG
GRMZM2G084005_P01      MER-KGGCCLAPRYA------ATAAAQQAGAAWQMGRIMLKFRPIAPKPAAMAPAPAPASAPVTGSAAGAGRGKRKAACGGGGRRGRKPKKAAKVAMVTAAPAATAAAQDVGDC------
At1g27461.1            -----MIKILNPHSH-----------HSQTTTLKTAEILSKYRPIAPKPGTPRVNDDDPSSSMS-----HKISQSPYLRNLWPQLQARPTRTRKRGRGGMGPSSLAMKR----P------
Os07g0585700-01 Sdr4   -----------MAMV-----------QPVDMAVKANEIMARFRPIAPKPVLPAAAAGVTGGGDG-------AAAVAATNRVLCQLQSRPCRARKRGRPSVVPPVSPPAGA---K------
GRMZM2G396402_P01      -----------MAMV-----------QPADTAVKANEILARFRPIAPKPTLAAAAAAAAAPVAQ-----AAAEGVVAANRVLCHLQSRPCRARKRGRPTVVPVSPKSGAQ---P------
GRMZM2G105302_P01      -----------MAMV-----------QPADATVKANEILARFRPIAPKPTLAAEGVVAANRVLC-------------------HLQGRPCRARKRGRPGPAVVAPSPESGLQ-P------
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At3g48510.1 DIG1       -----AKRCTRRKTSDKPVVH-------------GSAN------------------AVTLS-LL--PEKPIDLKAAVE------------------------KQKRQGP------LWLSF
At3g27250.1 DIL4       -----KGTCRGKSRSDLSDDR-------------EQTD------------------VVTLQ-LL--PEKSDISGEYSPLDQDSLDPS---------------VKSIIGEETQETNTWGMF
At5g40790.1 DIL2       -----SGSNNKKDITGKKNGC-------------DRGNIKTDLDKKIDGDDRTD--IVTLQ-LL--PEKDRDIGNNGDKAGEFCS-----------------DLSDMDP-----------
At5g40800.1 DIL3       -----KATCRSKTNGFRSSST-------------DPENGRED--------------IVTLQ-LL--PERSTPLSLDHNNLDPT-------------------VETINGDETCNTDTWLKF
At5g50360.1 DIG2       -----NGNSKRQRNDETKNGS-------------GGGRE-----------------IVTLP-LL--PETPEKKDSP--------------------------LKAKAAPELGAAALWLSF
At5g63350.1 DIL1       -----RRCNKKKRDLSGDTAT-------------TT--------------------AVTLS-LL--PETPEKRVFPDLNAFPVE------------------KQKRNGP------LWLSF
Solyc03g111100.1       -----NKRSSSGGCSPTPSRR-------------KRKARSVEENDSSAKSVSGGETAVTLP-LL--SEIPERKDNSVD------------------------MMKKNAP------IWLSF
Solyc02g093890.1       -----KNKNNKKEKSDGLLDE-----------------------------------VVTLQ-LL--PESSGGVKTSPEDR----------------------SYPKTIN------FLVQL
Solyc02g068030.1       -----KSNKEDEANKDGSSLY-------------EDNGA-----------------GITLQ-LM--PQSSSGVRNSL-------------------------ENSGSRP------FWMNF
GLYMA19G22560.1        -----VRKNNGDSNGKSNGNG-------------NDESSDVA--------------VVTLQ-LM--PEKDAPGGDVTLAGDSWCKNVDLDLTVEKIQI----VENRSAP-----------
GLYMA17G13720.1        -----KRRIRRRKNTSSPEKK-------------QKP-------------------VVTLP-LL--PETPDRKDSRAKDLTPSPAKPVRNNNNNNNKSKNLNIINKNVP------VWVSF
GLYMA06G18060.1        -----RGIRRRRNAPPPPPPP-------------PP--------------------AVTLP-LL--PETPDPKKTTSE------------------------LKNKNVP------VWLSF
