>kfl00266\_0050\_v1.1

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>kfl00339\_0070\_v1.1

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>kfl01173\_0020\_v1.1

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>AANG006772

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>AANG007497

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>AANG002657

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>AANG014577

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>Azfi\_s0117.g046584

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>Azfi\_s0139.g051166

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>Azfi\_s0158.g053902

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>Azfi\_s1840.g107359

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>Azfi\_s2076.g108990

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>Chabra1|335919|rna-CBR\_g32298

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>Chabra1|337629|rna-CBR\_g30118

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>Chabra1|339814|rna-CBR\_g37697

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>Chabra1|355109|rna-CBR\_g3422

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>Chabra1|356485|rna-CBR\_g2836

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>Chrsp31S04792

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>Chrsp6S00594

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>tr|E1ZJW9

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>tr|E1ZPY0

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>tr|E1ZTI4

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>TnS000331967t03

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>TnS000076667t02

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>TnS000022753t07

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>TnS000947333t01

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>TnS000060165t02

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>TnS000821935t04

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>ME000247S04224

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>ME000293S04947

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>ME000110S\_11048

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>Mesvi1549S03163

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>Mesvi1691S09237

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>Mesvi213S04226

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>OT\_ostta13g01940T0

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>OT\_ostta02g03420T0

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>Sacu\_v1.1\_s0028.g009859

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>Sacu\_v1.1\_s0098.g019462

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>Sacu\_v1.1\_s0146.g023088

MASSRDRASAHYAYRDDDAESGIYSTVVIHRGPDSGSDNSLTGADGDEVDDGVAGPGHIEPGDIYATMLRRDGDDDVDSPPPLLQSLAKRFAGTDAFDVTDDPSDIIPNFPPRDDDDSSVVLHSAATSTEDATALFKGDDFSAALRYMQKEAFSRMRVRQDEQEETDDSFSTFVVKKEDERGRKSTLGLGSSHGEASELYSTMLHRTGDASATVVTKHGDNSSSISKAVESFKNENEAFDKKRGFHDSPRSVHEKSQRSRRRASSPAQDNVIREDPTLKYELLDELGKGSYGAVYKARDRKTSDLVAIKVISLSEGEEGYDDICGEIEMLQECNHPNVVRYLGSYQAEEYLWIVMEYCGGGSVADLLQVTEETLEERQIAYICAEALKGLAYLHSIYKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTLSKRNTSIGTPHWMAPEVIQGTRYDGKVDVWSLGISAIEMAEGLPPRWNVHPLRVLFMIFREPAPMLEGKEKWSLIFHDFVAKCLTKETRLRPSATDILEHKFITKCNGNASCMLPRIEKARLIRLQTAPQRIPQDLDATVGVSLPQQWSWEKGNTVKMGEIYGATVLVKSDKTINSSDMEGTTIIRHDEVEYGVLSFHGNLLLLDSADFNTMVVHLDHPIDQTKEQVPSTQNDQSNLAEMPDSATREIIDSKVGSSSITTHLPNELSTPADLSESSVPQGTYASSSTSIQQNSVPEAREQVERGEPSIVPVPIVTPRGLHAGGRQVFALRDKLLSIYSGGTTVPIPFLRATDISPLALISNRIFGEEQVDKGNAVALGAVQELYNGGGLGDAPPKRGRKPHTSEQPLPASVHKRLSTSNTLANLARALAYHKLCYEEMPLQGQDVQECCHSAMQDLSVSRRWRISRQDRHSGCDIFVTKGNRNASCKHPRIEKTRLILSQTAAQRIPQDLDAAVGVTLLILKVSGLY\*

>Sacu\_v1.1\_s0149.g023298

MERKASFSSDSRTEKKVYPLVASDYKLLEEIGKGFSAIVFRAKCIPLGEFVAIKTVDLERCNGNLAYCSFVVEQSLWVVMPFMAGGSCLHIMKAAYPEGFEETIIASFLKETLKALEYLHQQGHIHRDVKAGNILVDGNGAVKLGDFGVSACMFDTGDRQRSRNTFVGTPCWMAPEVMEQVHGYDFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKKFSKSFKEMVAMCLVKDPSKRPSAEKLLKHSFFKHAKSADYIARTILDPLPPLWERVREVKMRDEARLAEKKMPYGEQEARSQNEYKRGVSSWNFDLEDLKAQAALNEVEPPMKDDIRKEFYAAEIHRASSPPCATSLPTTQDNNSCQQSDVPDHVSRVKSASLPPKPGNDSKFGHPPGKKEPKHFGRFDVFDDDPEQDALDSCNGNGDTKQQRKEEEKDNLTKEDDQGNGKECSFLLTTEKCMESSHAEEKTCEQDHTNQKYNHCSVVESADEGQEDGGIKSSGKQMDENATVSQPSKPPIPSSGPSVSSGAFYEGRCSNGLPTPSRLGDHKAHKESVEDKLKGQAVFQKKGRFSHGPSSRKNVSIQTSMQPVNKAPNVNDWHLERKNTGPPLSSQNPSLTTASGLNSAMVIPQLQTLFSQTALQQELIVNLMNSINPSEQSLSLKSSSFNAKNVSRSGGLSSVDSTMVEIITERERDLLSQVADLQYRVAALAEELQAVKSRNVQLERQLNAIFNKEEEERIRKEEAARDDG\*

>Sacu\_v1.1\_s0212.g025959

MDKKKYPLSAPYYTLLEEVGQGASAAVYRAKCIPTNEIVAIKILDMERCNSNLDDIRREAQTMSLINHPNVLSAYCSFVVEHSLWVVMPYMAGGSCLHIMKSAYPDGFEEPVIATVLKECLKALEYLHSHGHIHRDVKAGNILIDSVGNIKLGDFGVSACMFDTGDRQRTRNTFVGTPCWMAPEVLEQVHGYDFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKRFSKSFKEMIAMCLVKNPAKRPTAEKLLRHSFFKHSRSPDYIARTLLDNLDPLGQRFRDLKLKDAERLAQKKMPFDEKEERSQTEYKRGVSSWNFDIEDLKAQAASIEDDDGCYATGKEELEHMDTSNIASAMQTSASQDSINDIHDAVMVQSPSAEKTGRAFPRVLSGPSVAPLRSSSEEYTQPSGVQDVGCSDESSLATDAINVQLQTETPKGTEALYGRETKGELKKADKSFQQRGDLKKEDRLFQNIDEKDLRHERMQQEGRRASSGPLVAEHVLSAYRTRDEEKDNGRVSSRGDDDVPRARVNHRERAFSGPLSVHGTPFEHRVTNGFSSTAKQVAGSKDVPDKGLYVQKKGRFSVTSADVELMEDNATSTAPRRGASMQTLPQLSQSSASLQYPVAHSPNMIPTTAVVACLQNLLQHASSQQELLVSMMNSINRGDALQGVSENISTKLYYGNPSARPLESLELEISSDREHELLQQIADLQNRLAIATDELQTQKNKNSVLERQLNALCNRKEEERIRREDEAEES\*

>UM010\_0073.1

MKGEHRKPSGLLKGFSRLGHSKSRKQLAPEPSKWDDMDFPTTPDEYEIQQECGRGVSATVYQGICKTNNEKVAIKKLDLDEMGWGAHWEEVVREAHTMAAHHHPNLLPLLCSFTDGNQLWMVEPYITHGSMLNIMKYAHPHGLSEELIAVIAHETLRGLDYLHHHGMIHRDVKCGNILVDADGRVYLADFGVAAPLEVRGAWGEKPRNTFVGTPCWMAPEVMQESQYDFSADIWSLGITVLELAHGHAPFAKYPPFKVVMMTVQNPPPSLDSEPNSQRRFSKELHDLVASCLQKDPAKRPTARALLEHRFFKHVPKDRDYMRKHLMAGLPDVITRVRHMKDGVKGLPFEPALQEESRSNDQYVRGLSAWNFDVAELKRQAQLEPMEPLLEEEETGHADRVASTSFTSRTAAGDSAPMAAADGAAGLPRSSADSGVSAALPVAAPPPASVVSMDTVSGALASVGVPDVAGGASSVGAPLSEAGDAISRGASHTGEFALPSTALSSSPGQLGPTDHAGLPHSPYSNPPSQPPSNPPTSNAASDMHEEDDLAQATIGHSIAQASPSTCLPHSLAMSSSTGAPAAAPADSAAASSAAALSDALGGQPLPPGSVVAVTTSVTVATTALPVPAGSPVPAGAAVPPAEQVLPPTEVNIARHTHALAATVGPPPPQQKVGRFNIKKKMDLTASDNGSAATMPEWRHGVMAGEDAVPRPGPSNSPQDNPLPMFDPVADRAIVEGAKAASVAGMPIGDKDETSSRKSSKKGRFNVTAATMPLQRSSVNLLPAQPESERSLTVEALTALDTDPAAVAASHVARVTCDSDIAGRLTSDGAWASPAHTSSTHGEADAPAAAAAAAAAANAAAASVAVSTADAVLEAALTAPLGKDLSKSRKESRFKVVKVVDGRLPSEPGGVVQGARTTSESAAPQPGAMQQGVSQGGISVNGAQQDALGIVNKKLQELMQANQAQQEALRMVTAAVSEGAKGKDLLLSDLSRNPLVAVHLLGSESQHNALLEENARLRAELEDLKRKTRRDSEKNKALTKEKELLRSHVAALREQLEAARGVPPPIAALPPDLRTSAPLLTTPTPGPGDSRTSSPSGSILAAAAGGGGGGVRLLPLDMAIIGSGGVVAGAGAPGDMTACSGSSSTTPQELSPWPGGSSQSGEVGGGARYMPPVCPSTSMAMPTPVPAAAIRSPFAGTQHMMVAGDAPAAAAHSAQHAHLRPGTLPSDLSSLAQMTKSTAAQTAPAALDAGVPADAGPAAAPAATAAAAVDVDSAPATRPLSPVAEGAAEGSASSATGQADSMPGLPMVHSADHVAVLPSCGAAAAPAVAGHDRPAEPAS\*

>UM061\_0059.1

MGLSDPLADAISVHGRFDAGALIGKGSYGSVYEGVDTKNGNKIALKVIDLDELEDDISEVMQEITALANCDCPQITKYYDSMLLPDSSKLVIAMELMSCSGADLLELAPWPEAGIAYAMKQVLQALDYLHSQRRMHRDIKAANVLLSAEGVVKVADFGVSGQLTATLGYKRRTFVGTPYWMAPEAIESSEEGYTCSADIWSLGITAIEMAQQRPPHSELHPMRVLFVIPKAEQPVLAGGQHSAHFKDFVALCTAKDPQQRPSASALLAHPFLKAQEKPPAELLGLLKQAEAKRAAVAPTRSAATLSRRTTAQRTESSGPFWDFPDDDRGSGMHGRPAVGEPEAPPGSEQGTVRLQRLPPSSWQDTGDGTVRIMRPDSRISGGGGGGGEGPQFRTVTAADMAAYADESDVPLITAAAAKSNARMQQAPLRPPSLRAPSTRDASEGFAPVDTATILNQASTPATLKHVIGPALTAAGRPAEGAMPAAQAVGDAVDAFARLEAASPGACLAFVAQVMSEAVAAPIAGGGELVQLRKFATRMAAAVQSAPDEPEEEKPPMLEFLKQRWRSNLARDELRAAGLAGSIGS\*

>UM105\_0010.1

MRTRQSSAQQHPKKRYDLREQLGRGSYGSVYKAIDTVTSEIVAVKIIPLSVTEQDGFAEVKKEIEMLQMCNHPNIVNYISSIQAEDALWIIMEYCGGGSITDVIASNGLPLEESTIAYICSEALKGLSYLHSMNKVHRDIKCGNILLTETGEVKLADFGVAAQLTNTLSKRNTFIGTPHWMAPEVIQESRYDGKVDIWALGISAIEMAETIPPRWTVHPMRVIFLISREEPPRLSEWEKWTLTFHDFVRLCLTKDTTARPTGAQLENHKFVTQSRAAPRPNLQPAIHRAKLFLSAKAAAASEAFGLSLTSTVPEEGGRQSIAATESYQGTVLQRGTVGAGGTWGTVLMHDGDPPATPSPDFQDTVVHQGSVRRPAAPRAFGRGAAVPSTPERYGTTVIHEDTTEGGEDADAYGTVVVAGEPPAGGGGYLDAVRMAGEQYGSREPSPMGRSGGGGAVGGSPQSGYWAAVASASEGGPASAAVSPSPAREKTPTQKMLSRLNSVYESGNVMPVAFLKASHAAPLALLDPDPAPAAAAPLAPPPAPGGPTAGATSGGGGSGASRGGEPGSELSRRALRMVSDLAVDSMLAAVPQQMRDNYKKQARPFDAAIVKQLQEAPVLMNLARALAFHHATLDDAPLPPAEAAAQKEVVDDLTEMLRTIMCL\*

>Vocar.0005s0155.1

MERALTGLTARLTSRKSTKDLATLATGKEWPTDASAFKILDDCGRGVSATVHRAICLDNGAEVAVKLMNLESMNCDLEEIIHEAQTMRKYNHPNILPLYCSFVHEQELWMVMPFVAGGSVLHIMKYGHPEGLNETIIATIGREVLKGLDYVHKNGSIHRDVKAGNILVDGDGNVKLGDFGVAASLERGGSWGHDKQARMTFVGTPCWMAPEVMEQTSGYDFSADIWSFGITLLEMCHGHAPFAKFPPMKVLLMTLQNPAPTLEDKGQKHFSKALKDLVTRCLQKEKDKRPTAAQLLEHRFFKIAKDAKYLKDNLVGELPPLSDRVNRIRTGMAATNKQDNDRNLEKSQEEYRKGVSSWNFDLAALKAQAALEPDDETTHGANMLPTITESDEREETMTGTSAAVATPVEAERTAPQPTGAVAGPYTSTSTASVFATMNGQDATLRTNAIVPLLTSAASDGAPPQDQAGVSAGPSAERCNTQGELPPPSPGGGVSPATGLSREGSLGGNLADARAGQAATPTGGVLKQKKGRFEVSVHADVPASSAASAAAQALAQVPTMPASVPLAAAHPSVQLAHAPNSIGSNTLASMSTGSGVLISGGTVPDLQLLRGSTPGLDAASESRDEFPGTLLPAKTEVEESVTSVEPKQRGRFKIVAEQGTTSDSRPLSKASSMANLSDSNKDPSKQRSDGGNLSGKPPTAPTSMTTSVSVVLPKLQELMDHASAHQAALQKLIGAVQECEKGRVPLLLSRTQSTKSLFETSPSEAADDLRLQVVELRAKLSALEDENTRLRERNKVLETLHSAAHTVRFTLPAEAASAPGGGATSPKFEGAPTQQQLATSQPSLA\*

>Vocar.0007s0076.1

MASERYERRHCIGRGSFGDVYEGVDTETGNPVAIKVIDLENVEDDIQDIHKEIQALAGCKCKNITEYYGSVAPPGTAELCIIMELMACSVSDLVQHGPLDEPCIAYILSQVLNALVYLHSERRIHRDIKAANLLLSRTAEVKITDFGVSGQLTGTLGYRRKTFVGTPFWMAPEVIETSEEGYSEKADVWSLGITTIEMATGAPPHAALHPMRVLFLIPTRPPPQLEGDFSPEMKDFVTKCLQRDPGARPAAKDLLSHPFLVGAVEPPDHLPAMVQELVRHKKPLTSRRDVEDSMAACGTMPAWDFGTIGRKAAAAAAAAAVPTGTVRAVAAAMAAVGSGATIRNGDPLREALKLQQQQQQQQQQQQQQQLATAATVAAAPRLESTSRKAVGTAFTEGLASPNGAIAAVVPVIAAAAAPPAVTAPPSPGPGTAAAAAATTAPSTPGGHTSSSSLLQLAQQAEQQQQQPPQGIAVEAVKSPLASPGARTNGVADGIGGGSGVGGALGLGGALSPSAKTRGAAHALERHSSLPTAGQQPQQQPQQQLSQPQLPQQQQQPVQQEPAPQQPQRSAPILSEKFRTMSSAERRMYGDLISKGSPWAGSGVIGGGSGSATGSGGGSGSATGSGGGGGSEGTATTTEGLVRNSLSFGAPLPAGTPPSGIAAAAVATVSAGAKNAVHRYSATSDDSSEASSGRRRPAEHSVDGTAGDADKYGTMQSRASGTASGGASSGSPSHNSGSQRSSIATHSGGAGGPSTVIGSSSGGGVYGTVQSRKQVTPLVDGNHSGAPTAAAAGGLPPRGTSTTADGLAGNAGGGGAAAAAAAASGGDEIFKGLEPLWVHGVSLVVGVIVVVVITAGYQVPTPCSVYPTCPRSSCVKRIGAFLHACRDFCVMCSVQMPGASYRLVQELLVRLSCSSDPALQPLCASAIGLYATQLATSSAAGAIGIGGTSGPGLASTAAAAAAGGGGGSSSGRGSASSSGNGISMPAAAVAAVAAAAPHSHGKNRSLPDLGPLGEFLLGRWREEEAHELALLARSMSLSVAPRR\*

