Expression of OsMATE1 and OsMATE2 alters development, stress responses and pathogen susceptibility in *Arabidopsis*

Manish Tiwari[1], Deepika Sharma[1], Munna Singh[2], Rudra Deo Tripathi[1], Prabodh Kumar Trivedi[1]*

Fig. S1 An unrooted neighbouring junction (NJ) phylogenetic tree of MATE. All the MATE sequences (designated in the form of locus ID; Table S2) were aligned using ClustalW and phylogenetic tree was created by PHYLIP with PhyloDraw V0.82. Branch lengths are proportional to evolutionary distance with each other.

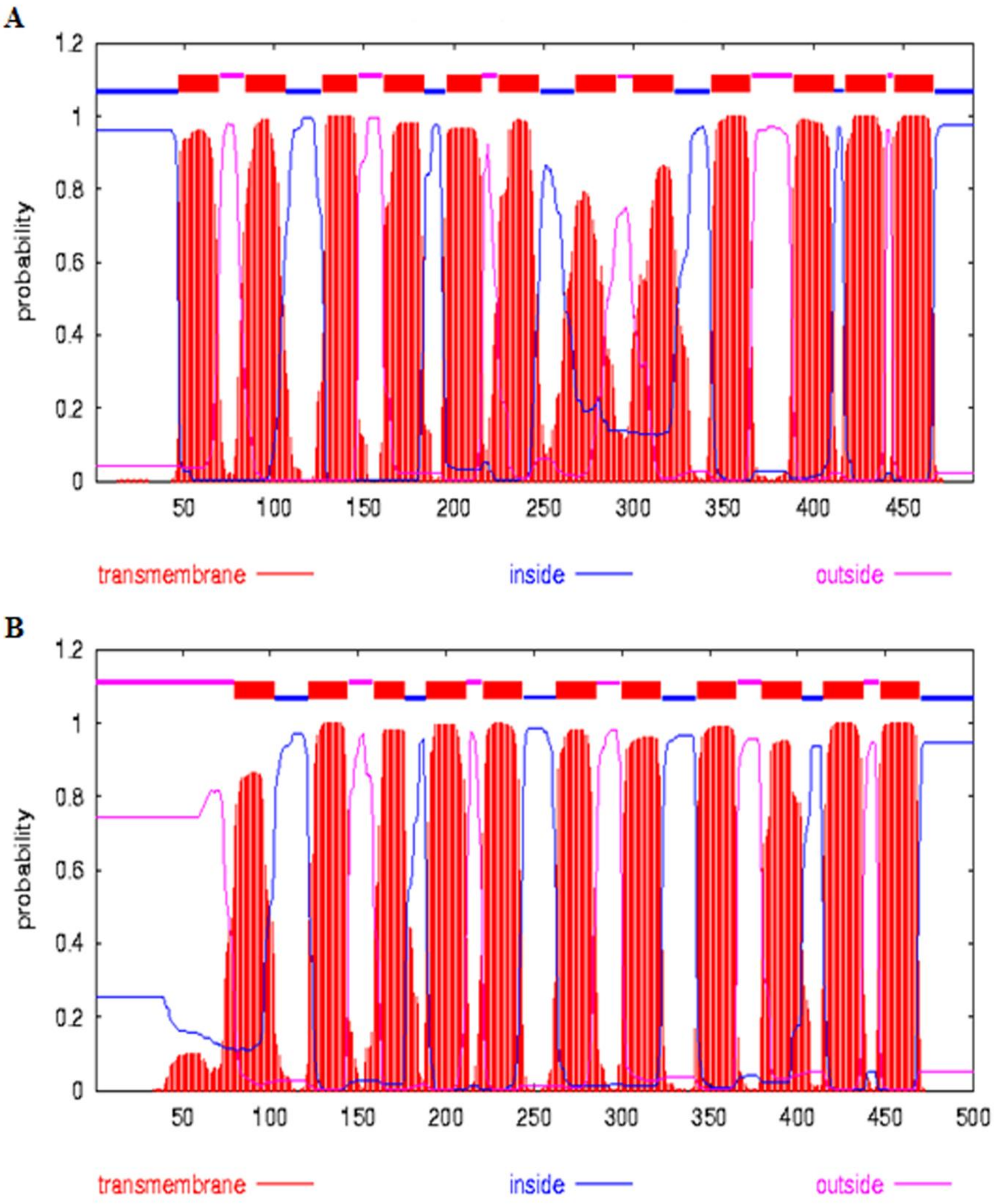

Fig. S2 Transmembrane helix prediction. Presence of transmembrane domain was calculated using TMHMM. Red colour represents the transmembrane helices. *In silico* prediction indicates the presence of 12 domains in OsMATE1 (A) and OsMATE2 (B).

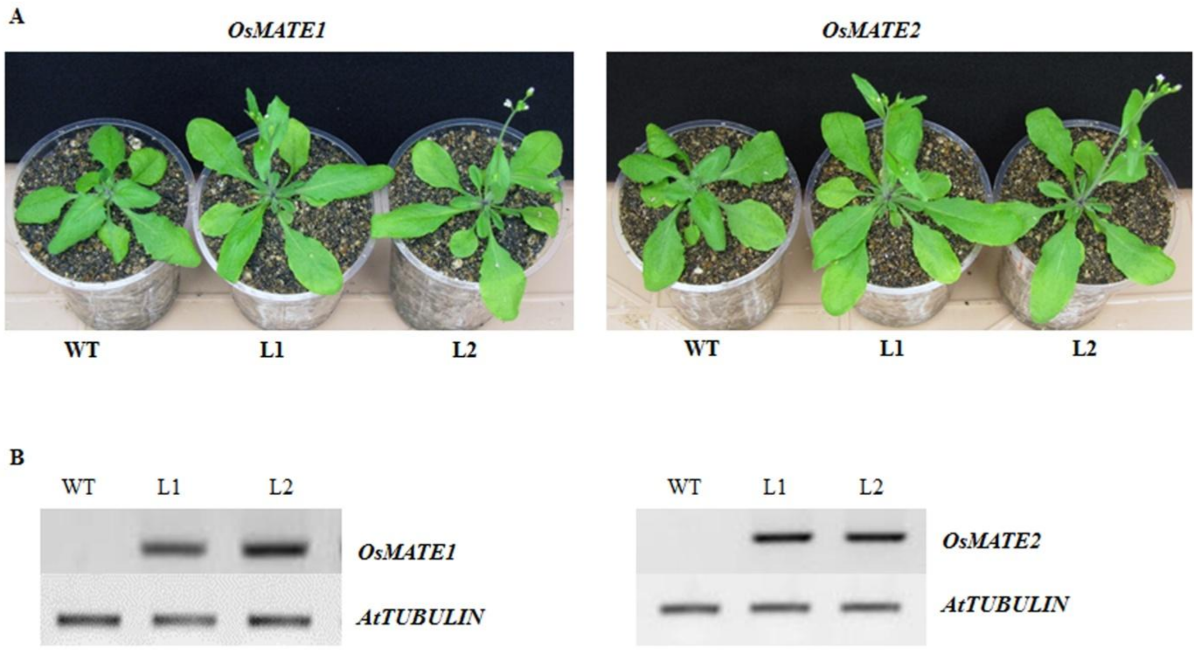

Fig. S3 Confirmation of transgene expression. (A) Photograph of two representative transgenic lines of *OsMATE1* and *OsMATE2*. (B) Transgene expression was confirmed through semiquantitative RT-PCR and *TUBULIN* was used as endogenous control.