GLYMA05G06810.1        -----VRKNNGNSNRKSNCNC-------------NDESSDVA--------------VVTLQ-LM--PEKDAPEGDVTLAGDSWCKNVDLDLTVEKIQI----VENRSVP-----------
GLYMA05G03080.1        -----RRICRRKNSNSSPEQK-------------QKQTTP----------------AVTLP-LL--PETPDRKDFPAKDLTPSPVRN-NNNNNSSNKSKKLNIINKNVP------VWVSF
GLYMA04G36920.1        -----RGIRRRRNAPPPPPSP-----------------------------------AVTLP-LL--PGSPGPKKITSE------------------------LKNKNVP------VWLSF
Os12g0242500-01        DCKEMEREKEKEKSLSSPSSS-------------SSGMTSVESSPPPPP-------SAMLP-LL--PVRPLDTTTT--------------------------TPPPVAP-----------
GRMZM2G084005_P01      -----REHCDKEKSSSSPSSS-------------SSGTSSVDSSPPPRPQQRQ---LATLP-LM--PVTAAEDKAAA-------------------------CPATVGP-----------
At1g27461.1            -----KSSCGSSSTSTISTQRVLGPIKTLSFQAFTHHRLPNLPQVGYGFENGVSSTLVTLP-LL--QCSPPSSKCMEPEIKGKGVI----------------DLNKTAEVIQERDFLTQL
Os07g0585700-01 Sdr4   -----RKRAPAYPVPVAPLRC-------------AAVATATRARVSVVVVPAPESAGGVSA-LA--PVSPSAGDSTRLSPTVVEVEDE--------------DEERGVV-----------
GRMZM2G396402_P01      -----PAKRRRASTPYPPLRC-------------AAATTGAHV-------------SAVVPGSA--RLPPASAGVEDIAKAAAAAAT---------------EEGRDVP-----------
GRMZM2G105302_P01      -----PAKRKRATTPYPPLRC-------------TGPRASAAVPG-----------SAGLP-LASASLPPAGAGAAEDLAKVA-------------------AEGRHVP-----------
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At3g48510.1 DIG1       ---------------KDGGGMLTPAYQTPEIVQRTVVISS---CMTVERVT---D-AWI---DG-YG----LGRSD---EERKMNLVRDTCPGFISDGSGRVTWTNDAYRKMA--RDIIP
At3g27250.1 DIL4       -----------------NGSVTAE-------------MET---WVTVESVT---S-VCEGSLSS-HA----VGITD---VEIVDNLGKDTCPAFVSDGSNRVVWVNEAYRRNV----SGD
At5g40790.1 DIL2       ----------KKSLYNSIIGLSSS--------FDRKVVES---WLTVECVS---D-TCT--DLGWYHILEQLGRMDQAEERVMRMLEVDTCPWLVSDGSNRVCWVNRAYRRMM----GAP
At5g40800.1 DIL3       ----------------NGGDDALQ----------QVPVET---WVTVESVN---SGLVS------HA----VGLTD---EELTYALDKDTCPGFISDGSNRVVMVNEAYRRIV----TGD
At5g50360.1 DIG2       ----------------NDGASYNRRYQTELMTET--VVSS---LLTVECVT---E-RLM---EGEYE----LGCTD---EERKMNLERDTCPGFISDGLGRVIWTNGSYRELV----VGK
At5g63350.1 DIL1       ----------------NGGGEILTPYKTAEISRRTVVVSS---CVTVERVT---D-AWI---DG-YG----LGETN---QERKMNLVEDTCPGFISDGVGRVTWTNEAYKKMAREDINIP
Solyc03g111100.1       GGNQGNNNDNSNNNNGQLQGVAMDR-SVVMFPQPVRVVGS---WVKVESVT---D-AWV---EG-YG----LGRTD---EEKLINLERDSCPGFISDGLNRVRWANKAYKGMV-------