>Vocar.0003s0077.1

MMSKDVAAGALCATWQRDQHPTDEMESEVASSRFQLQNVLGKGAYGTVYSAVDGQTGETVAIKVIPVTDQDREELTQIQKEIRFLADCNHPNVVRYLGSYRHPNELWIVMEYCGGGSVSDLLSATSEPLSEDLIAYVCGEALKGLAYLHGLGKVHRDIKCGNILLTTGGEVKIADFGVSAQLTATMSKRNTFIGTPHWMAPEVIQESRYDGKVDVWALGISAIEMAELRPPRWNVHPLRVIFMIGRDPPPRLSQLDKWSPVFQDFVSQALLKVKVSFNRVWFVFPPAPTSALSLLSPPFAFSPPPGSDPRFAPFRATHPVVRLSPRWHTQDAAAAAQKRQSVVEVTSLEGLATGRFTWRSGTARGHGAVGAVPETEDVALAAAATMRAGARNGGGGGGGATAAVSGAGFGAIVQPEAEPASVPRSAAARGGRTPAAAAGAQPPASSPLPATPLSAVRRISSGAGFDSTMVDKEDYYGTVVVHNEYDAAAVHSDGGAGGNGLAVALAAYRTPATPAGGPAGAAEYGSAMVVGGTMIERSGTVRRSNEMADASGDGADGCGGGGGGYLAAVRAAAAEAQNGDRHAKPLDSPLGSRPAAAHHLDEVERVRERLHSLYDGGLVVPLPFFKASQAQPLALLCPSEPFAGSCSHAVQGPLLPPPLPPPLAGSSRQEGAAAAVAAAGAPYRRVQHGGGGGGGGALTRSGGGVAAVPPPPASAAAAAAAGGTSWVGALQKTSQPSLPPLPPLQQQQQQLSSSPQQQSQPHVLQSNAAPPASLDLHGVDPEAYGVVLELVQQSAAMARQRGEVVSEPGSAAVDPLPPTVVTQLLFHPALQNLARTLTYNRRCLASLPLDRRAQEELQESCNQLSAALQCVLSL\*

>AL1G37450.t1

MTSSSGTKFPLDAKDYELLERIGDGVYRARCILLDEIVAIKIWNLEKCTKDLETIKKEVHRLSSIDHPNLLRSHCSFIDGTSLWIVMPYMSCGSCLNIMKSVYPNGLEEPVVAIFLREILKALVYLHGLGYIHGNVKAGNILVDSEGTVKLGVERMPTSSGNTFVGTPCWIAPEEDTQQVDGYGFKLDIWSFGMTALELAHGHSPFSKYPHTVAPPLTLQNSPCPVYEEDNKFSKSFRELVAACLIKDLEKRPTASKLLEYPFLQHTLSTEYLASTILDSLYPLGERFRKLKEEEAKLVKRIDGNSEKLSQVTIEGLLTSGKPASPVNPVSCNAAQILPMLQNLLIQNDIQRERVISLMQLYDPTAEIRIPVVNTEGGQISTPETDLLSEVHVLQQSVNKLEEEVEKQKTENAKLEGQINRLTRCTDPYRQNCFVLHLEGEAPLL\*

>AL1G61540.t1

MAPEVIQNSEGYNEKADIWSLGITMIEMAKGEPPLADLHPMRVLFIIPRESPPQLDEHFSRPLKEFVSFCLKKAPAERPSAKELLKHRFIKNARKSPKLLERIRERPKYQVKEDEEIPTNGPKSPVESSGTVRVAGDERGQGTSGTSFQVKTVRNAGWDFSFGGSQGAGTVRALKPPQARERRQEVSSNQTSQKTSRASGSQLSSTFGVPEISEGGFNKRDSYQNDNQEEDDSSGSGTVVIRSPRSSQPSSMYRDQSSGSANRYTSFDDASTSGTVVVRGQNDDSGSPRTPRSRLGLQERSSSASEDSISNLAEAKLALEAGFRRGNAREKLGNGKVNKRREQATDNSDYLRNSRDHSDKQKPVIRSQQVSDDEDDSKLASLSASLSLLLLPSLKEAVGGDDSKGSVGHRVSRSLVNMEREKPGSSEAFIAKLIEQLGSTKEVSVKEVQDMAIRVFAKTMNKDAENKRKQASKEFSSNANFSPLARFLFSRWLGQTSRDLNQS\*

>AL2G28310.t1

MDHNSPRSRRSRKPEPKSDIYSTFVVHSDSDSDQGRNRDKRKAKPEEDENVDLYATMVYKGDSDGEGEEDDEDDSMLPPLLKRLPKDFGGGASLDYDDDDGDETGDFGTMIVKTDRSSHSKNSPYSSKPRMGVSPRRRARGGDEESSDEEDEEEEDDDDDGEYGTFVVKSSSKKGKNKEKEIDMSTMGRAVASMQKSNFGGKTRKLDPSSSSSKLQGEDNRKMQQQNSKMSTTSLPDSITREDPTTKYEFLNELGKGSYGSVYKARDLKTSEIVAVKVISLTEGEEGYEEIRGEIEMLQQCNHPNVVRYLGSYQGEDYLWIVMEYCGGGSVADLMNVTEEALEEYQIAYICREALKGLAYLHSIYKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVIQENRYDGKVDVWALGVSAIEMAEGLPPRSAVHPMRVLFMISIEPAPMLEDKEKWSLVFHDFVAKCLTKEPRLRPTAAEMLKHKFVERCKTGASAMSPKIEKSRQIRAVMALQAQSVVAPSSEDTSTLGPKSNEEVGITVPAKPPQNSTEAPLTGTLNRQHITGNTVLAGEGGDFGTMIVHGEDEAEESDSRSQLVKEKEESSSSQVEGVSREVSGEELPDSWIHDKKNPPGIDLPIEASTSQSIQASSSHEHRTKLNNIAGTQIEGGSDASGSTLKNETVGRKAFALQDKLWSIYAAGNTVPIPFLRATDISPIALLSENMIGGMQQDGNGTVAVEALQELFTSDPQSKKGRRGQNEMPLPPSVYQRLTTSSSLMNLAQVLAYHRACYEEMPLQELQATQEQQTIQNLCDTLRTILRL\*

>AL2G29800.t1

MAGSSTKRFPLYAKDYELFEEVGEGVSATVYKARCIALNEIVAVKILDLEKCRNDLETIRKEVHIMSLIDHPNLLKAHCSFIDRSSLWIVMPYMSGGSCFHLMKSVYPEGLEQPIIATLLREVLRALVYLHRQGHIHRDVKAGNILIHSKGVVKLGDFGVSACMFDSGERMRTRNTFVGTPCWMAPEVMQQVDGYDFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPRLDYDRDKKFSKSFRELIAACLVKDPKKRPTAAKLLKHPFFKHARSTDYLSRKILHGLSPLGERFKKLKEAEAELFKGINGDKEQLSQHEYMRGISAWNFDLEDLRRQAAIVPNDEMCNSEIQELNTNGDVPKGKPVMQRSQTMPLEFFSEKDMMSESYSQLTGSLLPSFHRKFLPTIGYQVGILSDERNACCSSDGVAEKLALGKPHQLEPLADTEQIGKAGSEQEKPKNGYAVSPVNRESSTSKEPLADTKQIRKAGNEQEKPKNGYIVSPVNGESSPSKEILPLLQSLLVQNDIQRAKVIRLIRFFDRTAGTENPISKTEGVQVYPSKEKDLQSQVQFLEQSVEKLVEEVQRRKEINSQLEQQISSLISSSSSSNIP\*

>AL2G40330.t1

MEKKKYPIGPEHYSLYEVIGQGVSALVHRALCIPFDEVVAIKILDFERDNCDLNNISREAQTMMLVDHPNVLKSHCSFVSDHNLWVIMPYMSGGSCLHILKAAYPDGFEEAIIATILREALKGLDYLHQHGHIHRDVKAGNILLGARGAVKLGDFGVSACLFDSGDRQRTRNTFVGTPCWMAPEVMEQLHGYDFKADIWSFGITGLELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKKFSRSFKQMIASCLVKDPSKRPSAKKLLKHSFFKQARSSDYIARKLLDGLPDLVNRVQAIKKKEEDMLAQEKMADGEKEELSQNEYKRGISGWNFNLDDMKAQASLIQDMDCGFSDSLSGSTTSLQALDSQDTQSETQEDVGQITNKYLQPLIHRSLSIARDKSDDDSSLASPSYDSYVYSSPRHEDLSLNNTTVGSNHAINGKPTDSTSIPTNQPTEILAGNSALADRNGIPNKGESDKTQDHLQNGSNCNGAHPTVGGDEVPTELAVKPPKAASSLDESDDKSKPPVVQQRGRFKVTSENLDIEKVVAPSPILQKSHSMQVLCQHSSAPLPHSDVTLPNLTSSYVYPLVYPVLQTNILERDNILHMMKVLTNRELTDGRAVEQGSVQQPTVPPTEKSMLEAAHEREKELLHDITDLQWRLICAEEELQKYKTEHA\*

>AL3G27620.t1

MDDVAGLREAAGARFSHIELIGRGSFGDVYKAFDKDLNKEVAIKVIDLEESEDEIEDIQKEISVLSQCRCPYITEYYGSYLHQTKLWIIMEYMAGGSVADLLQSSNPLDETSIACITRDLLLAVEYLHNEGKIHRDIKAANILLTENGDVKVADFGVSAQLTRTISRRKTFVGTPFWMAPEVIQNSEGYNEKADIWSLGITVIEMAKGEPPLADLHPMRVLFIIPRENPPQLDEHFSRPVKEFVSLCLKKVPAERPSAKELIKHRFIKNARKSPKLLERIRERPKYQVKEDEETPRNGPKAPVDSSGTVRVAKDERSQGTPGSSFQGNTVKNAGWDFSVEGSQSIGAVRALKPPQARERRHEVSSNQISQQTTRDSGNQWSSSTGSTISEASEGGFVRRHPFQNDHEDGFHEEDDSSLSGSGTVVIRASRSSQSSSKFREQSSVSSGRYAPFDDASASGTVIVRGQYDDSGSPRTPKSRLGIQERTSSASEDSNANLAEAKAALDAGFRKGNARERLGMGKNNNDGKVNRRRDQMADDSDYSRNSGDKSSKQKAVPRSEQVSDEEDDSIWESLPASLSILLIPSLKEALGDDSKESIGRTVSRSLVMMEREKPGSCEAFVAKLIELLGSSKEASVKELHDMAVRVFAKTTPDAAENKRKQANKEFSSNTNVSPLGRFLLSRWLGQSSRDL\*

>AL6G25490.t1

MSLINHPNVLQAHCSFTAGHQLWVVMPYMAGGSCLHIIKSSYPDGFEEPVIATLLRETLKALVYLHAHGHIHRDVKAGNILLDSNGAVKLADFGVSACMFDTGDRQRSRNTFVGTPCWMAPEVMQQLHGYDFKADVWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKRFSKAFKEMVGTCLVKDPKKRPTSEKLLKHPFFKHARPADYLVKTILNGLPPLGDRYRQIKSKEADLLMQNKSEYEAHLSQQEYIRGISAWNFNLEDLKTQAALISDDDTSHAEEPDFNQKQCERQDESALSPERASSSATAPSQDDELNDIHDLESSFASFPIKPLQALKGCFDISEDEDNATTPDWKDANLNSGQQHLTKASIGSLADTTKEEDTAAQNTSLPRHVISEQKKYLSGSIIPESTFSPKRITSEADREFQQRRYQTERSYSGSLYRTKRDSVDETSEVPHVEHKGRFKVTSADLSPKGSTNSTFTPFSGGSSSPSSLNATTASILPSIQSILQQNAMQREEILRLIKYVEQTSAKQPGSPETNVDELLQTPPATPRERELQSQVMLLQQSFSSLTEELKKQKQKNGQLENQLNALTHRND\*

>AL6G44780.t1

MVSRLRLALEAVFGSRRRKKKMASTSSGGDKKKKKGFSVNPKDYKLMEEVGYGASAVVHRAIYLPTNEVVAIKCLDLDRCNSNLDDIRREAQTMTLIDHPNVIKSFCSFAVDHHLWVVMPFMAQGSCLHLMKAAYPDGFEEAAICSMLKETLKALDYLHRQGHIHRDVKAGNILLDDTGEIKLGDFGVSACLFDNGDRQRARNTFVGTPCWMAPEVLQPGSGYDSKADIWSFGITALELAHGHAPFSKYPPMKVLLMTIQNAPPGLDYDRDKKFSKSFKELVALCLVKDQTKRPTAEKLLKHSFFKNAKPPEICVKKLFVDLPPLWTRVKALQAKDAAQLALKGMASADQDAISQSEYQRGVSAWNFNIEDLKEQASLLDDDDILTESREEEESPGEQLHNKVNDRGQVSCSQLLSENMNGKEKVSDTEVVEPICEEKSTLNSTASSVEQAAPSSEQDVPQAKGKSVRRQTHSGPLSSGVVLINSDSEKGPGYERSESERQLKSSVRRAPSFSGPLNLPNRASANSFSAPIKSSGGFRDSIDDKSKTNVVQIKGRFSVTSENLDLARSSPLRKSASVGNWILDSKMPTGQPSKESSSHHASPSFILPQLQNLFQHNSIVQDLTLNLVNSLQQAAEATDGSQNGKLPPLPRGSDSNGTVVELTASERERLLLTKITELRARMKELTEELEKEKSKETQLQQKLKSVTGREQL\*

>AL7G29190.t1

MVGGGSSSGGGGVFRGGGSGKQQRGFSLNPKDYKLLEEIGHGASAVVYRAIYLPTNEVVAIKCLDLDRCNSNLDDIRRESQTMSLIDHPNVIKSFCSFSVDHSLWVVMPFMAQGSCLHLMKTAYSDGFEESAICCVLKETLKALDYLHKQGHIHRDVKAGNILLDDSGEIKLGDFGVSACLFDNGDRRRARNTFVGTPCWMAPEVLQPGEGYNSKADIWSFGITALELAHGHAPFSKYPPMKVLLMTIQNAPPGLDYDRDKKFSKSFKEMVAMCLVKDQTKRPTAEKLLKHSCFKHTKPPEFYVKKLFSDLPPLWTRVKSLQDKDAQQLALKRMATADEEAISQSEYQRGVSAWNFDVRDLKTQASLLIDDDDLEESKEDDEILCAQFNKVNDRVQVFDSLQLYETMNEKEKVSNTEVEEPTCEEKFTFITTASSLERMSPNSEHDIPEAKVKPVRRQSQSGPLTSKTVLCHSASEKGHIFERSESEQQTASTVRRAPSFSGPLNLPTRASSNSLSAPIKYSGGFRDSLDDKSKANLVQKGRFSVTSGNVDLAKDVPLSIVPRRSPQATPLRKSASVGNWILEPKMPTAQPQTIKEHSSHPTSSSSSLIVPQLQHLFQQNSIQQDLIMNLLNSIQPGEATEGSQSGKLPPLPRSDSNGNVEPVASERERLLLSSISDLRARLDDLTEELDIEKSKYSQLQQKLKAFTGRKHV\*

>AL7G41660.t1

MARNKIEFPLDAEAYEIICKIGVGVSASVYKAICIPMNSMVVAIKAIDLDQSRADFDSLRRETKTMSLLSHPNILNAYCSFTVDRCLWVVMPFMSCGSLHSIVSSSFPNGLPENCISVFLKETLSAISYLHDQGHLHRDIKAGNILVDSDGSVKLADFGVSASIYEPVTSSSGTTSSSLRLTDIAGTPYWMAPEVVHSHTGYGFKADIWSFGITALELAHGRPPLSHLPPLKSLLMKITKRFHFADYEINTSGSSKKGNKKFSKAFREMVGLCLEQDPAKRPSAEKLLKHPFFKNCKGLDFVVKNVLHSLSNAEQMFMESQILMKSVGDDEEDEEEDEKIAKNRRISGWNFREDDLQLSPVFPATDSDTSESSPREEDHIQDKQEDDNVTITGSELGLGLSNEEAKNQEGEVVGFDKDLVLEKLKVLKKSLEHQRARVSIIIEALSGDKEEKSREEELLDMVEKLKIELEAEKLRS\*

>AT1G53165.1

MDDVAGLQEAAGTRFSQFELIGRGSFGDVYKAFDTELNKDVAIKVIDLEESEDEIEDIQKEISVLSQCRCPYITEYYGSYLHQTKLWIIMEYMAGGSVADLLQPGNPLDEISIACITRDLLHAVEYLHAEGKIHRDIKAANILLSENGDVKVADFGVSAQLTRTISRRKTFVGTPFWMAPEVIQNSEGYNEKADIWSLGITMIEMAKGEPPLADLHPMRVLFIIPRESPPQLDEHFSRPLKEFVSFCLKKAPAERPNAKELLKHRFIKNARKSPKLLERIRERPKYQVKEDEEIPTNGPKAPAESSGTVRVAKDERGQGTSGTSFQVKTVRNAGWDFSIGGSQGAGTVRALKPPQARERRQEVNSNQTSQKTSRTSGSQLSSTFGVPEISEGGFNKRDSYQNDYQEEDDSSGSGTVVIRSPRSSQSSSMFRDQSSGSTRYTSFDDASTSGTVVVRGQNDDSGSPRTPRSRLGLQERSSSASEDSISNLAEAKLALEAGFRRGNARERLGNGKVNKRREQATDNSDYLRNSRDHSDKQRPVMRSQQVSDDEEDDSKLASLSASLSLLLLPSLKEAVGGDDSKGTIGHRVSRSLVKMEREKPGSSEAFIAKLIEQLGSTKEVSVKEVQDMAIRVFAKTMNNDAENKRKQASKEFSSNANFSPLARFLFSRWLGQTSRDLNQS\*