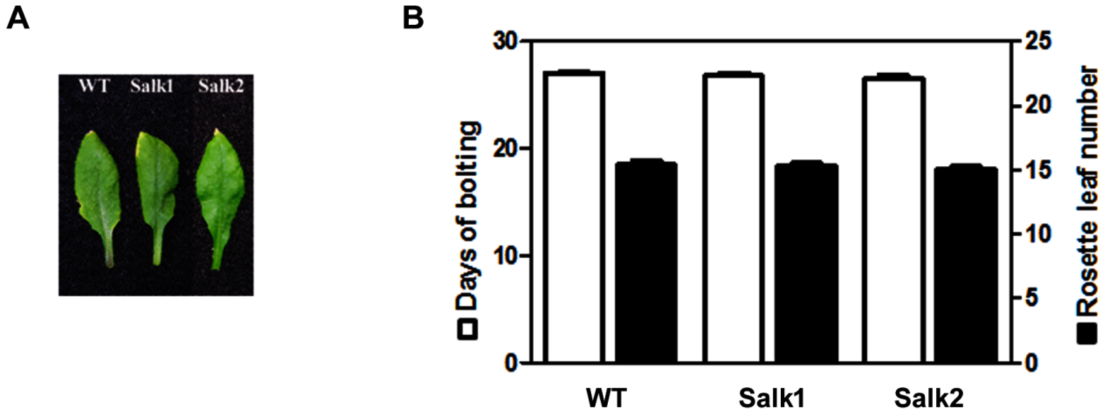

Fig. S4 Flowering days of WT and salk mutants. (A) Photograph of 8th leaf of salk mutant (three week old) along with WT are displayed. (B) Number of rosette leaf and days at bolting of WT and salk1 (SALK_045655C) and salk2 (SALK_124549C) grown under LD conditions (16h light-8h dark cycle). Bars are the mean and error bars are ±SE (n=8-12).