Solyc02g093890.1       --------DRSIWINKNILSIGAP--DPSVEIRSPMVVES---WVTVDGLT---NTTFV---DL-SA----LGSTD---MEKMMNLQRDTCPGFISDGLDSVKWVNLAYRRMI-----DP
Solyc02g068030.1       ----------QKSENSEIFPVGSDQIDRTVEMQKKRVVES---WVMVDQIT---N-ALV---DG-EA----LGSTD---TEKMKNLEADTCPGLISDGLDRVRWVNLAYRRMV----DPL
GLYMA19G22560.1        --------------PPRAAAEEGEGGKRSDLVAAAKVAES---WVTVESVT---G-TCMGEGDG-EGGRGLLDCTD---AEKVKSLEADTCPAFVCDGSLRVRWVNDAYKRMM---LEGR
GLYMA17G13720.1        ----------ENRSLTMMGG---------WCS-----------CVTVEGVT---D-TCL---ES-EW----LGSTD---EERRLNLSNDTCPGFISDGYGRVTWTNEAYGKMMMMKGEGD
GLYMA06G18060.1        -----------ENSFKNRGGTASEKVDPCWYSPA---AGS---VVTVECVM---D-RWQPQEEG-LG----LGRGD---VERKVKLEEDTCPGFISDGYGRVTWTNGAYREIM-------
GLYMA05G06810.1        --------------PPRLVVEEGEGAKGSDLVPAAKAAES---WVTVESVT---G-TCMGEGEGGRG---LLSCTD---EERVKSLETDTCPGFVCDGSLRVRWVNDAYKRMV---LEGR
GLYMA05G03080.1        ----------ANRSLTMMGG---------WCS-----------CVTVESLT---D-TWV---EG-EW----LGSTD---EERRVNLSKDTCPGFISDGYGRVTGTNEAYEKMM----EGD
GLYMA04G36920.1        -----------ENNFENRGGAASEKLDPCWYSQATAAAGS---VVTVECVM---D-TWQQQDEG-LG----LGSGD---EERKVKLKEDTCPGFISDGYGRVTWTNEAYRETV-------
Os12g0242500-01        ------------------AHAAAQSVVVAPPPRALLPAAA---VVTVEDVT---S-VWR---DGGSG------------AARAGD-DGDGAPAFVSDQWGRVTWKNAAFHRAV-----AP
GRMZM2G084005_P01      ----------------ELVPSQVATAARPLAPRAMRPAAAAAYLVTVEEVT---A-TWR---DG---------------EAPASATGHDEAPAFVSDQWGRVTLWNAAFVRAA----SAD
At1g27461.1            --------------QGPITTTTTATTSRVISPQPIRPVCS---KINVAYIN-----PLTNPSPTSQT----SKKSP---REVEEDVESDDLPSVITDSNSRVRLVNSAYKEMM----GQP
Os07g0585700-01 Sdr4   ------------LVERDLLRKLLEP-RKLLEPRAVRPVGS---TIHVESVHIDVGRTTA---AAAAA----APKTA---EEVEAELESDSLPAVVSDSSNRVRLVNDAYKRMV----GQP
GRMZM2G396402_P01      -------------VERDLLRKLLEP--RVISPRAVRPVWS---AIHVGCIHRTDDAACT---DAA------VSKTA---VQVEAELEVDALPAVVSDSGNRVRLVNDAYKEMV----GQP
GRMZM2G105302_P01      -------------VERDLLRKLLEP--KVISPRAVRPVCS---AIHVGCIHRADA-TCA------AA----VSKTA---VRVEAELEVDALPAVVSDASNRVRLVNDAYKEMV----GQP
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At3g48510.1 DIG1       VEEGAPEITSGDSFHVI--VRLVMRER------PMLTS----PGFTCRMK-LQYTCQNRERGSVTVPCDVWRMDVGGG----FAWRL---DVKAALCL----------
At3g27250.1 DIL4       DSTAS------VSPEVV--VWLVAEEATAA---MHCNY----QAFTCRVR-MQYTW-KETKYTKTVPCDVWKME-FGG----FAWRL---DTTAALTLWL--------
At5g40790.1 DIL2       DVDVI-----------R--VWLVVAMDLMEEIACMVEL---YGAVTCRVR-VRYEP--STWRKMTVPCDVWRIR-SGG----FAWRL---DVESALRLGM--------