>AT1G69220.1

MDHNSPKSRRSRKPEPKPDIYSTFVVHSDSDSDQGRDRDKRKAKPEEDENVDLYATMVYKGDSDGEGEEDDDDDSMLPPLLKRLPKDFGGGASLDYDDDDGDESGDFGTMIVKTDRSSHSKKNSPYSSKPRMGVSPRRRARGGDEESSDEEDEEEDDDDDDGDYGTFVVKSKDKKGKKKDKEIDMTTMGRAVASMQKSNFGGKTRKLDPSSSSSKLHGEDNRKMQQQNSKMSTTSLPDSITREDPTTKYEFLNELGKGSYGSVYKARDLKTSEIVAVKVISLTEGEEGYEEIRGEIEMLQQCNHPNVVRYLGSYQGEDYLWIVMEYCGGGSVADLMNVTEEALEEYQIAYICREALKGLAYLHSIYKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVIQENRYDGKVDVWALGVSAIEMAEGLPPRSSVHPMRVLFMISIEPAPMLEDKEKWSLVFHDFVAKCLTKEPRLRPTAAEMLKHKFVERCKTGASAMSPKIEKSRQIRATMALQAQSVVAPSLEDTSTLGPKSSEELGITVPSKPPQNSTEAPLTSTLNRQHITGNTVLAGEGGDFGTMIVHGEDETEESDSRSQLVREKESSSSQFEGVPREFPGEELPDSWIHDKKKPPAIDLPVEASISQSMQASSSHEHRTKLHNIAGTQMEGGSDASGSTLKNETVGRKAFALQDKLWSIYAAGNTVPIPFLRATDISPIALLSENMIGGMQQDGNGTVAVEALQELFTSSDPQSKKGRRGQNEMPLPPSVYQRLTTSSSLMNLAQVLAYHRACYEEMPLQELQATQEQQTIQNLCDTLRTILRL\*

>AT1G70430.1

MAGSSTKRFPLYAKDYELFEEVGEGVSATVYRARCIALNEIVAVKILDLEKCRNDLETIRKEVHIMSLIDHPNLLKAHCSFIDSSSLWIVMPYMSGGSCFHLMKSVYPEGLEQPIIATLLREVLKALVYLHRQGHIHRDVKAGNILIHSKGVVKLGDFGVSACMFDSGERMQTRNTFVGTPCWMAPEVMQQLDGYDFKYLAHGHAPFSKYPPMKVLLMTLQNAPPRLDYDRDKKFSKSFRELIAACLVKDPKKRPTAAKLLKHPFFKHARSTDYLSRKILHGLSPLGERFKKLKEAEAELFKGINGDKEQLSQHEYMRGISAWNFDLEALRRQASLVIIPNEEIYNSEIQELNRNGDVPKGKPVIQRSQTMPLEYFSEKASDMVSESSSQLTGSLLPSFHRKFLPALGNACNSSDRAAEKLAFEEPRQVLHPLADTKKIRKAGSDQQEKPKNGYADSPVNRESSTLSKEPLADTKQVRKPGNEQEKPKNGYIVSHVNRESSTSEEILPLLQSLLVQNDIQRAQVIRLIRFFDRTAKTENPISKTEGVQEKDLQSQVQFLEQSVEKLVEEVQRRKDINSQLEQQISSLISSNNIS\*

>AT3G15220.1

MDDVAGLQEAAGARFSQIELIGRGSFGDVYKAFDKDLNKEVAIKVIDLEESEDEIEDIQKEISVLSQCRCPYITEYYGSYLHQTKLWIIMEYMAGGSVADLLQSNNPLDETSIACITRDLLHAVEYLHNEGKIHRDIKAANILLSENGDVKVADFGVSAQLTRTISRRKTFVGTPFWMAPEVIQNSEGYNEKADIWSLGITVIEMAKGEPPLADLHPMRVLFIIPRETPPQLDEHFSRQVKEFVSLCLKKAPAERPSAKELIKHRFIKNARKSPKLLERIRERPKYQVKEDEETPRNGAKAPVESSGTVRIARDERSQGAPGYSFQGNTVKNAGWDFTVGGSQSIGTVRALKPPQARERRQEVSPNRISQRTTRPSGNQWSSATGSTISEASEGGFVRRHPFQNDHEDGFHEEDDSSLSGSGTVVIRTPRSSQSSSVFREPSSGSSGRYAAFDDASASGTVVVRGQYDDSGSPRTPKSRLGIQERTSSASEDSNANLAEAKAALDAGFRRGKARERLGMGNNNNDGKVNRRREQMADDSDYSRNSGDKSSKQKVVPRSEQVSDEEDDSIWESLPASLSVLLIPSLKEALGDDSKESTVRTVSRSLVMMEREKPGSCEAFVAKLIELLGSSKEASVKELHDMAVCVFAKTTPDNAENKMKQANKEFSSNTNVSPLGRFLLSRWLGQSSRDL\*

>AT4G10730.1

MVSRFRLALEAVLGSRRRKKMASTSSGGGGGGDKKKKKGFSVNPKDYKLMEEVGYGASAVVHRAIYLPTNEVVAIKSLDLDRCNSNLDDIRREAQTMTLIDHPNVIKSFCSFAVDHHLWVVMPFMAQGSCLHLMKAAYPDGFEEAAICSMLKETLKALDYLHRQGHIHRDVKAGNILLDDTGEIKLGDFGVSACLFDNGDRQRARNTFVGTPCWMAPEVLQPGSGYNSKADIWSFGITALELAHGHAPFSKYPPMKVLLMTIQNAPPGLDYDRDKKFSKSFKELVALCLVKDQTKRPTAEKLLKHSFFKNVKPPEICVKKLFVDLPPLWTRVKALQAKDAAQLALKGMASADQDAISQSEYQRGVSAWNFNIEDLKEQASLLDDDDILTESREEEESFGEQLHNKVNDRGQVSGSQLLSENMNGKEKASDTEVVEPICEEKSTLNSTTSSVEQPASSSEQDVPQAKGKPVRLQTHSGPLSSGVVLINSDSEKVHGYERSESERQLKSSVRRAPSFSGPLNLPNRASANSLSAPIKSSGGFRDSIDDKSKANVVQIKGRFSVTSENLDLARASPLRKSASVGNWILDSKMPTGQAIKESSSHLSFIIPQLQNLFQQNSMQQDLIMNLVNTLQQAAETTDGSQNGKLPPLPRGSDSNGTVVELTAAERERLLLTKITELRARMKELTEELEVEKSKQTQLQQKLKSVTGREQL\*

>AT4G14480.1

MARNKLEFPLDAEAYEIICKIGVGVSASVYKAICIPMNSMVVAIKAIDLDQSRADFDSLRRETKTMSLLSHPNILNAYCSFTVDRCLWVVMPFMSCGSLHSIVSSSFPSGLPENCISVFLKETLNAISYLHDQGHLHRDIKAGNILVDSDGSVKLADFGVSASIYEPVTSSSGTTSSSLRLTDIAGTPYWMAPEVVHSHTGYGFKADIWSFGITALELAHGRPPLSHLPPLKSLLMKITKRFHFSDYEINTSGSSKKGNKKFSKAFREMVGLCLEQDPTKRPSAEKLLKHPFFKNCKGLDFVVKNVLHSLSNAEQMFMESQILIKSVGDDDEEEEEEDEEIVKNRRISGWNFREDDLQLSPVFPATESDSSESSPREEDQSKDKKEDDNVTITGYELGLGLSNEEAKNQEGEVVGFDKDLVLEKLKVLKKSLEHQRARVSIIIEALSGDKEEKSREEELLEMVEKLKIELETEKLKTLRADKDSVLG\*

>AT5G14720.1

MESGSEKKFPLNAKDYKLYEEIGDGVSATVHRALCIPLNVVVAIKVLDLEKCNNDLDGIRREVQTMSLINHPNVLQAHCSFTTGHQLWVVMPYMAGGSCLHIIKSSYPDGFEEPVIATLLRETLKALVYLHAHGHIHRDVKAGNILLDSNGAVKLADFGVSACMFDTGDRQRSRNTFVGTPCWMAPEVMQQLHGYDFKADVWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKRFSKAFKEMVGTCLVKDPKKRPTSEKLLKHPFFKHARPADYLVKTILNGLPPLGDRYRQIKSKEADLLMQNKSEYEAHLSQQEYIRGISAWNFNLEDLKTQAALISDDDTSHAEEPDFNQKQCERQDESALSPERASSSATAPSQDDELNDIHDLESSFASFPIKPLQALKGCFDISEDEDNATTPDWKDANVNSGQQLLTKASIGSLAETTKEEDTAAQNTSLPRHVISEQKKYLSGSIIPESTFSPKRITSDADREFQQRRYQTERSYSGSLYRTKRDSVDETSEVPHVEHKGRFKVTSADLSPKGSTNSTFTPFSGGTSSPSCLNATTASILPSIQSILQQNAMQREEILRLIKYLEQTSAKQPGSPETNVDDLLQTPPATSRERELQSQVMLLQQSFSSLTEELKKQKQKNGQLENQLNALTHRND\*

>AT1G23700.1

MTSSPETRFPLVAKDYEILEEIGDGVYRARCILLDEIVAIKIWNLEKCTNDLETIRKEVHRLSLIDHPNLLRVHCSFIDSSSLWIVMPFMSCGSSLNIMKSVYPNGLEEPVIAILLREILKALVYLHGLGHIHRNVKAGNVLVDSEGTVKLGDFEVSASMFDSVERMRTSSENTFVGNPRRMAPEKDMQQVDGYDFKVDIWSFGMTALELAHGHSPTTVLPLNLQNSPFPNYEEDTKFSKSFRELVAACLIEDPEKRPTASQLLEYPFLQQTLSTEYLASTFLDGLSPLGERYRKLKEEKAKLVKGVDGNKEKVSQENVEALLMEPASLVNPVSCDTAQVLPILQNILIQNDIQRENVEALLTEPAILVNPVSCDTAQVLPIVQNILIQNDIQRKRLIGLMQLCDPTAGKFAVLSLEFASSLCYKFHDLILIFVQKSEFRLAIQKLGRYQQQRQIYCLRFTFCSRGNDKFHKL\*

>AT1G79640.1

MEKKKYPIGPEHYTLYEFIGQGVSALVHRALCIPFDEVVAIKILDFERDNCDLNNISREAQTMMLVDHPNVLKSHCSFVSDHNLWVIMPYMSGGSCLHILKAAYPDGFEEAIIATILREALKGLDYLHQHGHIHRDVKAGNILLGARGAVKLGDFGVSACLFDSGDRQRTRNTFVGTPCWMAPEVMEQLHGYDFKADIWSFGITGLELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKKFSRSFKQMIASCLVKDPSKRPSAKKLLKHSFFKQARSSDYIARKLLDGLPDLVNRVQAIKRKEEDMLAQEKMADGEKEELSQNEYKRGISGWNFNLDDMKAQASLIQDMDCGFSDSLSGSATSLQALDSQDTQSEIQEDTGQITNKYLQPLIHRSLSIARDKSDDDSSLASPSYDSYVYSSPRHEDLSLNNTHVGSTHANNGKPTDATSIPTNQPTEIIAGSSVLADGNGAPNKGESDKTQEQLQNGSNCNGTHPTVGGDDVPTEMAVKPPKAASSLDESDDKSKPPVVQQRGRFKVTSENLDIEKVVAPSPILQKSHSMQVLCQHSSASLPHSDVTLPNLTSSYVYPLVYPVLQTNILERDNILHMMKVLTNRELTDGRAVEQGSIQQPTVPPTEKSMLEAAHEREKELLHDITDLQWRLICAEEELQKYKTEHAQVSMSN\*

>AT4G24100.1

MVGGGGGSSGRGGGSGSGSSKQQRGFSMNPKDYKLMEEIGHGASAVVYRAIYLPTNEVVAIKCLDLDRCNSNLDDIRRESQTMSLIDHPNVIKSFCSFSVDHSLWVVMPFMAQGSCLHLMKTAYSDGFEESAICCVLKETLKALDYLHRQGHIHRDVKAGNILLDDNGEIKLGDFGVSACLFDNGDRQRARNTFVGTPCWMAPEVLQPGNGYNSKADIWSFGITALELAHGHAPFSKYPPMKVLLMTIQNAPPGLDYDRDKKFSKSFKEMVAMCLVKDQTKRPTAEKLLKHSCFKHTKPPEQTVKILFSDLPPLWTRVKSLQDKDAQQLALKRMATADEEAISQSEYQRGVSAWNFDVRDLKTQASLLIDDDDLEESKEDEEILCAQFNKVNDREQVFDSLQLYENMNGKEKVSNTEVEEPTCKEKFTFVTTTSSLERMSPNSEHDIPEAKVKPLRRQSQSGPLTSRTVLSHSASEKSHIFERSESEPQTAPTVRRAPSFSGPLNLSTRASSNSLSAPIKYSGGFRDSLDDKSKANLVQKGRFSVTSGNVDLAKDVPLSIVPRRSPQATPLRKSASVGNWILEPKMPTAQPQTIKEHSSHPTSSSPIMPQLQHLFQQNSIQQDLIMNLLNSLQPVEATEGSQSGKLPPLPRSDSNGNVEPVASERERLLLSSISDLRARLDDLTEELDIEKSKYSQLQQKLKAFTGREH\*

>ATR0150G013.1

MSDSSINDIELRFSSLEQIGRGSFGDVYKGFDKVLNKDVAIKVIDLEEAEDEIEDIHKEISVLSQCRCPYITEYYGSYLHQTKLWILMEFMAGGSVADLIQTGPPLDEMSIACILRDLLHAIEYLHSEGKIHRDIKAANILLTANGDVKVADFGVSAQLTRTISRRKTFVGTPFWMAPEVIQNTDGYNEKADIWSLGITAIEMAKGEPPLADIHPMRVLFIIPRENPPQLDDHFSRPMKEFVSLCLKKNPSERPSAKELLKHRFIKNVRRSPRLLERIRERPKVLVRNPDTQRNGHTAFEDVSNPVRETKGLKDEETVRARNAGWDFSVRGNLGGGTISNAVSPPQVNATKEKFSDAQYTQVLPRVSSELDSRYSTLGNTPQDSTLNFTTEIKGRDQQTDEREEISLGDGKVSANSSGTVISRTPRVTQKSSFFTDQSTASSSSRRSSSGDLSPSGTIVVRGPLDEADPPSRTPRSRLGIQEKASRASQEDSAVNLAEAKAALQAGLRKGNTRERFQLGKLHIDGQESKVAERPTSSDSSRDSHEYLDAPNLLSRLGRSSDDESGARYAAAVSSPSLSLLLIPALKEASGNDSEGAVVRAVTNSLIEMEHALPSSCEVFVSRLLQQLGSTKEPSVKGLQELAARIFAKTSAPPNMESANNEATSSKPSNGKRQPNVDQTENSGLSPLARFLISRWQGQVSRDLNSV\*

>ATR0580G015.1

MERKKYPIKAEDYRLHEEIGHGVSAKVFRAICIPLNEIIAIKVLDFEKTNSNLDNIRREAQTMILVDHPNVLKAHCSFVHEHTLWVVMPYMAGGSCLHILKHAYPDGFEETIIATVLREALKGIAYLHHHGHIHRDIKAGNILVEATGAIKLGDFGVSVCLYDSGDRQRSRNTFVGTPCWMAPEVMEQLHGYNFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKKFSKSFKQMIAMCLAKDPSKRPSAEKLLKHAFFKQARSNDYMARTILDGMPSLGDRIRHLKDKEADMLAQKKMPDGEKEERSQNEYNRGISAWNFNIEDVKAQASLIPDVDDILPDKDQGMLGFYDSLEKDSNCQPAVMDISDMVATDGGHATGPGDAHLPLPGQDPKIIRFKAHGFEDDFDALSLTGEGSARQSTSVMELQCNNADIEKFANEQEVVSNPFLPLATYKGERLDSVIYDK\*

>ATR0620G134.1

CRDYGEDCGKFLVIMGRMGGQKSYSALPGDYKLLEEVGHGASAVVYRAIYLPFNEVVAVKCLDLDRCGSNLDDIRREAQTMSLIDHPNVIRAYSSFVVDHSLWVVMPFMAEGSCLHLMKIAYPEGFEEAVIGSVLKETLKAVEYLHRHGHIHRDVKAGNILLDSDGGVKLADFGVTACMFDRGDRQRSRNTFVGTPCWMAPEVLQPGSGYNFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTIQSAPPGLDYDRDKRFSKSFKEMVAMCLVKDPMKRPTAEKLLKHSFFKHAKPPEATVPGLLVNLPPLWERVKALQLKDAAQLALKKMPSAEEEALSQDEYKRGVSAWNFDVEDLKSQAALVQDDDDPSVLKEEDEDLGPLVNDRVFSVSKSGAGKSISTNDLYCKGNIDGAGCLDSRCFGAREENSESESPAAENLEQRDGRENGSINDPIHSLSKRDPEQSNSRNQLFKHRQTHSGPLMPIRVLSMPSSERGRFSERDEGDYPSAMERGCKHDGRKEPNLSGPLMLPSRASANSLSAPIRSSGFREGLDDKTKANVIQIKGRFSITSENADRVKDIPLCSVSRRSSQGSPLRKSASVGDWLVDTKQTRPKEASNLPIPVSVLIPQLQNLFQQTIFQQDLVANLLRTVQQTELVEGGKWAPPTQSLGSDSSNDPAVSERERLLSVKVAELQNRMINLTDELTAAKLKHVQLQQQLTEAHGREEDRIRKEEKEYS\*