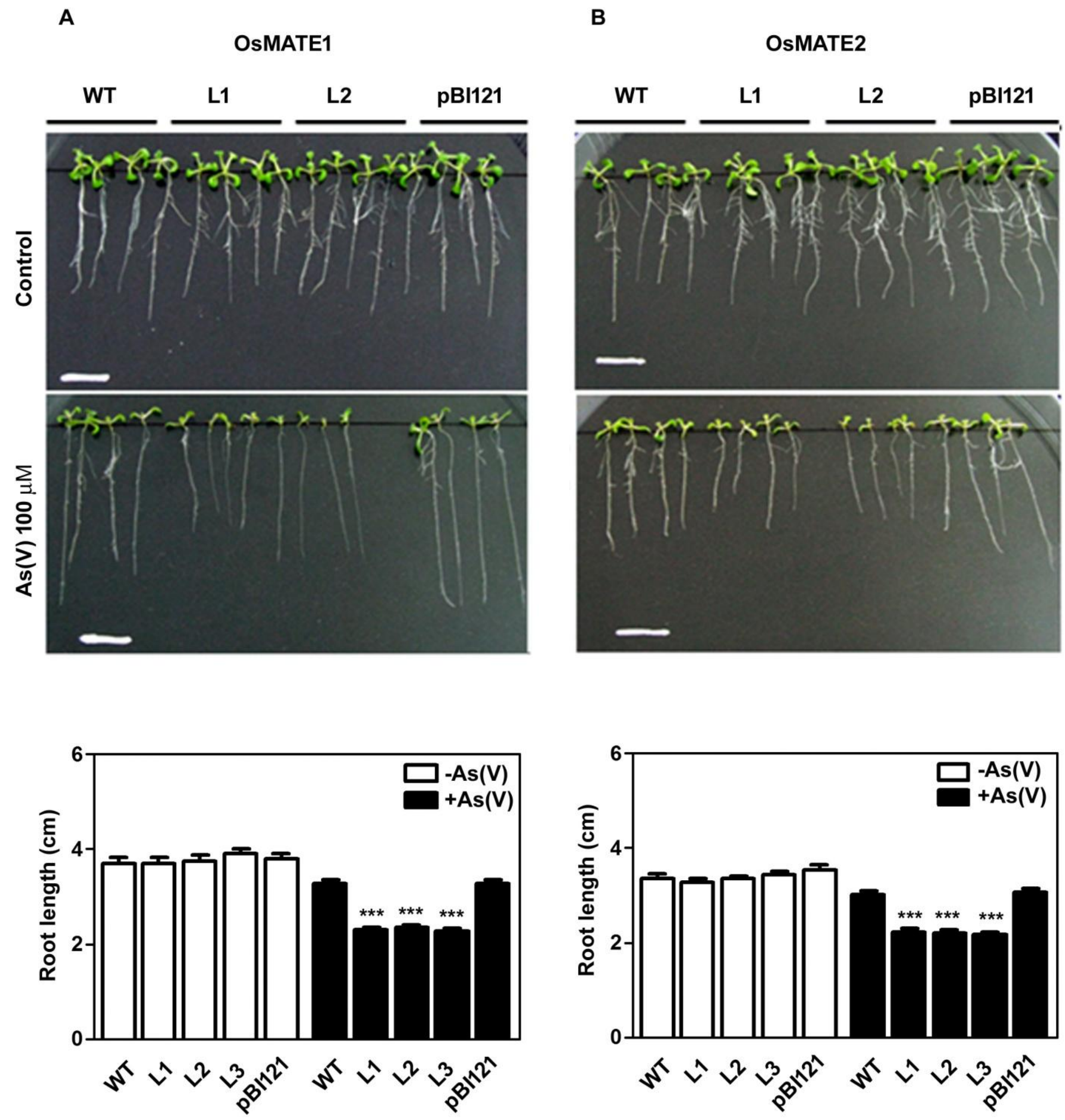

Fig. S5 Expression of *OsMATEs* in *Arabidopsis* leads to sensitivity for As(V). (A) Phenotypic changes of WT and two transgenic lines, expressing *OsMATE1* grown on control (half strength) and in the presence of As(V). (B) Sensitivity of transgenic lines, expressing *OsMATE2*, reflected towards AsV. Lower panel depicts the graphical representation of root length and while line depicts 1 cm scale bar. Bars are the mean of root length of 15-20 plants of each genotype and error bars represent ±SE. Significance was determined by One-way ANOVA (Newman-Keuls used as post hoc test). *** Significantly different from WT ($P < 0.0001$). Experiments are performed more than three times and result is the representative of one set.