At5g40800.1 DIL3       GGFGR---------EVI--VWLVVDQTA-----TFCDY----RTFTCKVR-MEYTW-RETKYTKTLPCDVWKME-FGG----FAWRL---DTTAALTLWL--------
At5g50360.1 DIG2       DHEQC--------SKMS--VWLVMKEK------PLVTY----RTFTCRMR-LQYTCRDKEVSSITSFCDVWRMS-DGG----FAWRL---DVDAALCLGR--------
At5g63350.1 DIL1       MEEGVPEDISYDNFHVN--VRLVMKER------PMLTY----PAFTCRVR-LQYTCQDRERGSVTVPCDVWRMD-GGG----FAWRL---DVKAALCL----------
Solyc03g111100.1       -GDGA--------GEVV--VWLVMKDA------VRLPESKSTAAFTCRVRVVR--C-GKEKNSLILPCDVWRMD-GGG----FAWRL---DTEAALSLGR--------
Solyc02g093890.1       EEEGG------EATEMV--VRLVVKEDKRAPVLLLLPS------FACIVR-IVYTW-NKVKQSRTMPCDVWKMD-CGG----FAWKF---DAKAALSLGR--------
Solyc02g068030.1       EGSGN-------SPELV--TWLVVKEK------ILLPN---SSAFACTVR-ILYT-----KNSQTMPCDVWKME-FGG----FAWRL---DAKAALRLGR--------
GLYMA19G22560.1        EGEGE---------NIV--VWLKVKDSA-----IASWWCYSHPAFTCGVR-LQYTW-RNEKCTKMVPCDVWRLD-CGG----FAWRL---DVKAALSLGL--------
GLYMA17G13720.1        EGQGP--------------VLLVNKVN------TVVPH----ASFTCLVRVVQYSC-GKERNSLTVPCDVWRMD-CGG----FAWRL---DVKTALSLRLGY------
GLYMA06G18060.1        -GEGG--------------VWLAMKVT------VPCLY----RGFTCRVR-VQYAC-GKER---TVPCDVWRMN-SGG----FAWRL---DVKAALSLSLAL------
GLYMA05G06810.1        KGEGE---------DIM--VWLKVKDSA-----CAAWWCYSHPAFTCGVR-LQYTW-RNEKCTKMVPCDVWRLD-CGG----FAWRL---DVKAALSLGL--------
GLYMA05G03080.1        EGQGP--------------VLLVNKVN------TVVPH----ASFTCLVRVVQYAC-GRERSSLTVPCDVWRMD-SGG----FAWRL---DVETALSLRLGY------
GLYMA04G36920.1        -GAGG--------------VWLAMKVA------VPYPY----RGFTCRVR-VRYAC-GIER---TVPCDVWRMD-SGG----FAWRL---DVKAALSLSLAF------
Os12g0242500-01        DAAAP--------DQAR--VALAARDGDAA---AAVPAWGTCAGFTCRVR-VHPSPYSPRRSSVVAPCDVWRLD-AGG---CYLWRL---DLQAALSLSLGALP----
GRMZM2G084005_P01      DGDEA--------------AAPVVLG-------GALPAWGTCAGFTCRVRARHWSA-RRVGSPVVAPCDVWRLDAAGS----YLWRL---DLQAALTLGGCL------
At1g27461.1            ECSWL--DSMVRGKRIC--GEVMINFCE-----SKIPVMTENNGFSCWVR-IDWGR-DGKEEYMHAFCDVTKLA-CDSKDYVFTWRF---HTTTDRR-----------
Os07g0585700-01 Sdr4   ECPWLDAVATAASRRISGEVALVVSEPAAAA--AALPE--TCKGFSCSAK-IAWER-DGKWSSVHAPCDVTRLQ-CESRDYVFAWRF---RAAGDECNTHRRAAGDA-
GRMZM2G396402_P01      ECPWL-DAVAATSRRISGEVALVVADR------SSLPD--SYGAFTCTAK-IEWED-DGKVTSIAAPCDVSRLQ-CESRDYLFAWRFRTAAADADASVGHSSEEISES
GRMZM2G105302_P01      ECPWL-DAVAATSRRISGEVALVVANQ------SSLPE--SYGVFTCTAK-IEWED-DGKVASIDVPCDVSRLQ-CESREYLFVWRFRTADADADASVGCSSEEISES
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