>ATR0686G134.1

MATDPRLRVPYPLEASAYRIVHEIGQGLSSVVYLAECLPLGSTVAIKALDLDRAPTHRLDDIRCEAQTMTLLSHPNVLTAHCSFTVDHSLWVVMPFCSAGSLHSILSASFPSGFDETVIAIVLRDTVRALNYLHQQGHVHRDIKAGNILLDSMGLIKVADFGVSASLFDPSSLTKLQEMAGTPYWMAPEVIDSAARGGPGYDYKADVWSLGITALELAHGKLPRSDVPLGKAIVLSATKPFPASSRKKFSKAFREMVGLCLTHDPVKRPSASKLLKHSFFKHCKSSEYLVKHVLNDLPSVEVRFKAMAEAGRIPKQMVDDEEDEAHELQKTRRISGWNFDEDCFRFVPVFPFQEEQGAKNQENDERGAQKEQDQEINATGAQKEQDQAKNHEIDETGAQKEQDQANNQEIEAEEESEEAKNQEIRAGGVNKERESGDQEEREGETNQEGGEAKTVVSGGRMAAMIPELERILEHSEAQRQGLVRLVDMFVDGRREVELLDLLGSLQLEHDRLTSELEILTKRNEELQRQWEEATGVGRIEQPDMEGANPELQEP\*

>ATR0712G038.1

MASPRPFSRKSKSSNQADMYSTVVIHGDTGDSDQRDPDPRKDEEEEEDIYATMITKDHEDPSLPPLLKRLPKDFGAAIDYEEEEHNYSGSVIVRSNRSSVSKYPRKPPGIDPRSRGSLRKKPEVEDPYSTFLVKSSVRSRGGTFRGSPFGTMLSRTGSNFSTSMSKAVESIRGGAGMEFTPQMRDFHVEEGRKAMRRSVSSLPDSVTKEDPTNKYELLNELGKGSYGAVYKARDIKTSEMVAIKVISLCEGEEGYEEICGEIEMLQQCNHPNVVRYLGSYQGEDYLWIVMEYCGGGSVADLMGTTEETFEEHHIAYICREALKGLSYLHSIFKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVIQESRYDGKVDVWALGVSAIEMAEGLPPRSTVHPMRVIFMISSEPAPMLEDKEKWSLVFHDFVAKCLTKEPRLRPNATEMLKHKFIEKCKWNASVMLPKIEKARIIRAAMSAQALHQVPGTSFPGGSDINESHADTVPTEPSKIPTHEVRDETSKVHDEEPPREGESGTFIVHMQLEREAKEIAPAGTKDMTTSMDVRIPSSHALEDRQPKFEVDMERTSPGGVPSVASSHLPQDINDSFPSLDTFPEKSMQKEKAAPLQRDSGDPQMGGESTSGSTLKTATIGRQGFALQDKLWSIYAAGNTVPIPFLKATDISPLALISDNDNGDRDPDGNGTTALEAIQELYSGDGTARKGRRAQNNEVPLPSSVHKRLTTSSTLFNLAQALAYHKMCYDEMPLQGLQAAQEQRTIQNLGDTLRTILRL\*

>ATR0730G015.1

MDHAYEKKYPLSSKDYRLYEEVGEGVSASVYRALCIPLNEIVAIKVLDLEKCNNDLDGIRREVQMMSLIDHPNLLRAHCSFTADHNLWVVMPYMAGGSCLHIMKTTYPEGFDEPVIATLLREVLKALVYLHGHGHIHRDVKAGNILVDGNGAVKLADFGVSACMFDTGDRQRSRNTFVGTPCWMAPEVMQQLHGYDFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDRRFSRNFKEMVAACLVKDPKKRPSSEKLLKHHFFKHARSNEYIARTILDGLSPLGDRFRALKAKEADLLLQNKAMYGDKEQKSQHEYIRGISAWNFNLDDLKAQASLIQDYDENPGSNDINMNGKEKAGFNDAPDPLSPNNANHDTSEIVEEDGDHILKDRERPFPSSFPLHPLEALKGYFDVTEDDINSSSPKEGIQSEFEPQEDDQEPKPNENEGFERSFSSSKVIINPLPGRGNKFLSGSLIPERVTRSGNGDGDR\*

>Bo1g037530.1

MQTLSPQSLRWKSNPLIVSESYVFNPKALNFQLSSLSSPHRRTRNWRISSSPEENAANSSDGGDLKKSLSGIVGNQVEELLSREENKSLLDGLEKASMRVETAKRELAEIERQELEAKLLQDYVDKLESRAAEIAECQQEIVAARTMVEEAERSLSLAETAATKSSENGYSIDKDKERLESAKAAAIAAAVGTVAEVPFALSQVSTIEQLVLPLGVAFASCALFGVTFRYVIRRDLDDSHLKSGAVAAFGFVKGLGMLSRGPPLELSWESLFSHGIDGAVLVSQSVLIFAFASISLDFCFKLKLLKPFPSSAQMAVFGGKRRKKMVRGSSSSGAVVRGGGGSSVKQKGFSMNPKDYKLMEEVGHGASAVVYRAIYLPTNEVIAVKCLDLDRCNSNLDDVRRESQTMSLIDHPNVIKSFCSFSVDHSLWVVMPFMAQGSCLHLMKTAYSDGFEESAICSILKETLKALDYLHKQGHIHRDVKAGNILLDDNGEIKLGDFGVSACLFDNGDRQRARNTFVGTPCWMAPEVLQPGNGYNSKADIWSFGITALELAHGHAPFSKYPPMKVLLMTIQNAPPGLDYDRDKKFSKRTFSCEQSFKEMVAMCLVKDQTKRPTAEKLLKHSCFKHTKPPELAVKSLFADLPPLWTRVKSLQAKDAAQLALKRMATADEEAISMSEYQRGVSAWNFDVKDLKTQASLVNDSPVLYENMNGKEKVSTTEVEEPNCEEKFTFITNASSVTPNSEHEVPEAKVNKPVRRQSQSGPLTSRAVVSHSASEKEKAFKSNPTFETLLRSESEHQAAPSVKRAPSFSGPLNLSTRASSNSLSAPIKYSGGFRDSLDEKSKGNLVQKGRFSVTSGNLDLAKDVPLSIVPRRSPQPTVQPQTIKELSSQTMSPSLIIPQLQHIFQQNSVQQDLLMNLLNSVQPAETTDGSQSGKLPPLPRSETNGTVDSVPSERERMLLSSISELRANKSLLSAYRCQNFQAERLNGGTRFREIKIQPTTAETESIHWSRTSVSRSGKRGRKKLSCTEPVGERVEKSYQ\*

>Bo2g012140.1

MLLKYIYIIMESGSEKKFPLDAKDYKLHEEIGDGVSATVYRALCIPLNEVVAIKVLDLEKCNNDLDGIRREVQTMSLINHPNVLQAHCSFTARHQLWVVMPYMAAGSCLHIIKSSYQDGFEEPVIATLLRETLRALVYLHAHGHIHRDVKAGNILLDSSGTVKLADFGVSACMFDTGDRQRSRNTFVGTPCWMAPEVMQQLHGYDFKADVWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKRFSKAFKEMVGICLVKDPKKRPTSEKLLKHPFFKQARAPDYMAKAILNGLPPLGERYRTIKSKEADLLMQNKSEYEAHLSQQEYIRGVSAWNFNLEDLKNQAALISDDDSSHAEEPDFNRKQCEIQDESAISPERASSSETAPSQDDELNDIHDLESSFASFPSKPLQALKGCFDIDEDEDNETIGTQAHTTKEEDTAAQISSLPRHVISEQKKYSSGSILPEGTFSPKRTSSDAERDFQQRKYQTERSYSGSLYRTKRDTVDETSEAPYVEHKGRFKVTSADLSPKGSTNSTFTPFGGGSSSPSSLNATAVSILQSILQQNAMQREEILRLIKYVEQTSVKQSGSPETNLNELLQTPPATLRERELQTQLMLLQQSFLSLTEEVKKHKQRNGQLENQLNVLTQRND\*

>Bo2g062870.1

MDQNSPRSRRTRQTDPKPDIYSTFVVHSDSDSDQDNKRNAKPEDDDDENVDLYATTVYKGDSDGGGDEDDDDDSFLPPLLKRLPKDFGGGASLDYDDDDNGDFGTMIVKKDRDSHSSSKPRVAASPPRRIADEESSEEEEFGTFVVKPSSKKGKEKEKEKEMDLSTMGRAVASMQESSFGGKKNRKSRPSSPSSHRRMQQQNSKMSTTSLPDSITREDPTTKYEFLNELGKGSYGSVYKARDLKTSEIVAVKVISLTEGEEGYEEIRGEIEMLQQCNHPNVVRYLGSYQGEDYLWIVMEYCGGGSVVDVMNVTEEALEEYQIAYICREALKGLAYLHSIFKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVIQENRYDGKVDVWALGVSAIEMAEGLPPRSAVHPMRVLFMISIEPAPMLEDKEKWSLVFHDFVAKCLTKEPRLRPTADEMLKHKFIQRCKTGASAMSAKIEKSRQIRASMALQAQKVAASSEDTSTLGLKSSEEMKITVPYTEALPACSLNPQHISSNTALSGEGGDFGTMIFHGEDEADEIHSGSQLAKEKESSSSVGFSGEEVTRIHERKNLPTTDVAVETSTSQSVRGTLSSIEHKKRLSNISGTQTEGGSDASGSTLKNETVGKKAFALQDKLWSIYAAGNTVPIPFLRATDISPIALLSENMIGGMQQDGNGSVAVEALQELFTSDPQSKKGRRGQNEMPLPPSVYQRLTSSPPLMNLAQVLAYHRACYEEMPLQEMQATQEQQTIQNLCDTLRTILRL\*

>Bo2g068160.1

MAGSSTKRFPLYAKDYELFEEVGEGVSASVYRARCIALNENVAIKIMDLEKCRNDLDTIRKEVHIMSLIEHPNLLKAHCSFIDRNTLWIVMPYMSGGSCFHLMKTVYPQGFEQPIIATLLREVLKALVYLHRQGHIHRDVKAGNILLHSRGVVKLGDFGVSACMFDSGERMRTRSTFVGTPCWMAPEVMQQVDGYDFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPRLDYDRDKKFSKSFRELIAACLVKDPKKRPTAAKLLKHPFFKHARSTDYLSRKILHGLSPLGERFKKLKEAEAELFKGINGEKEHEYMRGISAWNFDLQDLRKQASLNPDNEMCSSESQVVGVDVPKRNPMIQRSKTMSLEMFKISDKDLMSASNSLTIGPLLPSFRRKFLPAIGYKVGILSDESNACRQRAAEALALEEPNQLELLAVDTKQTPALEELHQLEEPLAVETKQTPALEESHQVEPLAEKPKNGYTVSSVSRCAANEVLPLLQSLLVQNDIQREKVIRLIRFFDGTVSETQNPTSKNEAVQIYPSREKELQSQVNFLEQSVEILVEEVKRRKEINDQLEEQIRSLTSSSSRRSNSRSGA\*

>Bo2g109270.1

MWSGGEKKGFSVNPKDYKLMEEVGYGASAVVHRAIYLPTKQVVAIKCLDLDRCNSNLDDIRREAQTMSLIDHPNVIKSFCSFAVDHHLWVVMPFMAQGSCLHLMKAAYPDGFEESAICSMLKETLKALDYLHRQGHIHRDVKAGNILLDNTGEVKLGDFGVSACLFDSGDRQRARNTFVGTPCWMAPEVLQPGSGYNSKADIWSFGITALELAHGHAPFSKYPPMKVLLMTIQNAPPGLDYDRDKKFSKSFKEMVALCLVKDQTKRPTAEKLLKHSFFKNAKPPEICVKKLFADLPPLWTRVKTLEAKDAAQLALKGIASADQEAISQSEYQRGVSAWNFNVEDLKEQASLLDDDDSLAESREEDELCGEQLHNNNIKAKEKKLNPEVEEKTASSAEQTTPSPKCNVPQGKAEPVRRQTQSGPLSPGTLLTNSDSDKGHGYYLRPESERQPAPSAQRAPSFSGPLNLPNRASANSFSAPIKSSGGFRDSMDDKSKPNVVQIKGRFQVTSENLDLARASPLRKSASVGNWILESKMQQPTGQPIKELSNPVSPSFIMPQLQNLLQQNLIQQDLIIKLLNSLQASEATDASQNEKLPPLPRGSDSNAVIELTSSERERLLLNKMSEIRARMKELTEELEEEKSKDTRLQQKLKSVTCQL\*

>Bo5g127370.1

MDDVAGLQEAAGARFSQVELIGRGSFGDVYKAFDKELNKEVAIKVIDLEESEDEIEDIQKEISVLSQCRCPYITEYYGSYLHQTKLWIIMEYMAGGSVADLLQSGHPLDETSIACITRDLLHAVDYLHSEGKIHRDIKAANILLTENGDVKVADFGVSAQLTRTISRRKTFVGTPFWMAPEVIQNSEGYNEKADIWSLGITVIEMAKGEPPLADLHPMRVLFIIPRENPPQLDEHFSRPLKEFVSLCLKKVPAERPSAKELIKHRFIKNAKKSPKLLERIRERPKYQVKEDEETPRNGPKAPFESSGTVRVARDERSQGTPGSSFQGKTVKNAGWDFSIGASQGIGTVRALKPPHARERRQEVPSNQTSQRTSRAGGSQLSPTSGITVNDHEDGFHDEEDSSVSGSGTVVIRTPKRSQSSSIFREQISASSSGYASLDDASASGTVVVRGQHDDYASPRTPKSRLGNQDRTSSASEDSIANLAEAKAALDAGFRRGNARERLGMRNNNKDGNVNRRREQMTEDSDYSRNSGDKSGKQKALPKSQQASDEEEEEEEEEEDPIWDSLPASLSVLLIPSLKEALGDDSKGSIGRALSRSLVAMERENPGSCEAFVAKLIELLGSSKEASVKELQDMAVRVFSKTAPADAENKRKPANKEFSSNTNVSPLGRFLLSRWISQSSRDL\*

>Bo6g029300.1

MDGVAGLQEAAGARFSQVELIGRGSFGDVYKAFDSELNKEVAIKVIDLEESEDEIEDIQKEISVLSQCRCPYITEYYGSYLHQTKLWIIMEYMAGGSVADLLQPGHPLDEISIACITRDLLHAVEYLHTEGKIHRDIKAANILLSENGDVKVADFGVSAQLTRTISRRKTFVGTPFWMAPEVIQNSEGYNEKADIWSLGITMIEMAKGEPPLADLHPMRVLFIIPRESPPQLDEHFSRPLKEFVSFCLKKAPAERPSAKELLKHRFIKSARKSPKLLERIRERPKYQVKEDEDSPTRDPKSPAESSGTVRVARDDRGHGTSGTSFQGRTIKNAGWDFSIGGSQSAGTVRALKPPQSRERRQEVTSDQSFQKSSRASASQLSSTSGAVVPEISEGGFLKRDSYQNDGQEEDDSSLSGSGTVVIRSPRSSQSSSVFRDLSSGSTSRYTSFDDASTSGTVVVRGQNDDSGSPRTPKSRLGLQERSSSASEDSIANLAEAKVALEAGFRRGNARERLGNGKVNKRREQEKDSSDHLRSSRDDSEKQKPLIRSQQVSDDEDESELASLSASLSLLLLPSLKEAVGGDTSKGSVGHRVSRALVKMEREKPGSSEAFIAKLIEQLGSSKEVSVKEVQDMAIRVFGKTVNNDAENKRKQASKEFASNTNVSPLGRFLFSRWLGQTSRDLNPS\*

>Bo6g080900.1

MMLVDHLNLLKSHCSFVSDHNLWVVMPYMSGGSCLHILKAAYPDGFEEVIIATILREALKGLDYLHQHGHIHRDVKAGNILLGARGAIKLGDFGVSACLFDSGDRQRTRNTFVGTPCWMAPEVMEQLHGYDFKADIWSFGITGLELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDRKFSRSFKQMIASCLVKDPSKRPSAKKLLKHSFFKQARSSDYIARKLLDGLPDLVNRVQAIKKKEEDMLAQEKMADGEKEELSQNEYKRGISGWNFNLDDMKAQASLIQDIDCGLSESSLSESTTSLQALDSQDMQLETQEDTCQLPNKYLQPLIHRTLSIARDKSDDDISLASPSYDNYVYSSPRHEDLSLNNTTVASAHAINEKSTDSTSITANQPTEILAGSCVSKGESDKTQDQLQNGSTCNGAHPTVGGDEVPTELAVKPPRALSASLDESDDKSKPPVVQQRGRFKVTSENLDIDKVVPSPILQKSHSMQVLGHHSAASLPPSVSGADVPLPNLTSSYVYPLVYPVLQTNILERDNILHMMKVLTNRELTEGRSAEPGSVQQPNVAPTEKSMLEAAHEREKDLLHDITDLQWRLICAEEELQKYKTEHAHV\*