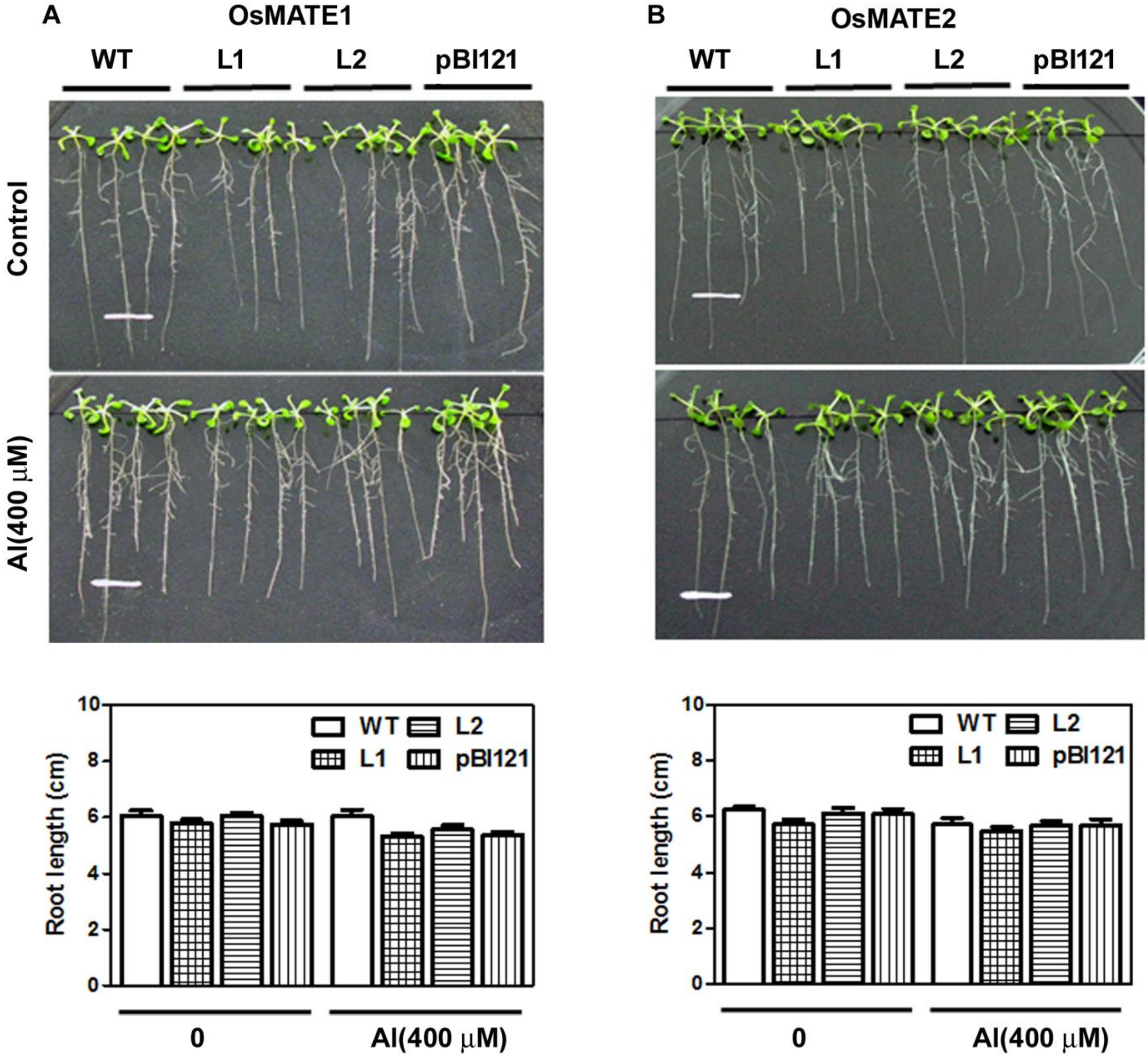

Fig. S6 Effect of Aluminium on growth of transgenic *Arabidopsis* lines. (A) Phenotypic changes of WT and transgenic lines, expressing *OsMATE1*, grown on control (half strength) and in the presence of Al. (B) Appearance of transgenic lines, expressing *OsMATE2*, during supplementation of Al (400 μM). White scale bars are equivalent to 1 cm length. Lower panel depicts the graphical representation of root length. Bars are the mean of root length of 15-20 plants of each genotype and error bars represent ±SE.

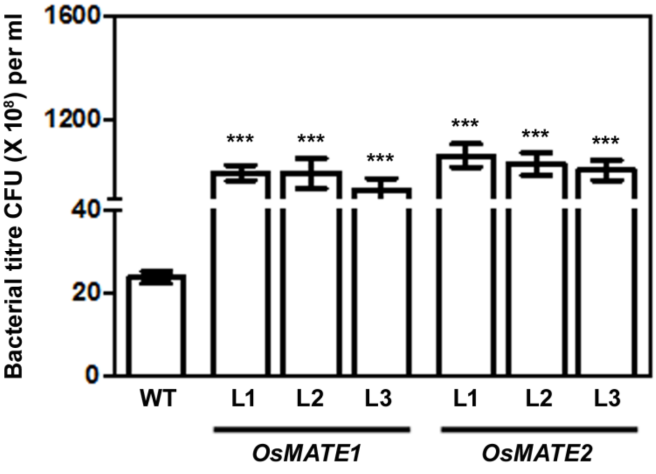

Fig. S7 Bacterial growth after *in planta* sprayed inoculation. Three week old plants were spray-inoculated with *Pst*DC3000 and bacterial growth was measured after 7 dpi. The experiment was performed two times with similar results. *** indicates significant differences ($p<0.0001$) in bacterial titre compared to WT (One-way ANOVA, Newman-Keuls used as post hoc test).

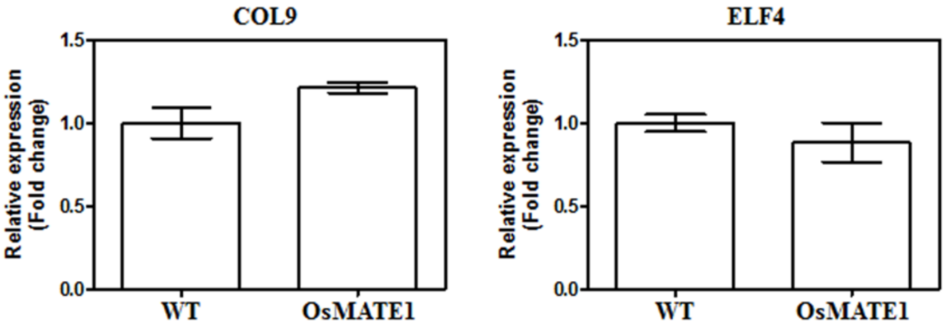

Fig. S8 Relative expression of *COL9* and *ELF4*. Transcript level of *COL9* and *ELF4* measured in WT and transgenic plants expressing *OsMATE1* by quantitative RT-PCR.

Table S1 List of oligonucleotides and their use in the study

S.No.	**Primer Name**	**Primer sequence (5’-3’)**	**Use in the study**
1.	MATE1F1	CAGAGGAGGTTGGATTGTTCGTTC	Gene specific primer for cloning
2.	MATE1R1	TCTGGTGACGAGCATATTAGCTC	Gene specific primer for cloning
3.	MATE1Xba1	TCGGACGACACGGTCTAGAGGCGAT	For cloning in pBI121 and 326sGFP
4.	MATE1Sac1	ACCGAGCTCGGATCCCTTGTCCATG	For cloning in pBI121
5.	MATE1BamH1	ACCGGACTTGGATCCCTTGTCCATG	For cloning in 326sGFP
6.	MATE1RTF	GACAAGTTCGCGCTCATCTTCAC	For semiquantitative RT-PCR
7.	MATE1RTR	ATGGCCAGAATTAGCGTCTGCAC	For semiquantitative RT-PCR
8.	MATE2Fl	CGGTCGGTGGAGGCGACGACGACG	Gene specific primer for cloning
9.	MATE2R1	TCAGTTCGCGTCAACGGATCAGGAT	Gene specific primer for cloning
10	MATE2Xba1	CGGTCTCTAGAGGCGACGACGACGA	For cloning in pBI121 and 326sGFP
11	MATE2Sac1	TCAGTTCGCGTCAACGGATCAGGATG	For cloning in pBI121
12	MATE2BamH1	GAATCAGGATCCCGAATTCGTTGCAT	For cloning in 326sGFP
13	MATE2RTF	TCATTGCATTCTTCAGCAACTGGC	For semiquantitative RT-PCR
14	MATE2RTR	TCAGTTCGCGTCAACGGATCAGGATG	For semiquantitative RT-PCR
15	AtTubulinF	CTCACAGTCCCGGAGCTGACAC	Endogenous control Arabidopsis
16	AtTubulinR	GCTTCAGTGAACTCCATCTCGT	Endogenous control Arabidopsis
17	ProMATE1F	GAATCAGGATCCCGAATTCGTTGCAT	For cloning in pCAMBIA1303