>Bo6g108650.1

MAHNSPRSRRSRKPDPTPDLYSTFVVHSDSDSDQGRDPDKPDEDETVDLYATMVYKSDSDEDSMLPPLLKRLPKDFGGGGASYDGDGGFGTVIVKKDSKNSPRVPVVNPADEESSDEGEEYGTFVVVKPCSSKKGKEKEKETDLSTMGRAVASMQESSFGGKNNRKSTPSLQQQKQKQSSKMSTTSLPDCVREDPTTKYEFLNELGKGSYGSVYKARDLKTSEIVAIKVISLTEGEEGYEEIRGEIEMLQQCNHPNVVRYLGSFQGDDYLWIVMEYCGGGSVTDLMNVTEEPLEEYQIAYICREALKGLAYLHSIFKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVIQENRYDGKVDVWALGVSAIEMAEGLPPRSAVHPMRVLFMISIEPAPMLEDKEKWSLVFHDFVAKCLTKEPRLRPTADEMLKHKFVQRCKMGASAMSPKIEKSRQIRASMALQAQNVVASSEDTSTLGPKSSDEMGITVPYKPPNNGYQNTTQAPPTSTGEGGDFGTMIVHGEDETEESYAGAQLAKEKESSASQVDGVSVGFSGDQVAGSWIHDKNNRSAADVPVDESTSQSVRGTPPSVSISLEHKTKLNSISRTQTEGGSEASGGTLKSETVGKKAFALQDKLWSIYAAGNTVPIPFLRATDISPIALLSENMIGGMQQDGNGTVAVEALQELFTSDPQSKKGRRGQNEMPLPPSVYQRLTSSPPLMNLAQVLAYHRACYEEMPLQEMQATQEQQTIQNLCDTLRTILRL\*

>Bo6g111030.1

MAGTSTKRFPLYAKDYELFEEVGEGVSATVYRARCIALNENVAIKIMDLEKCRNDLDTIRKEVHIMSLIDHPNLLKAHCSFIDRNSLWIVMPYMSGGSCFHLMKSVYPEGLEQPIIATLLREVLKALVYLHRQGHIHRDVKAGNILVHSRGVVKLGDFGVSACMFDSGERMRTRNTFVGTPCWMAPEVMQQVDGYDFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPRLDYERDKKFSKSFRELIAACLVKDPKKRPTSAKLLKHPFFKHARSTDYLSRKILHGLFPLGDRFKKLKEAEAELFKGINGDKEQLSQHEYMRGISAWNFDLEDLRKQASLNPDSEMCSSEVGDEVPKRKPMDLMMSSSNSLTYGAVLPSFHRKFLPAVGYKVGTFSEERKARRGRTAESLALEEPHQPKEPLEDTKQVGTAGSGQEKQKNGYTVSPVNQASCTATEILPLLHSLLVQNDIQREKFIRLIRFFDPTAETENPISKTTQGVQIYISSRERELQSQVDFLEKSVEILVEEVKRRKEINDQLEGQIRSLTSSTSNSLP\*

>Bo6g124030.1

MEKKKYPIGPEHYTIYEVIGQGCSALVHRALCIPFDEVVAIKILDFERDNCDLNNISREAQTMMLVDHPNVLKSHCSFVSDHNLWVVMPYMSGGSCLHILKAAYPDGFEEVIIATMLREALKGLDYLHQHGHIHRDVKAGNILLGARGAIKLGDFGVSACLFDSGDRQRTRNTFVGTPCWMAPEVMEQLHGYDFKADIWSFGITGLELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDRKFSRSFKQMIASCLVKDPSKRPSAKKLLKHSFFKQARSSDYIARKLLDGLPDLVNRVQAIKKKEEDMLAQEKMADGEKEELSQNEYKRGISGWNFNLDDMKAQASLIQDIDCGLSESSLSESTTSLQALDSHDMQPETQEDIGQLANKHTQPLIHRTLSIARDKSDDESVASPSYDNYIYSSPRHEDLSLNNTTVASMHASNGKPMDSTSVATNQPTEIPAGNCVNKGDSDKIQDQLQNGAHPGDEVPTEIAVKPPKAAASLDESEDKSKPPVVQQRGRFKVTSENLDIDKVVVPSPILQKSHSMQVLSQHSAASLPPSVSGSDVALPNLTSSYVYPLVYPVLQTNILERENILHMMKVLTYRELTDGRSGEPGGFHQPSVAPTEKSMLEAAHEREKELLHDITDLQWRLICAEEELQKYKTEHAQV\*

>Bo8g038040.1

MARNKLEFPLDAEAYEIICKIGVGVSASVYKAVCIPMNSTVVAIKAIDLDQSRADFDSLRRETKTMSLLSHPNILNAYCSFTVDRCLWVVMPFMSCGSLHSIVSSSFPEGLPENCISVFLKETLNAISYLHDQGHLHRDIKAGNILVDSDGSVKLADFGVSASIYEPVTTSSGTTSSSLRLTDIAGTPYWMAPEVVHSHTGYGFKADIWSFGITALELAHGRPPLSHLPPLKSLLMKITKRFHFADYEINTSGCGKKKFSKAFREMVGLCLEQDPAKRPSAEKLLKHPFFRNCKGVDFVVKNVLHGLSNTEQMFIESQALIKGVEDDEDDDEEIVKNRRISGWNFREDDLQLSPVFPTTESDTSEFSPREVDPIQDKPEGDKVVITGSEVCLGLSNRNEEAKEQEGEVCGFDRDLVLEKLKLLKKSLEHQRARVLVIIEALSGEKEERNREEELLEMVEKLKIELEAEKMKTLRAEKESVLS\*

>Bo9g089620.1

MVSPLRQVIQAFISRRRRKKMASGGGTSSKEKKGFSVNPKDYKLMEEVGNGASAVVHLAIYLPTKEVIAIKCLNLDRCNSNLDDIRREAQTMSLIDHPNVIKSYCSFAVDHKLWVVMPFMAQGSCFHLMKAAYPDGFVEPAICCILKETLKALDYLHRHGHIHRDVKSGNILLDDTGEIKLGDFGVSACLFENGDWQRSRNTFVGTPCWMAPEIMQPGSGYDSK\*

>Bo9g165690.1

MSEKKFPLKAKDYKLQEEIGDGVSATVHKALCIPLSEVVAIKVLDLEKCNNDLDGIRREVQTMSLINHPNVLQAHCSFTAGHQLWVVMPYMAGGSCLHIIKSSYQDGFEEPVIATLLRETLRALVYLHAHGHIHRDVKAGNILLDSNGAVKLADFGVSACMFDTGDRQRSRNTFVGTPCWMAPEVMQQLHGYDFKADVWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKRFSKAFKEMVGTCLVKDPKKRPTSEKLLKHPFFKQARPPDYLAKTILNGLPPLGERYRTIKSKEADLLMQNKSEYEAHLSQQEYIRGISAWNFNLEDLKSQAALISDDDSSHAEEPDFNRKQCERQDESALSPERASSSETTPSQDDELNDIQDLESSFASFPIKPLQALKGCFDVGEDEDNATTPDWKDASLMSSGQQHLTKASSIGSLAHTTKEEDTAAQNSYLPRHVISEQKKYSSGSLIPESTYSPKRISMEADREFQLRRYQSERSYSGSLQRTKRDTVDEMSDSPHVEHKGRFKVTSADLSPKGSTNSTFTPFSGGSSSPSSLTTASILPSVQSMLQHNTMQREEILRVIKHLEQTSVKQQPGSPETSVDELLQMTPTTARERELQTQLMLMQQSFLSLTEEVKKLKQRNGQVENQLNALTQRND\*

>Cre07.g317300.t1.1

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>Cre12.g544400.t1.2

MTAAAADRYERGCCIGRGSFGDVYEGLDTVTGQQVAIKVIDLDDVEDDIQDIHREIQALAGCKCRNITEYYGSVLRPGSAELHIIMELMACSVADLVHHGPLDEASIAYVLAQVLNALVYLHNEHRIHRDVKAANILLSRGGDVKITDFGVSGQLSGTLGYRRKTFVGTPFWMAPEVIDTSEEGYSEKADVWSLGITAIEMATGSPPHSSLHPMRVLFLIPKGPPPALEGDAFSPELKDFVATCLRKDPAARPAARDLLAHPFVAAATQAPEHLPAMVAELARHKKPLSSRRDADEALIAAGGTMPAWDFGTAGAAAAARGKAAAAAAAAVAAAPPAGTVRAMAAAISAASSGGTIRGGAGAEALRETLRASGSAAAGAAAARVETISRTAGVALKEALAAANGSGSAGGSGGGSAPSTGTLRHTNGSAAGPMPPAVPGQYDSLVLPAPPASLPPASAGGAPALFMSGNGGGGAVGAVSSPPRGLPRGAPPPAAKFATMSTAEARMYRDLMGRGAGAGAGATNTSSVGVSSGSVGGGGGAGGAAGTSMGGDGHSGTVVAAGLARNSLSVGTGATVGPAASKAANRYAAAPAFSISSDDSSQQQQPSLPGAEGSGGGSVTSPSAAAAAATASAGALADGYGTVQSRPAGAGAGAGAGAGSDSASASAAPSGSLRSTSATTTTTSGNGAGAAGPSAYGTVQSRKQVEAGPSSGAPSGSAGAAAAHTGTLLLDSSALAGLVAREGSPAESGAVLSRLLGPCARSAFNSADKASQAALAGVLSGLGQLEKMMPGASYRLVQELLVRLSCSAEPTLEPLRASAIGLYATAASASAPASAAATAVRGEGAAAQPPAAPAAAGAALGGVPRAVPDLGPLGEFLLGRWREEEAHEVALLARSQTAGAAAAAGLGMGAPSGTGGSVRR\*

>Cre12.g550300.t1.1

MFKSRSAAALHELRAAAAARTYPTDPAQYELLEECGAGVTSTVHRARCVPLGGEVVAIKRCDLTDLADADLQVVIEEVAQMRRYQHPAVLPLLCSFVTAAGELWLVMPYMEGGSVAHVMRYAHPDGLEEAVVATIAREVLRALDYLHKQGAIHRDVKAGNVLLGGDGAARLGDLGVAATMERSGTWGRGRVGRRTLAGTPCWMAPEVLQDCVYDDKADMWSFGITLLEMAHGSAPFANQPPLKVLLNTLQNPPPQLEDRIGARTFSKSMREVVALCLQKEPAARPPARQLLEHRFFRHHARDRAYLVKHLLAGLPPLTERVRQLRAGHGGRVPTRQAHSRELKSRASYMTGVLGWDFNLPCAQPQQQLPQLQPVTELQPSGSPAPPLHQAASGLSCVSSSTTGASLATVTGGGGGSSATSSYSPGANTAAGTGGSSPTAATAPTTPAAAPPSPAGSASTTPPGGGSSIPGGGSSTPGGGSPTSSAGPVLGSRAQQSPSHFHPQPRHWPFLSPGPPSVSPTRQPRPGGGGAASPFGAAVSQAAAASAAAAAGGGSGTDTDHSSMPGTGGARGAAPDEGEEDEEEEWAAAEGVPRRPSLRSSVSSPDLHRRRTQQPPPHALPPPPDLPSVALPQPYQSPKQQQPLLQPQPLLPSLSPAAQPLTPAPAAGAAPAVASPTAVSRSPFSGAGGGGGGPGGGGGCHHSGHHHRVSFAPDVAGLGSSSSGPPPPTPLLGSGGSSGALSVQRKGRFQVIETTQPAAKPQHPPPPWLTSPGAAAASAHARGGGASTASTSGTGAAACGGAGRSSSGGHVFTSPTSTSPLTSPRSHSGQHGQQHQHQHQHQQLTQLPQPQQPLQLARAHSGGKPPLPPRPPPPPAATAAANHPTAAAGASNHPHQLLPMAVGSHGHGHGHGHSSHLLARTPSLRTSTSTSGSSTRSPPPSPPGSVAAAVAASGGGSAAAPPSPPPLSFPSVTSPLLPLPQPPAAPTLPPSSMLPSAPASPFASAVGGMAAAAPPPAVSVGAARSDWLKGLYKRWSDAAVHSLLAAVHRPDESHQLSLALTSAAAPRHVPTIRVTAAPPELAAALVAAAALKPPQSSLTAPRAAPSSAAQSLTSAGTSTEASAAAAAGAPPAKAPSPRLPIITLAHLVPSQPHHWFTPLLDRLMPHHPAAGTPATATSAPATLATDSTGGTGGATVTAAAMERAQQRRLQQAELRGGGGGRHRRLLVPSIYPPLEMDSGWCGCGSEADASASSDSSSGEGGAVDTAGGAMGGAGGEGLWGGHTRGHTDGSTQHTLTGSSTAPSTSTAPSTATGATATGTSGTGSQASGSDSAGHRGNREARAAAAAAAAPSTDVVPAADASASVTTSRSEALQTKHRRPHHHHHHHHHDLHDRGAAGGSMYGSMYGGGGGGGLVVVEVDPSHPDYNALAECYAGAGGTCWAPTARLLQPLLRTLPVELERAQHTCGDGNSGGGSGAAGGGGEAQGAATAAAAALDAENASTTTPVVTPGLATSPTPPLSLPPPPEPLLLPHRPLQPPAASLMPGAPRRTPHAQPSLPTLQEKPAAAPGGTFPTAHDGGAAATIVPSRVPFHGVVPEAAAAAAEAQRRRRQAELQRHLEAALMTFGVAPEEIEELERVQSGGGGDGGAGLWSPKLVPAAAAAAEGKREVAGKAAMERVEEGEEGEEGDSSESTVSDADEEAAEDEPPDGVSPAAPATLASQGRGQGQGDGLDRGGGARSSTTAAAVSRRTTANTAGAPQQAWVPAGPAQHGPQAQAAGPAPAANAAAAVAAPPQTPAQVTLGGSSTRTAGGLGGSSSNSSSSNSTSGSAAASALAQGTGAGAAVAACALQAAATGALSPAAAAQLLPIVSATSLVPSLPSPPHAQAQAQALGAPGEAPPPLQPFQSYWFAVSPPRSAVLPQPPRTGPGGGSSTCWRATAAAPAATAGASPATAAQAASAFEAWRQQGDLAGIPPLAPLAPSSQLQPLQPPPPLPMGLGGAAPLLPRHSSSSANSGSRRSSLNLPPGSHTPHGAGLEGSSPMLEGTGSGGCSNAAVAAAVAAAAAATAATVLGSSGGSGSSGGGGGAHSPGLDSAGVPRPDAAVSAGEDSGGAGPVQLRGGAGVAVTGAADHPGGSGPRGIADGPMTRWHAGGMAPTTPASPNSAMGAGSGVSAPGRLVLPAGPRAPGAAGRLQPPQRHRQPPQTAQERAVAAAAAAATAAAMAAAAAGRGVARGRFVVVNETMQQPQAGRGRG\*

>Cre03.g164900.t1.1

MERAISGITSKLSSRKSTKDFSALAGGKEWPTDANQYQILDDCGRGVSATVHRAKCLTNGEIIAVKLMNLESMNCDLDEIIHEAQTMRMYNHPNILPLYTSFVHGQELWMVMPFVAGGSVLHIMKYAYPEGLDEVVIATIGREVLKGLDYVHRNGSIHRDVKAGNILVDGDGIVKLGDFGVAASLERGGSWGHDKQARMTFVGTPCWMAPEVMEQTMGYDFSADIWSFGITLLEMCHGHAPFAKFPPMKVLLMTLQNPAPTLEDKGKRHFSKALKDLVARCLQKESDKRPTAAQLLEHKFFKIARDSKYLKEFLVGNLPALADRVNRIRNGMAATNVTDNDRNLEKSQVGAPPDAASLHADELEEIKAREEYRKGVSSWNFDLAALKAQAALEPDDDSSAHGAASMLPTISESDEREDTLTGTSAAAAQAFLVAQAEEQAAAAAGAGAGGTGAGSAAAAGEAARSFMSAFATVSGQESTARTGSVLPLAAPSPTPAPMTVDVSAPVAAPLRAVASGEGLAGGDRGAMPGYGDMPPPSPGGGVSPAAGLSREGSVGGNMGGMATTPTAVTKQKKGRFEVSEHPAVPVASAAAPHGVVASGSAVALPSLATTSVAGAPHMVSASSAGSLSTYNTFSGPSISGGTVPDLSALRGSATGLADMAGAGGGAALLGGAAAHGEEGLMMGAAAAVAPGPQPTLRTEVEESVTSVEPKQRGRFKIVAEQGAESRPLSKTSSLANLSDAGKSRSDGGGGALLGKPPTGPSGPSSITPPISIMLPKLQELLDHANAHQAALQKLLGAVQECDKGRVPLLLSRAQSTRSLFDGTPGMVLSPAAAGEGAEELRTAMAELRARLATLEDENARLRERNKVLETLHDASQQSAAVAASAGAPAPSGPSYNTSLGGTSVRFNLPDSSGGALQSPTLSVSPKLPAADLPPAPGSGAQPSAL\*

>Glyma.01G061500.1

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>Glyma.02G119700.1

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>Glyma.05G006700.1

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>Glyma.06G238000.1

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>Glyma.07G002900.1

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>Glyma.08G223700.1

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>Glyma.10G173000.1

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>Glyma.12G132600.1

MNSAAVAIKSIKLNRSRPDLDDVRCEAKTPSLLSYPNILKAHCSFTVDRCLWVVMSFMAAGSLQSIIYHSHPNGLMEPYITVVLRDTLNALSYLHCQHLHRDIKVGNILIYTNGQVKLADFGVSASIYESTTTTTTSSSSSLKFTNVVGTPYWMAPEVIHSHTGYSFEADIWSFGITALELAHGRPPLSHLPPSKFMMLKITKRFPFSDDFDDKENMITQLKNAQRH\*