18	ProMATE1R	TCACCCATGGCCGCCGACCGTGTCGTC	For cloning in pCAMBIA1303
19	ProMATE2F	TGTGTTAAGCTTCGGTTGTTAACGTG	For cloning in pCAMBIA1303
20	ProMATE2R	TCCTCCATGGCGGCCGCAGTGCGCGCG	For cloning in pCAMBIA1303
21	At5g39610RTF	TCTGCTACTGCCATTGGTGA	For Real Time expression analysis
22	At5g39610RTR	TCTCCCATCTTAGCCTTCCA	For Real Time expression analysis
23	At3g20810RTF	CCACATCATAATATACTTGCTCAGGTT	For Real Time expression analysis
24	At3g20810RTF	TCTCAGATAAGGGTAAAGTTCGTC	For Real Time expression analysis
25	At1g07590RTF	GGGTGATGGGTTTCCAGTT	For Real Time expression analysis
26	At1g07590RTR	CCCTGATTATCCACTCCATCA	For Real Time expression analysis
27	At1g77450RTF	CAACAATTGGGCCTTAGCC	For Real Time expression analysis
28	At1g77450RTR	TGCTTCCTGAAAATAACAACACA	For Real Time expression analysis
29	At4g15490RTF	AGCAAGAGCAGATGGAGGAG	For Real Time expression analysis
30	At4g15490RTR	GCCGAACCACCCATAAGAC	For Real Time expression analysis
31	AT2G29490RTF	AGACAATCGGATTCTTGGACAT	For Real Time expression analysis
32	AT2G29490RTR	TCCAATACCTTTCCAAAGTCTAGC	For Real Time expression analysis
33	At2g14610RTF	GATGTGCCAAAGTGAGGTGTAA	For Real Time expression analysis
34	At2g14610RTR	TTCACATAATTCCCACGAGGA	For Real Time expression analysis
35	At3g57260RTF	GCTTAGCCTCACCACCAATG	For Real Time expression analysis
36	At3g57260RTR	CCCGTAGCATACTCCGATTT	For Real Time expression analysis

37	At1g75040RTF	CGGACTACTCGAGGATTTTCA	For Real Time expression analysis
38	At1g75040RTR	GTGCTCGTTTCGTCGTCATA	For Real Time expression analysis
39	At3g25010RTF	CTAATGCACCACCAGCACAT	For Real Time expression analysis
40	At3g25010RTR	GCCTTCCCAGTTCAACACTT	For Real Time expression analysis
41	At4g23150RTF	GCCATTGGTACACCACCAC	For Real Time expression analysis
42	At4g23150RTR	GCTACCACGACCACATTTGA	For Real Time expression analysis
43	At2g43570RTF	CATCTCCAAACGCGAAATC	For Real Time expression analysis
44	At2g43570RTR	GCTGGTCCATCAATTTCCTC	For Real Time expression analysis
45	At5g24530RTF	TGATCGATCTTTTCTCATCCAA	For Real Time expression analysis
46	At5g24530RTR	TTGTTAACTCCGTGATTTATGACC	For Real Time expression analysis
47	At3g27690RTF	GCGTCGTACCGTCAAGTCTAC	For Real Time expression analysis
48	At3g27690RTR	GGAAAATGGTCCTAGGTATTTGG	For Real Time expression analysis
49	At2g18660RTF	TCGATGCATTGGTGCTACAT	For Real Time expression analysis
50	At2g18660RTR	TCCCGGCAGAAATCAACTAC	For Real Time expression analysis
51	ELF4RTF	TGAAGAGGAACGGCGAGA	For Real Time expression analysis
52	ELF4RTR	CGGTCAAGATTCTCCCACAT	For Real Time expression analysis
53	COL9RTF	CTAAAGTTTCTGGATTCAACTTCTGA	For Real Time expression analysis
54	COL9RTR	TGTTCACCACAGAAGTCACACA	For Real Time expression analysis

Table S2: Polypeptide sequences of MATE proteins identified from rice and present in *Arabidopsis* and other plants