>Glyma.12G226300.1

MGNELFVSLLFNLISRFDRELNKLVAIKVIDLEESEDEIDDIQKEISVLSQCRCPYITEYYGSYLNQTKLWIIMEYMAGGSVADLIQSGPPLDEMSIACILRDLLHAVDYLHSEGKIHRDIKAANILLSENGDVKVADFGVSAQLTRTISRRKTFVGTPFWMAPEVIQNTDGYNEKADIWSLGITAIEMAKGEPPLADLHPMRVLFIIPRENPPQLDDHFSRPLKEFVSLCLKKVPAERPSAKELLKDRFIRNARKSSKLSERIRERPKYQIKEDEETPRNGPSGMGEASGTVKVARDLRGEENNRPSDQGKTLKSAGWDFSIGGSQGTGTFRNVSRPPQFRDKITEVSHNQLTQRKAPQSGYQGGSVNRSALNESLESSFGRDLRVPHHDEHLDNHLEDDELSGNGSGTVVIRSPKGSRSSAFRDQSSQSSSSYASFEDASSSGTVVLRGQHDESDSPQTPRSRLGLNDRNSNASMEDSAANLAEAKAAILRKSNAREKLARGKINNDRQESKRDQKASSSDSSRPHGEYDAHKGMLRSHHASDGEESAKIMSSSVPLSVLLIPSLKEAIADDPELVRAVINSLINMEGTKPKSCDVFVKKLLQRLASSKEDSLKDLQGLADQLFSKTKSAQETRNAEADNRKKQQNKEHNSNSNLSPLARFLLSRWQGQTSRDLNPS\*

>Glyma.13G001900.1

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>Glyma.13G274500.1

MADVAGLVEASGSRFSSLELIGQGSFGDVYKAFDRELNKLVAIKVIDLEESEDEIDDIQKEISVLSQCRCPYITEYYGSYLNQTKLWIIMEYMAGGSVADLIQSGPPLDEMSIACILRDLLHAVDYLHSEGKIHRDIKAANILLSENGDVKVADFGVSAQLTRTISRRKTFVGTPFWMAPEVIQNTDGYNEKADIWSLGITAIEMAKGEPPLADLHPMRVLFIIPRENPPQLDDHFSRPLKEFVSLCLKKVPAERPSAKELLKDRFIRNARKSSKLSERIRERPKYQIKEDEETPRNGPSGMGEASGTVKVARDSRGEENNRPSDQGKTLKSAGWDFSIGGSQGTGTFRNVSRPPQFRDKKTEVSHNQLTQRKAPERGYQGVSVNRSALNESLESSFGRDLRVPHHDEHLDNHLEDDELSGNGSGTVVIRSPKGSRSSAFRDQSSLSSSSYASFEDASSSGTVVLRGQHDESDSPQTPRSRLGLNDRNSNASMEDSAANLAEAKAAILRKSNARERLARGKINNDRQESKRDQKASSSDSSRPHGEYDAHKSMLRSHHASDGEESAKIMSSSVPLSVLLIPSLKEAIADDPELMRAVINSLINMEGTKPKSCDVFVKKLLQRLASSKEDSLKDMQGLAGQLFSKNKSAEETQNAEADNRKKQQNKEHNSNSNLSPLARFLLSRWQGQTSRDLNPS\*

>Glyma.13G349800.1

MAATNEAEEAAGGKRVQYPLDSSSYKLLNEIGEGVSAVVYKALCIPMNSAAVAIKSIDLDRSRPDLDDVRREAKTLSLLSHPNILKAHCSFTVDRRLWVVMPFMAAGSLQSIISHSHPNGLTEPCIAVVLRDTLNALSYLHGQGHLHRDIKAGNILVDTNGQVKLADFGVSASIYESTTTTSSSSSLKFTDVAGTPYWMAPEVIHSHTGYSFKADIWSFGITALELAHGRPPLSHLPPSKSMMLKITKRFRFSDDFDDKYRKGNGKKFSKAFKDMVASCLDQDPSKRPTADKLLKHPFFKNCKGTDFLVKNVLQGLPSVEKRYRESKGNLHEDDDDGDDDDDDPSMQVKQRRISGWNFNQDGLELDPVFPNDVKEVRFGGETVIQQAAGMEKVNNNSSSREGMLATLNVLKGSLEQELWQVKFLVNTIQGDHHDTQVPEEQEISRLRAQLENERMKNLQLELQLQTSKLHQKSDSN\*

>Glyma.19G007300.1

MEHVLEKRFPLNSEDYKLYEEVGEGVSASVYRALCVPLNEIVAIKVLDLEKCNNDLDGIRREVQTMNLIDHPNVLRAHCSFTAGHNLWVVMPYMAGGSCLHIMKSNYPEGFEEPVIATLLHEVLKALVYLHAHGHIHRDVKSGNILLDSNGAVKLADFGVSACMFDAGDRQRSRNTFVGTPCWMAPEVMQQLHGYDFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKRFSKAFKELVATCLVKDPKKRPSSEKLLKHHFFKQARASKYLARTILEGLAPLGDRFRLLKAKQADLLVQNKALYEDKDQLSQKEYIRGISAWNFNLEDLKSQAALIQDDDIPNAEESQRDKKQKDRLDDFKVSAERLSPGAANHSDDAPTQDKEDGFNNLPDLESSLASFPSKPLQALKGCFDMCEDDVNNSSPRNLDHDGRIDNESSGTSTSLQQNATSHQKKFPSGSLLPDNFLFPKKIVTDGDRDYLQTKYSSDRNHSGPLQYRQKRDTNNLPLVDDTSDGAFVQFRGRFKVTPADLSPMGPSNSTSGPLVSPTSPPNPNFLSVAILPSLQCILQQNGLQREEIIKLIKYAEQSSGKNTESMEAGIVDILQAPPATTRERELHFQVIQLQQSNGILFEELQKQKMKNVQLEKQLSSMINKVEK\*

>Glyma.20G067600.1

MGGYSTNPADYKLLEEIGYGATATVYRAMYLPFNQLVAIKSLDLDRCNINLDDLRREAQTMSLIDHPNVVRAHCSFAVERSLWVVMPFMDQGSCLHLIKIALSHGFQEDAIGSILKETLKALHYLHRHGHIHRDVKAGNILLDTSGAVKLSDFGVATCLYDAVDRQRCRNTFVGTPCWMAPEVLQPAGSGYNSKADIWSFGITALELAHGHAPFSKYPPMKVLLMTMQNAPPGLDDRDKKFSKSFKEMVAMCLVKDQTKRPSAEKLLKHSFFKHAKPPELSVKKLFADLPPLWNCVKSLKLKDAAQLAVKKMPSADEEAISQSQYQRGVSAWNFDIDDLKAQASLVMDDNDNAEMREDENKFFTNYKASAIDSQSGTVKMNTEKSPQNKITSLVGAFDIKQTEQNEYLNKKEKNLESDLQEPGLPRNIIWKRNGSIMEATTSTIEKDIGMSHQTQSGLPGTVLSHSASERRRTLERLENGNQLLGEKNNREARQPPSFSGPLMLPTRASANSLSAPIKSSGGFRDSLDDKSKATLVQIKGRFSVTSENLDLVKDIPVSSVSRQSSQGSVSPLRKSASVSDWMLDSKQMATEDSATDSISASLLTTHLQNLLQQTSIQQDLIMNLLNSVQSAEAIEVSQNGKLPPLPRSSEINGSVDTAASERERLLLLKILELQTRIITLTDELTAEKLKYMQLQQQLTLYSQEQNMDKREEIA\*

>Glyma.20G217200.1

MGNGSRSYSANRSDYKLLEEVGYGASATVYRAIYLPYNEEVAVKCLDLDRCNINLDDIRREAQTMSLIEHPNVVRAYCSFVVERSLWVVMAFMAQGSCLHLMKAAYPEGFEEAAIGSILKETLKALEYLHRHGHIHRDVKAGNILLDDNGQVKLADFGVSACMFDTGDRQRSRNTFVGTPCWIAPEVLQPGTGYNFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTIQNAPPGLDYDRDRKFSKSFKEMVAMCLVKDQTKRPSVEKLLKHSFFKQAKPPELSVKKLFADLPPLWNRVKSLQHKDAAQLALKKMPSAEQEAISQSEYHRGVSAWNFDIDDLKAQAALMQDGDDIAEMREEDENKFFSSYKGTADSQFIVDEKNSNNLQQYEFTSQVGSNDIPQCEKRNGSVAEATPSTLENDVGTSKVKTQSVKLGKTQSGPLMPGLVLGHSSSERGRTFERFENENQLAGEKSNRDIRRAPSFSGPLMLPNRASANSLSAPIKSSGGFRDSLDDKSKANLVQIKGRFSVTSENLDLVKDIPVSSVSRRSSQGSPMRKSASVGDWMVDYKQMPIGQSSNDSANINIPASLLVPHLHNLFQQTSIQQDLIMNLLNSLQTAEAIDTSQNGKLPPLPRNSENNGSADTAVSEREQLLLGKISELQSRMINLTDELTYEKLRYVQVSFCTSFYISLSVQDFASAILFSCLDYIHVTSNLESI\*

>Glyma.U025600.1

MADIAGLAEAAGARFSSLELIGQGSFGDVYKGFDKELNKEVAIKVIDLEESEDEIEDIQKEISVLSQCRSPYITEYYGSFLNQTKLWIIMEYMAGGSVADLLQSGPPLDEMSIACILRDLLHAIDYLHNEGKIHRDIKAANILLTDNGDVKVADFGVSAQLTRTISRRKTFVGTPFWMAPEVIQNSEGYNEKADIWSLGITAIEMAKGEPPLADLHPMRVLFIIPRENPPQLDEHFSRYMKEFVSLCLKKVPAERPSAKELLRHRFIRNARKSPKLLERIRERPKYQIKEDQTTPRNAPRGMGEASDTIKVAKDLRGDETNQPSGQGKTLRSSGWDFSIGGSQGTGTFRSVSRPPQFRDKKTEVSDHQLNQRKIPESGYQGESGNKSALNELLETSFGKDLGVPYHDEHPDNHLENQDEFSGNGSGTVVIRSPKGPQPSMFRDQSSQSSSSYASFEDVSTSGTVVVLHSQHDDSDSPQTPRSRLGLNSRNSNASLEDSATNLVEAKAAIQGGLRKVNVRERFALGKLNNDVQDSKRDQMSSSSDSSSIFFRPSREYFDAPKAFSRSHYSIDDEESAKIISSSVPLSVLLIPSLKEAIADDPDGSIVQIVINALVNMESTKPQSCDVFVKKLLQQLASSKESSFKDLQELAGQIFSKTKSSEETRNAESDNKKQNKEVHSNSNLSPLARFLLSRWQGQTSRDLNPA\*

>HORVU2Hr1G047960.1

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>HORVU4Hr1G088910.1

MVRGGSMRRPSLAAAAEPAVPEFTVSPDDYRLMEEVGFGANAVVYRAIFLPANRTIAVKCLDLDRVNSNLDDVRKEAQIMSLIDHPNVIRAYCSFVVDHNLWVIMPFMAEGSCLHLMKVAHPDGLEEPVICSILKETLKALAYLHGQGHIHRDVKAGNILIDSPGVVKLGDFGVSACLFDRGDRQRSRNTFVGTPCWMAPEVLQPGTGYNFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYDRDRKFSKSFKEMVAMCLVKDQTKRPTAEKLLKHSFFKNTKAPQLTVKSILTDLPPLWDRVKALQQKDAAHLASSEQEALSMSEYQRGVSAWHFDIEDLKAQALLINDDDPPELKEDDDSARVTEIDKGTSFESHFGQSALLNGNNHRLNHERTCTTAVNPGGNGPETSDEFASDLGNADSPRMVDGRITQGTENDSLSSTSKQGSEAGNPRSEVRQRQRTFSGPVMYSGTRSSSLIERGHIIDKDAGGRSLSNKQKSDTGRIDDLSGPLSLSTRASANSLSAPIRSSGGYVGSLGDKPRVEIKGRFSVTSENVDLAKVQEIPVIKISHKPQEVRTQVSTMKKSASVGAWPVKSKSMSNSHHRKEFRDSSVSASILIPHLENLVQQTTFQQDIITNLMSNLQQNEKPNGPQTRVQNMEGDTGVETGSAERERKLLAKVFELQSRMISLTDELIASKLKHVQLQEELNTLYIQEEIADTREDGNGEA\*

>HORVU5Hr1G059030.1

MHCYSGPHLSCHLSTFLLITSDHGHPQSSRFSSPALSSSVCCIRNATYVSPVYHYHYHYLHPFLSFPGRPPTDMADDAGAGGEAKYPLNPECYRLLCKIGSGVSAVVYKAACLPLGSVPVAIKAIDLERSRANLEDVWREAKAMALLSHANVLRAHCSFTVGSHLWVVMPFMAAGSLHSILAHGFPDGLPEPCVAVVLKETLRALCYLHEQGRIHRDIKAGNVLVDSDGSVKLADFGVSASIYETPPPASSFSGPLTHVPQVVLSSSSYFSEMAGTPYWMAPEVIHSHVGYGIKADIWSFGITALELAHGRPPLSHLPPSKSMLMRITSRVRMEDAEISKNKKLSKAFKDMVSSCLCQEPAKRPSAEKLLRHPFFKGCRSKDYLVRSVLGTVPSIEERCKDVTSLCGCAAGGARCVSPCHGGQASVVKNRRMSGWNFGADCPRKEDTDSFEELDRTQTAARLFLPLDDEDIVPERACDGAGEDGDKGIMEQQGDREENEEFGVKGVVVPHLVTILESLEVQKRMLAQELEGGCCYHHDGNCCRETTAREEMLLAYVRQLEQRVEVLTLEVEEEITRNXXNHH\*

>HORVU6Hr1G029780.1

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>HORVU6Hr1G084460.1

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>HORVU1Hr1G048230.1

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>HORVU5Hr1G095970.1

STFPVLLRSHPPPMAFSPRSPWSRSKKPDIYSTVVVHDDEDDAHGGGAARAEDDDDDDPSALPPLLQRLPKDFGGASFDDDDDPYSSDLDDASLSATVVIKRGAPASTSSSSRSPFLDLRRSSPRAAEADPYSTFVVHGTARSGGASSPRESVSGTFIRHSGGPPSPRESVSGTFIRHTRGSSSPRESYSGTFIHHTSGASSPRDPASGAGAGFGSSFMTPSTGQAEEDRQPSLLMQQQQSRRQASMSSVPDSVTREDPSTKYELLHELGKGSYGAVYKARDLRTQELVAVKIISLTEGEEGYEDIRGEIEMLQQCSHPNVVRYFGSYQGEEYLWIVMEYCGGGSVADLIGITEEPLDEPQIAYICRETLKGLAYLHTIFKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVIQESRYDGKVDVWALGVSAIEMAEGMPPRSTVHPMRVIFMISSEPAPMLEDKEKWSLLFHDFIAKCLTKDARLRPAAIEMLKHKFIEKCNTGASKMLAKIKEAKIIRETAVQNQLPDSDDAMDATVRINEDYGETVPTNSQSTHETKNDGSGGDFGTMIVHPEDGDEAVESSIFPRAEFIPGLGSINSFTHDPKRAELISKFWAENTADSDATKGRDLDGLPDTQEPKAMPRSIGTFKHHKGVEGTVLRHDNTASPGVASTMTKLSSSPSRKAFSVQDKLWSIYAAGNTVPIPFLKAIDISPLALVSDSVAGNGPAGSSTTDALEAVRELFSGDGQAKKGRKGQNEVCCRLFLSSVAKRHYFSCPDVCLILDLIALGPSSSRCARQIDDKPYIDEPGAGSRLP\*

>HORVU7Hr1G047720.1

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>MCO05G399.1

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>MCO12G367.1

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>MCO16G480.1

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>Mapoly0008s0135.1

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>Mapoly0102s0039.1

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>Mapoly0133s0001.1

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>Medtr1g077800.1

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>Medtr2g100030.1

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>Medtr5g045190.1

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>Medtr6g006770.1

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>Medtr2g078740.1

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>Medtr4g005730.1

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>LOC\_Os02g08240.1

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>LOC\_Os02g54900.1

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>LOC\_Os03g47470.1

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>LOC\_Os03g54780.1

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>LOC\_Os06g29120.1

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>LOC\_Os10g37480.1

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>LOC\_Os03g02320.1

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>PAB00014937.1

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>PAB00026846.1

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>PAB00040610.1

MDHHHQKSYSLISSEYRMVDEIGHGVSATVYEAKCLVLDETVTIKSIDLELLNATLDDVRREAQMMSLVDHPNVLRAHCSFIVQQSLWVVMPYMAGGSCQSIMKKSFPNGFEELVIALILKETLKALEYLHQQGHLHRDVKAGNILIDSRGGVKVGDFGVSACVFDSRDGQRLKQNTFVGTPCWMAPEVIDHGNGLITRPIYGRLGLLHSSSRMAMPRSLSSRQSKPSSCSSRAPRQVWTMKPIRSFLEVKDTQLYYESNFVPEPKNTQIDYESNCVLKPKNTQVASEANSIPSPENTQVVSQTNCVLDPKNTQVDSQSNCVPGPKNSQVASEAYCMPEPESIIEFGHKPQSDAESNTMPRH\*

>PAB00040641.1

MGNFMQDDIRREAQTMSLIDHPNVIRAYCSFVVDRCLWVVMPFMAEGSCLHIMKIAYPDGFEEYAIATILKETLKALEYLHRQGHIHRDVKAGNILVDTSGAVKLGDFGVSACMFDTGDRQRSRNTFVGTPCWMAPEVLQPGSGYDFKADIWSLGITALELAHGHAPFSKYPPMKVKSTSTHPMSENQFVCIPRLLKFSSYNVMIFLIVSFISSGCILLTSIFNI\*

>Pp3c11\_21850V3.1

MSSSDPRGSPGLIRSESRRREQLGVDNLDSSKSPSSPPSIFATVITKPDEVSSSSQFSTVIQHISGTDPYSTVVHKAAESFRKDGGGSVQRRDGGGRPRGKSDWAGGIEGSSGALSGDVRDRTSLLQENVAFEDPSLKYELLNELGKGSYGAVYKARDLLTSELVAVKVISLTEGEEGYEEIRGEIGMLQQCNHPNVVRYLGSFQGEDYLWIVMEYCGGGSVADLMNITDEALEEQQIAYICREALKGLTYLHSIFKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVIQENRYDGKVDVWALGVSAIEMAEGLPPRSNVHPMRVLFMISREPAPMLEDKERWSLVFHDYVAKCLTKEPRLRPTASALLSHKFIEKCKGTASSMLPQIEKARRIRAEMAAQAANYVQEQGTTSSGGQYGSWEKGQTVKMHDTSAGTMLVRDTVVKSLSDTFKEGTGTIRGPVSAELDSRRSMYEATMSMETSPNREDSKSSLDTRDQDTDQGRNSTPESTVGSRKHFKDGVRLTLETPTTYSSSYAVFSPIPHQPVGVHSSISRRSLSSMEATLGPGTPVGGGNRPGFGIQDKLLSVYAAGNTVPIPFLKATDLSPIALTFDRIFADGRPDRTRNVALEAIQDLYVGEGHVRRGRKAPNSEMPLPPSVYQRTATSTTLPNLARSLAYHKRCYEELPSQGWQAAQEQQIIHNLSDTLRTILRL\*

>Pp3c12\_5150V3.1

MEGQGKEQKNGVGEEGGDEEGRRGYPLSASDYRIMEELGRGASCTVYSALCLPYNELVAIKVLQLDEGTRISSDFWTASKSRIQHPNVLTAYCSFTTSHNVWVVMPFMAGGSCLDIMKAAFSNGFDESVVCTFLKESLMGLNYLHHHGRIHQDVKAGNIFVDGNGRVKLADFGISTCILNAGDQQQSRSSLLRSCYWMAPEMIEQVHLYDSKADIWSFGITALELVHGIVPFSKYPMKVFFNTLQNKISEMNCACFKMFSKSFKDMIAICLAKDPSRRPTTEQLLRHPFFKQARSPEYIYQHVLDGLSSLGERSKNLKIIEAAQLALKKSPHSKEKLSQGEYLRGLHNWICNAHDIRKTETEVAIFKGGPADLAAQMDVDWESSCLHSKSASSIEIMDIIAERDAALMEKSTALAEKMAAYAERDAAILQRDIASADRDAAILTRDAALAALARLERKSSGRGRRPSQTALDESMHGSKLLQRMDLAEHSAFSSEFHPTAANPSHSGIMLLDPDSAHLQGVHRFSRDKESQIEIFVRTKRKATEMAEATHRGKHPRAAPKKSRNWPVTHQGQQPVQERESQAQVANEEEGGQIREPELVSSRIFRSQTVPTPIPYCSCTGMNQQCYRWGNGGWQSACCTTLISMFPLPLNPKKRGSRLAGRKMSAGAFDKLLEKLVSEGVNINLPVDLREHWAKHGTNRYVTLR\*

>Pp3c17\_14200V3.1

MEHDEDVDDEIHGAVDSAMEARFENLRLIGKGSFGDVFSGFDKELNKEVAIKVIDLEEAEDEVEDIQKEISVLSQCRSPHITEYYGSYLHATKLWIVMEYMAGGSVLDLLETGPPLDEVSIACILRELLLSLDYLHSEGKIHRDIKAANILLTANGDVKVADFGVSAQLTRTMSKRKTFVGTPFWMAPEVIQNSGDGYDEKADIWSLGITAIEMAKGEPPYADLHPMRVLFLIPKNNPPQLDDHYSRPFKEFVSFCLKKNPAERPSAKELLRHRFVKNARKSTRLLDRIRERPKSHISKSKDVPRPAEAFENESSSKEMGAKGDNGVYPPLSSRRKPLRDASWDFGTGTIHTTGTLRSGSTNLYTDQDRTGGNENTVLSGSEALPSLLSKAELDYQIDAGLRDASMDGNGFRRNSFGIQRKLDTEQYSPSDYGSYASASGTVKAASTLERPSLKSLSTSLANTGGNRNEEASEIFASGTIVRSSTPDEGGSVPGTPKAKQEPREDSATNLAEAKAALQAGMRKGGPRGPAPVKLRKEALEYASDPRETPRETPKATPRASARASEEDVARAAAAGASAALALLLIPALKETAAEQSEGPALRAAADAADALMDLERLAPGACEVLVSKLLRQLARKDQAPVKGLQNLARRLLSSSDNGSEVGHIPSSRDQPGNVRHRFQRDKTDDSGLSPVASFLLHRWQNQVAKDLNARR\*

>Pp3c1\_23810V3.1

MEYYVYVDEEVHGLIDGAMEARFENLELIGKGSFGDVFRGFDKELNKEVAIKVIDLEEAEDEVEDIQKEISVLGQCRSPHITEYYGSYLHTTKLWIVMEYMAGGSVSDLLETGPPLDEVSIASILRELLLSLDYLHSEGKIHRDIKAANILLTANGDVKVADFGVSAQLTRTMSKRKTFVGTPFWMAPEVIQNSGDGYNEKADIWSLGITAIEMAKGEPPYADLHPMRVLFLIPKNNPPQLDDHYSRPFKEFVSFCLKKNPSERPSAKELLRHRFVKNARKSSRLVDRIRERPKSHVSKAKDTPRPSEAFKNESDSKGVRMRSDNGVYPPLSSRRRDASWDFGTGSIHTTGTLRSSSKTFGQIDQDRPRGTDNSLHQGSDVLPTLLSKAELDYQIDAGLRDASVDINALRRNSFGTQKRLDAEPYFSRDPGPHASGDSSMEGRSQARPFLGSLSATTVNTTGGSRNEEASEGFSSGTIVRSSTPDEGGSIPGTPKINLEAREDSATNLAEAKAALQAGMRKGGPKGPTPVKLRKDAHEHLSDPRETPKAASRQSRRASEEDVARAAAAGASAALTLLLIPALKETAAEQSEGPALRAAADAADALMDLERLAPGACEVLVSKLLRQLIRKDEAPVKGLQSLARRLLSDNGGEKDGHVPSSHIRSGTARLRSQRDKSYDSGLSPVAAFLLHRWQGQVSKDLNFRR\*

>Pp3c11\_1950V3.1

MPSGGGTMVEAEKRSYPVLASEYKLYEEIGQGVSAIVYRAHCVTYNEIVAIKSLDLEKCNSNLDNIRREAQTMSLINHQNVVKAHCSFVVGQNLWVVMPHLAGGSCLHIMKAAYPDGFEEPVIATILKESLKALEYLHRHGHIHRDIKAGNILVDSNGSVKLGDFGVSACMFDTGDRQRSRNTFAGTPCWMAPEVMEQLHGYDFKADIWSFGITALELAHGHAPFSKYPPLKVLLMTLQNAPPGLDYERDKKFSKSFKEMIAMCLVKDPAKRPTAEKLLRHSFFKQARSFDYIARHILEGLPPLGETVNNLKIKDANRLAQQIQPYDEQEAQSQNEYKRGVSAWDFNVEDLKAQAALIQDDEEVVPKLLKVALNTEAEEISQAPVTPVKEEITEGDLQCSSPLSQPPLCRESSFNRVQMPVTIHSIIAETTNDAGERVTRIRSGPLPNPVQPKSANISRTALPSGRKEPKHIGRFDVWDEHDGESLSWHGSPRENRKSEARRERDDREQRRGDDRDRKEEREQRRSDERSERDEIRRVGSERVLSSIRGLTTMDERERDRDRDYRQGGRGSDYSGRMMQRERSFSGPVNTISDRSSFDQKSTNGLQAVSRQTPTQVNLNKEISEDKVKAPVQKGPVLHKGRFSVTSDDTQFEESSQLNPRKTSNTQASLHKSASSGDFMSGERRLPVSQHSSSSQHALLSQHSHSSLHVSSPNGLISHQNSQVTTPTAAVLSQLQQIFQQAQKQQDSILHLIQSLNPQDAASVISTSSMSRFSRTSSTNSGVEHSRNSVGARLRVNQVEVSTDRERELLHQVSDLQFSLRGS\*

>Pp3c21\_3370V3.1

MGGGVASEGQMEKRKYPYGASDYKLFEEVGQGVTATVYRAHCIPYNETVAIKSLDLEKCNTNLDDIRREAQTMSLIDHPNVVKAYCSFVVEQSLWVVMPFMAGGSFLHIMKSAFPDGFDEPVIATVLKETLKALEYLHRHGHIHRDVKAGNILVDAAGAVKLGDFGVSACLFDTGDRQRTRNTFVGTPCWMAPEVMEQLHGYDFKADIWSFGITALELAHGHAPFSKYPPIKVLLMTLQNAPPGLDHERDKKFSKSFKEMIAMCLVKDPAKRPSADKLLRHSFFKQARSGDYIARNVLYGLPPLGERVKKLKVNDANRLAQNEQEVQSQNEYKRGVSGWNFDLDDLKAEAALIQDGDEDLSMVVGKDVIVVEEQEVTKLQVLPFMETDGDVPSHCLTPSPPPSLSRQPSIDRFQQPVTIHSIIAETTSDAGERVTRVRSGPLPNPVQTKPTNGMRGRFEVWEDNNPESPVSHGSPRESRRSAEDKEPSRRERDSREFRKADDRERKEDREQRRSDERGDRDAFRRVGSFGSERVLSSIRGLTMDSREQDRDRDIRQNGRNGSKETLEEKTKYLGQKGSVLQKGRFSVTSDDMNLEDSPHVSSRKYSNVPTPLHKSASASEWSNDRKVLGLQNPASPSQQSIASSQNISGAISLCAGIMPQLHQILQHGQRQQEGILNLIQSLSPTDAANLQALNSASRYLRSLSANSVDSSSGCGSPRSPQCGSRNRPSQVEASHKGYYNCQLEVSTDKERELLHQVSELQARMANLVDELQTVKLRNVSLERQLNAIYNKEEEERIRKEDAARESG\*

>Pp3c4\_10780V3.1

MEKQSERKGPYPVTATQYQVLEEVGHGLGATVHRAICLPFNEVVAIKKLDLESRNVNVDDIRREAVTMSLTNHPNLVKSYCSFVVDQSVWIVMPFMAGGSCLHIMKAAFPDGFEEPVIATLLKESLKALEYLHRQGHIHRDVKAGNILLDGDGSVKLGDFGVAASMFDKGDRQRSRITVKGTPCWMAPEVIEKTHGYDFKADIWSFGITALELAHGHAPFSKYPPLKVLLMTLQNAPPRLDNERDKKFSKSFKEMISMCLVKEPTKRPSAERLLRHSFFKQARSSDYILRHVLDGLPPLGERVKHLRMLDAAQIAEKKMPFEEQEEKSKTEYKRGVSNWNFNIEDLKAEAALISGDGGYAEAVKEEDDTPKQQTQKGLDDYLPPKNAEPSARDRELRQRGMSAEDLSRCRERAFSGLLPSDERATSDQGPASGFQGVPRPSSGSKEGSEEKSKGPAQKFPIVQRGRFSVTSNDLDLQDPPQGSTRRRSASSQALQLQAPSVASSLSNVSGSSVSLAALLPHLQNALNHAVMQQDTLMNLLNSINASEASSSLRRSSRSSSSHSMTEISSDREKELLHQIAEFQSKISVLVDELQALKLKNMSLERQLNAHHNREKEERIRKQTNIGDG\*

>Pp3c4\_15760V3.1

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>Pp3c7\_24190V3.1

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>Potri.001G084700.1

MGRMGKMYTVNPNDYKLLEEVGYGASAVVYRAIYIPFNEVVAIKCLDLDRCNSNLDDIRREAQTMSLIDHPNVIRAYCSFVVDQNLWVVMPFMAEGSCLHLMKIAYQEGFEESAIGSILKETLKALEYLHRQGHIHRDVKAGNILLDTNGIVKLADFGVSACMFDTGDRQRSRNTFVGTPCWMAPEVLQPGSGYNSKADIWSFGITALELAHGHAPFSKYPPMKVLLMTIQNAPPGLDYDRDKKFSKSFKEMVAMCLVKDQTKRPTAEKLIKHSFFKNAKPPELSVKKLFADLPPLWNRVKAIQLKDAAQLALKKMPSAEQEALSQSEYQRGVSAWNFDLEDLKAQASLVRDDDDIPETREEDESIKFGGGKAAIGSQSSSVKVNSNSEIQLVEYSRQLSGGELPQADNFIRKGKLPESDLLETSSLEKVGWKRNGSSSEAKASTSESVMAQAKAKTVKSRQTHSGPLMPGTVFSHSLSERGRTSERFENEIHPTAERATREVRKAPSFSGPLMLPNRASANSLSAPIKSSGGFRDSLDEKSKTNLVQIKGRFSVTSENLDLVKPVNQPPKEVSNNSVHALLFPHLQNLFQQTSIQQDIIMSLLNSLQPAEAIEAAQNGKLPPLPHGSENNGSVEAASSEREKSLLIKITELQNRMVNLTDELNAEKLKYEQLQQQLKAISGREENGERSEVDA\*

>Potri.003G146000.1

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>Potri.004G194700.1

MSASSSSSRADGKVQIQYPTGADAYRILEQIGGGARATVHKATCVNNDIRYSGLVSIKIIDLEQYSAADLDGLRRESKAMSLHSHPNFLGSLCSFTVDHHLWLVMPYMAAGSLQSIVSSFFPDGLLEPCIAIVLKETLKGLSYLHRLDYLHTDIKAGNILLNHTDNGSIKLEDSGMSVWIYDSNSIEKSSSLSSSSKMRLTDVAGTPYWMAPEVIQDSNTGYSFKSDIWSFGVTALELAHGGPPFSYLPPSKSLMLKIKKRFGLSDYDYDEKSKKDFKNNHFSQAFKDMVASCLDQDPSRRPSADQLLQYSLFKNCEGLDLLFNEFFRGLPNVEERFKEPNASSDGTSSQITSGTDTDSAGSSVKTTRISGWKFNESKFELEPEFHAESKDDVVKTVHFGGETIIDTDTNIGFSESSSGSGDLEGLVGDHAGANMSGIEGAVETLNQETVAEKASSRYDCSVTTRV\*

>Potri.008G163800.1

MAHFQDQRTKSQRVQYPVDSNAYKILDEIGVGVSATVYKAICVPMNSTLVAIKCIDLDQSRADFDSVRRETKTMSLLSHPNILESHCSFTVDRHLWMVMPFMSAGSLQSIISSSFPDGLPEPCIAVVLKEILNALSYLHDQGHLHRDVKAGNIVIDSNGKVKLADFGVSASIYEFNTLERSSSLSCSSRMRLTDLAGTPYWMAPEVIHSHTGYSFKADIWSFGITALELAHGRPPLSHLPPSKSLIMKITKRFRFSDCHEENRKKSCRNKKFSKAFKDMVASCLDQDPSKRPSAAKLLKHSFFKNCKGLDYFVKNVLHGLPSVEERFKEAKVLSGISSQSGTDVEEEEKGDIDGDSVIQRVKTRRISGWNFNEEGFELDPVFPTDSKNDSVVKQVRFGGESIIQDKKIEFSESDGSGDLVDSAKPSILNSLAPVKEEMSQVGDHIGVNMSGVGGIVEGLNQVTMLEGLVALKRSLEEQRRHVAIIIGLLGGETDGEDQMVQMSENLKEELDIEKQKNLKLEMELEFIKIVISGAFAAASFPN\*

>Potri.010G157400.1

MWRMDHPSPSRRTRTSKTPNKSELYSTVVIHNSDSDSEPESKSKTDDNNIYATMLYKGGGENNSKDDDVDVEEEDEESLPPLLKRLPKDFGGGDDDDDADFGTMIVKASRGRHQNQSWSSSSSVAPPRKPYSAPFTEFESRINDIGDNSDGDDDGRGEFGTFLVKSTVVRRSGSGGGGSTMGKAVASMQASGELGFGKERKGSGLLGEEGKQHQQKQSKMSSSSIPESVTREDPTTKYELLNELGKGSYGAVYKARDLRSSELVAIKVISLTEGEEGYEEIRGEIEMLQQCSHPNVVRYLGSYQGEEYLWIVMEYCGGGSVSDLMNVAEEPLEEYQIAYICREALKGLAYLHSIFKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVIQESRYDGKVDVWALGVSAIEMAEGLPPRSTVHPMRVLFMISIEPAPMLEDKEKWSLVFHDFVAKCLTKEPRSRPMASEMLKHKFIDRCKVGASAMLPKIEKARQIRTAMSLQAQNLAPAESEPTEGPQLNEVYGDTVPSNRLPMVNEVHSSSDGVDMAGGDYGTFVVHGGEETDKTGLQTALYDVGGILQDHPGNIEGLSVSGTGGKSADPWLDNATGVAANNPLVGESLPALQTIQTSTPEVSGYSEQNLKKNTVSKVHVEGGGGLGSSTLKNETVSRKAFALQDKLWSIYAAGNTVPIPFLRATDISPIALLSDNVLGGIQCDNSGTVAAEALQELFSGDGPSKKGRRIQNEMPLPPGVYQRLTSSSTLLNLAQALAYHKMCYEEMPLQELQATQEKQTIQNLCDTLRTILRL\*

>Potri.016G049500.1

MADELDQESEAQLQYPTDPNAYRLVDEIGGTGARAKVHKAICIHNIWKSTFVAIRIFDLEQYPADFDGLRRETKTMSLHSHPNVLASHLSFAVDSYLWVVMPYMAAGSLQPIISTYFPEGLPEPSIAIILKETLQGLCYIHDQGRLHTDIKAGNILIDTENGSIKLADRGKSVSIYDLRSVVGSSPLSPSSRMRLTDVAGTPYWMAPEVIHDLDAGYSLKADIWSFGITALEIAYGGPPFSDLPPSKSLIMKIKKRLGFSNYHDEKHKKDFKNKKFSKEFKDMVASCLDQDPSKRPSADQLLEYSFFKNCRGLEFLFKKVFDGLPNVEETFKELKALQGTPSQITAGTDVEEEEERPESVGPSEKTRWISGWKLNEYEFNLVPEFSSDSEDDSVVKLVRFGGETIIPDTNIGFSVSSIGSSDLEGSVEDHTGENMSGIEGIVEEFNQVTVLEGIMALMRSLDEQRRQVARMIALLGGEADGEEQLVQRIENLMRELDLEKEKNLKLEMELENINIVISGAYNDASAAAAADDDDAAIDDID\*

>Potri.001G037900.2

MEKKKYPIGSENYLLYEEVGQGVSASVHRALCVPFDEIVAIKILDFERDNADLSNISREVQTMILVDHPNVLKSQCSFVSDHNLWVVMPFMAGGSCLHILKAAYPDGFEELVIATILREVLKGIEYLHQQGHIHRDVKAGNILVDGRGAVKLGDFGVSACLFDSGDRQRMRNTFVGTPCWMAPEVMEQLHGYDFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDLERDKKFSKSFKQMIASCLVKDPLKRPSANKLLKHSFFKQARSNDYIVRTLLDGLPDLGDRIKDLKRKEEDMLAQKKMPDGEMEELSQNEYKRGISGWNFNLEDVKAQASLIPDAEDHTTDSNPGGSSNSLSTLDAVEKQSEPRNSSLGQVTEMMEDKDMQNRAAPLPSVNSAINITKVRSVKSDDDSINASPCHERHVSQNSSSLSDRVEGNATERPASDINGKPSDKLQNQPPNNSNINGAIINQDGDDVPSENPSKPFKSSGASSEELDEKAKPPVVQQRGRFKVTSENVDIEKAVSPLVLQKSHSMQVRNFEVLTQHPGTPSPSPSETIPSTVLDHSVFPLLLSLLQTNITQRDGILHLMRQLYGGDTAGNRTTDGGWATAQGGSTEKSLIEAAHDREKELLHEITELQWRTNSKNLTSYTGEAHRGDSP\*

>Potri.001G349300.1

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>Potri.001G397600.2

MADAAGLMEAAGARFSSLELIGRGSFGDVYKAFDKELDKEVAIKVIDLEESEDEIEDIQKEISVLRQCRSPYITEYYGSYLHQTKLWIIMEYMAGGSVADLLQSGPPLDEMSIACILRDLLHAIEYLHNEGKIHRDIKAANILLSENGDVKVADFGVSAQLTGTVSRRKTFVGTPFWMAPEVIQNSEGYNVKADIWSLGITAIEMAKGEPPLADLHPMRVLFIIPRENPPQLDEHFSRPMKEFVSFCLKKVPAERPTAKELLRHRFIRNARKSPRLLERIRERPMYQIKDAETPRNGPIGIGEGFDTVKVVRDLRADGTVRASGQGKPFKNAGWDFSIGGSQTTGTIRSAARPPQESLELSYGKDARDPYHDDHQDNSYDDDDLSVSGSGTVVIRTPKGYQSSALFRDQNNASSSTSTSFEDASTSGTVVFRGQHDESDSPRTHKSRLGMQERTSSSSLEDSALNLAEARAALQGGLRKVNARERFVPSNNNRYGLENRRREQLTNSSDSSRSSREYFDAPKAFPRSQQASNVEESARIASASLSVLLIPSLKEAVADDSERALFHAVTNSLVNMERVKPGSCDIFVRSLLQQLASSKESSLRDLQELAAHLLSKGKTTPEETQNGNTDVDSRKKQPTKEFNSNANLSPLLIQMPI\*

>Potri.003G186700.1

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>Potri.011G116300.2

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>Sobic.001G085700.1

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>Sobic.002G313100.1

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>Sobic.004G064200.1

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>Sobic.004G327000.1

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>Sobic.008G011200.1

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>Sobic.010G139600.1

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>Sobic.001G193000.1

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>Sobic.001G533700.1

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>Solyc02g086790.2.1

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>Solyc03g117790.1.1

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>Solyc05g012130.2.1

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>Solyc06g053730.1.1

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>Solyc06g068590.2.1

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>Solyc07g062940.2.1

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>Solyc08g008550.2.1

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>Solyc08g083040.2.1

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>SMO116G0224.1

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>SMO134G0223.1

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>SMO169G0133.1

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>SMO351G0517.1

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>SMO356G0010.1

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>PGSC0003DMT400074400

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>PGSC0003DMT400036874

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>PGSC0003DMT400036872

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>PGSC0003DMT400036873

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>TraesCS1A02G181900.1

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>TraesCS1B02G199100.1

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>TraesCS2A02G233400.1

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>TraesCS2B02G249900.1

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>TraesCS2D02G232200.1

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>TraesCS4B02G395600.1

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>TraesCS4B02G398400.1

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>TraesCS5A02G187400.1

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>TraesCS5A02G392500.1

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>TraesCS5B02G196400.1

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>TraesCS5B02G397300.1

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>TraesCS5D02G203600.1

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>TraesCS5D02G402300.1

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>TraesCS6A02G353400.1

MVGSGSKHAAGGSGLGGGGERRKYPIRAEDYELYEEIGQGVSAIVYRALCRPLGETVAVKVLDFERTNSNLNNIMREAQTMILIDHPNVVKAICSFANNQTLWVVMPYMAGGSCLHIMKSVYPDGFEEAVIATLLREVLRGLEYLHHHGHIHRDVKAGNILVDSRGGVKLGDFGVSACLFESGDRQRARNTFVGTPCWMAPEVMEQLHGYDFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKKFSRHFKQMVAMCLVKEPSKRPTATKLLKQSFFKQARSHDYIVRKLLEGLPGLGARYQALKEKDEHLLAQKKMPDGRKEEISQVLILNL\*

>TraesCS6A02G353500.1

MVGSGSKHAAGGSGLGGGGERRKYPIRAEDYELYEEIGQGVSAIVYRALCRPLGETVAVKVLDFERTNSNLNNIMREAQTMILIDHPNVVKAICSFANNQTLWVVMPYMAGGSCLHIMKSVYPDGFEEAVIATLLREVLRGLEYLHHHGHIHRDVKAGNILVDSRGGVKLGDFGVSACLFESGDRQRARNTFVGTPCWADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKKFSRHFKQMVAMCLVKEPSKRPTATKLLKQSFFKQARSHDYIVRKLLEGLPGLGARYQALKEKDEHLLAQKKMPDGRKEEISQDEYKRGISSWNFDIDDLKSQASLISECEDTISSKDTDISSIYDFDTSLQEQALEGSLFSMKYDTDIENDVMANDKSAVSSPEQSVCLSRKHSSMESCDLDLQEKDLDAIPTSSFQERKCSFSSCSSDGFLSSKESSFSSKPQINIHNRDKGSGGVLQVADEPSPEAISRAPKSLVSNVDEHDDRSKPPLIQQRGRFKVTPGNVELDKAHSPGLQKSHSMQTISQLSALSIPSSAEAASSIIGGSLYIQLYNVLQTNLLQREQILHAMKQLYISDSISPVRMHSLSRSPSPSSALSVDRSMLLSTDSAAAQQNLNQRANPAESDSRNPLPKSEPKAEAAQDVLSKI\*

>TraesCS6B02G177800.1

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>TraesCS6D02G335800.1

MVGSGSKHAAGGSGGGGGGERRKYPIRAEDYELYEEIGQGVSAIVYRALCRPLGETVAVKVLDFEHTNSNLNNIMREAQTMILIDHPNVVKAICSFANNQTLWVVMPYMAGGSCLHIMKSVYPDGFEEAVIATLLREVLRGLEYLHHHGHIHRDVKAGNILVDSRGGVKLGDFGVSACLFESGDRQRARNTFVGTPCWMAPEVMEQLHGYDFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKKFSRHFKQMVAMCLVKEPSKRPTATKLLKQSFFKQARSHDYIVRKLLEGLPGLGARYQALKEKDEHLLAQKKMPDGRKEEISQDEYKRGISSWNFDIDDLKSQASLISECEDTISSKDTDISSIYDFDTSLQEQALEGSLFSMKYDTDIENDVMANDKSAVSSPEQSVCLSRASLCGTSNGVLVNGHVRKHSSMESSDLDLQEKDLDAIPTSSFQERKCSFSSCSSDGFLSSKESSKPQINIHNRDKGSGGVLQVADEPSPEAISRAHKSLVSNVDEHDDRSKPPLIQQRGRFKVTPGNVELDKAHSPGLQKSHSMQTISQLSALSIPSSAEAASSIIGGSLYIQLYNVLQTNLLQREQILHAMKQLYISDSISPVRMHSLSRSPSPSSALSVDRSMLEAAQEKEKELVNEVLELQWRLLCAQDEVQRLKAKAAQI\*

>TraesCS7A02G232300.1

MERAPRNRGFPTDPKEYKLYEEVGEGVSATVYRALCVPLNTFVAIKVLDLEKCSSDLDGIRREVQTMSLLDHPNLLRACCSFANDHQLWVVMPFMAAGSALHIIKTNFPDGFEEAVIATLLWEVLKALVYLHSQGHIHRDVKAGNILIDTNGAVKLGDFGVSACMFDTGNRQRARNTFVGTPCWMAPEVMQQLHGYDYKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKRFSKSFRDLVAVCLVKDPQKRPSSEKLLKHSFFKQARSADFLAKSILEGLTPLGDRFRALKAKEADLLLNNKLGPESKEQLSQKEYIRGISGWNFNLEDLKTAAALLDSSNGTYHFDGANNKDRNGLQDVYNESENIYQERVNHGASARHDEHEIQEVEDLDGDLASSFPTRPLEALKSCFDVGGDDDPDPTATNLPVQPSMESISPVQQFSEMDHSRSDNCNGENLERSVSVPSNLGNSVYPKFSSGSLIPEHVLSPYKNVGSDSRRNEFHQKNPSSRNRSGPLFFRQMKDTRPHLSVAPDEASEGNVVQRRGRFQVTSDNPGQKVASSASSNSRPNLPSGVTRPASNSSTILPTLQFLMQQNSMQKEVLSRLISSIEETSDASDASTVGLSQSFGSLAREKGLESYVVQLQRSVTELSEEVQRLKLRNNQLEQQINGLSKKDERLRREGSTKQ\*

>TraesCS7B02G130700.1

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>TraesCS7D02G232400.1

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>TraesCS1D02G185000.1

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>TraesCS5A02G556400.1

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>TraesCS6A02G149900.1

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>TraesCS6B02G386100.1

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>TraesCS6D02G139200.1

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>TraesCSU02G115300.1

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>TCA.XM\_007045769.1

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>TCA.XM\_007039347.1

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>TCA.XM\_007031422.1

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>TCA.XM\_007034971.1

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>TCA.XM\_007024752.1

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>TCA.XM\_007021490.1

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>TCA.XM\_007021757.1

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>TCA.XM\_007021772.1

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>TCA.XM\_007021774.1

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>TCA.XM\_007021777.1

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>TCA.XM\_007021791.1

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>TCA.XM\_007021794.1

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>TCA.XM\_007045768.1

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>TCA.XM\_007039346.1

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>TCA.XM\_007039348.1

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>TCA.XM\_007031421.1

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>TCA.XM\_007024753.1

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>TCA.XM\_007024754.1

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>TCA.XM\_007024755.1

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>TCA.XM\_007021491.1

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>GSVIVT01012233001

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>GSVIVT01013739001

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>GSVIVT01014297001

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>GSVIVT01016074001

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>GSVIVT01019643001

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>GSVIVT01027718001

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>GSVIVT01032461001

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>Zm00001d018352\_T001

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>Zm00001d023240\_T001

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>Zm00001d045967\_T001

MEHVLSSRRFPTDPNEYKLYEEIGDGVSATVYRALCVPLDILVAIKVLDLEKCNNDLDGIRREVQTMSLIDHPNLLRAYCSFTNGHQLWVVMPYMAAGSALHIMKTSFPEGFDEPVIATLLREVLKALVYLHSQGHIHRDVKAGNILIDTNGAVKLGDFGVSACIADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYERDKRFSKSFKDLVATCLVKDPRKRPSSEKLLKHSFFKHARSAEYLARSILDGLPPLGERFRELKSKEAELLLNNKLGQESKEQLSQMQLFAFQKEYIRGISGWNFNLEDLKNAAALIDSSNGTCYLDVRENRVKDDSQEAYNGPEHIYQERLNHVASRRPEEDEIQEVEALNDAVSSSFSSRSLEALKSCFDVCGVDDPSPTATDSRAQPSVGTLPFQQLQKFEHCKSGDCNGESLERSVSVPTNLVTSGYHKHSSGSLIPEQVLSPYLSSDLERYFFLKFIFPCPTQFGLSHPFLRAVAPDESSEGKIIRRRGRFQVTSDSISEKVATSSCNSSRINLPIDAARSSPKLSAILPTLQFLMKQNTMQKEVLSRLISSIEETSGMHEYSSLF\*

>Zm00001d013836\_T001

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>Zm00001d021584\_T001

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>Zm00001d027340\_T001

MVRSGSIRRSAVPAPMPAPAFTVSPADYRLLEEVGYGANAVVYRAEFIPTGRTVAVKCLDLDRVNSNLDDVRKETQTMSLIDHPNVIRSYCSFVVGHNLWVVMPFMSEGSCLHLMKVAYPDGFEEPIIASILKETLKALDYLHRQGHIHRDVKAGNILIDNPGVVKLGDFGVSACMFDRGDRQRARNTFVGTPCWMAPEVLQPGTGYNFKADIWSFGITALELAHGHAPFSKYPPMKVLLMTLQNAPPGLDYDRDKRFSKSFKEMVAMCLVKDQTKRPTAEKLLKHSFFKNAKPPELTVKNILTDLPPLWDRVKALQLKDAAQLALKRMPSSEQEALSMSEYQRGVSAWNFDIEDLKAQASLICDDDPPEIKEDDDTGRITDIDKDTSSDDYFGKTAPSNGNNCSDRSSVPANPGQNGPEINEILSSNNGNAYSERKPDGRKNPESENDSLPSTSKHDADGKDYRCDFRQKQRTYSGPVLQSGPNNSSMTERGHIIERDAGVQSVSDKQKNGTRRANNLSGPLSLPTRASANSLSRANNLSGPLSLPTRASANSLSAPIRSSAGYVGSLGDKPKRTMVEIKGRFSVTSENVDLAKVQEIPGSSASRKLQEGPSLRKSASVGDWSANDKTTSTNHQRKELCNSSVSTSILIPHLQNLVKQTAFQQDLITNLLSSLQQNERVDAAQSRVQSTTSDTVVEAATAEREHSLLVKIFELQSRMISLTDELIAAKLKHVQKHAFKTIINDRLRQLCTCLTYDPLCCYQLQEELNVLYCQEEILDMREDESEEA\*

>Zm00001d032440\_T002

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>Zm00001d034055\_T001

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>Zm00001d052051\_T001

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>Zm00001d053735\_T001

MWKGKKSGPLAPRGRKREFPIRAADYELLEPIGDGATAVVRRARCLPHGGEIVAVKVMNMAHRTESDVNNASEEVKTMIMIDHPNLLSAYCSFTEGEALWIVMPYMAGGSCYHLMKSSYPKGFDDENFIAFVLRETLKGLEYLHENGHIHRDVKAGNILLDQDKGVKLSDFGVTASLYDSIINRHGKRKTLVGTPCWMAPEVMEQKDYDFKADIWSFGITALELAIGHAPFSSQPPAKVFLMTLQHAPPSLHNTKEKKFSDSFKSMIATCLIKDPTKRPPAKKLLKHPFFRRARSDHNAVKCMLNKLPSLAERMQFIKENEAKLQADKKPLDNCKEKASQEEYRRGVSEWNFDIADLKAQAALYPDENEAEDFLRFLFELDIVDETTQLKDIRAESHSINNDGTNVADDGLGKSNSTSPMSSSQSVKQLDKGSPNGLVRSESFEIHSISPAKQLTTAVSTCNDVDEYLEKTAFQKGRFKVIHDYSKLEGATPREKELLDRISSLEQMLLATQDEVERLKAKES\*