S.No.	Locus ID	Amino acid sequences
1	Os01g31980	MGSSDSQAPLLLPRGSHRKEEEEEEYAAAGKVRGCCGGDGEGGWWREATAEAGRLASLAAPMIAVALLQLMMQLISTVMVGHLGEVALAGAAIANSLTNVSGFSVLMGLACGLETICGQAYGAEQYHKLALYMYRSIIVLLVVSVPIAIIWVFIPEVLPLIGQQPEIASEVGKYALWLIPGLFAFTVAQCLSKFLQTQSLIFPMVLSSSITLALFIPLCWFMVYKVGMGNAGAALSVSICDWVEVTVLGLYIVLSPSCEKTRAPLTWEAFSGIGSFLRLAVPSALMICLEWWSYELLVLLSGILPNPALETSVLSICISTVVLVYNLPHGIGTAASVRVSNELGAGNPEGALVVGVALSVILCSAVLVSVTLLALRHFIGIAFSNEEEVINYVTRMVPVLSISVITDSLQGVLSGVSRGCGWQLGAYVNLGAFYLVGVPVALFFGFAMHLGGMGFWMGMVAGGATQVTLLSIITAMTNWRKMAEKARDRVFEERIPTQSV
2	Os01g49120	MAAAAREEQPLLLRREEGEEEGEEVGWRRRWGSEAGKLAYLALPMVAVSLTNYAVQVFSNMMVGHLPGVLPLSSAAIATSLASVTGFSLLIGMASALETLCGQAYGAKQYHTLGVHTYRAILTLLVVCIPLSLLWVFMGKILVLIGQDPLISHGAGRYIVWLIPGLFANALIQPITKFLQSQSLIMPMLVASVATLVFHIPLCWLMVFKTGLGYTGAALSISISYWLNVAMLVAYILLSSSCKETRTPPTIEAFKGLDGFLRLALPSALMICLEWWSFELLILMSGLLPNPELQTSVLSICLTSITLLFTIPYGLGAGGSTRVANELGAGNPEGARSAVYVVLSVAVTEALIVCGTLLASRRLLGRAYSSEEEVISFVAMMVPLVCITVVTDGLQGVMSGIARGCGWQHLGAYVNLGSFYLLGIPMAILLGFVLHMGAKGLWMGIVCGSISQITLLSAITFFTNWQKMAENARERVFSEKPTEPSRYHLVE
3	Os01g56050	MAPPAGTEAAGAGHRKNWRGESGNLWRIAGPVILTEIFQFLIGFVTAAFVGHIGKVELAAVSVVNGVVEGLAFGLLVKNHARTLGMGSALETLCGQAVGAGQPRMLGVYLQRSWVICLATSLALLPLYLLASPALRLLRQSAAISSVAGRYARWCAPQLFAYAVNFPMQKFYQAQSRVWAVTAISAAALAAHALLNWLVVARLGHGVVGAALVGDVSWWLLNAAQFAYLVGGSFPEAWSGFSRKAFTSLGGFVKLSLSSAVMLCLEMWYYTAVLILVGCLKNPEIQVGAISICMNYQLWTLMVAVGFNAAVSVRVANELGANHPKAAKFSVIVAVVTSAAVGLVFTLVALVARKQLPRLFTDDDVLVRETAKLGYLLAATIFLNSIQPVLSGVAIGAGWQSSVAFVNIGCYYLVGLPIAAVFGFRLSLNATGIWVGMLIGTILQTVILLVILYRTKWQKEAMLAEERIKVWGGGVELPTIQEAS

4	Os01g69010	MARSSSAPESMEADHQLTATVTAAASGDMPVTEQQQQKQMVAVAAPPATENADAAGGGGGDNGDHLPPTATSLLGGARRTGLHLFVLNARSALRLDELGAEVLRIAVPASLALTADPLASLIDTAFIGRIGSVEIAAVGVAIAVFNQVMKVCIYPLVSVTTSFVAEEDAILSKGAAGADDDNDDGHDAKGHGASAAAVADPEKQQVVGVDSAETNGAEVSTAAVRTTDDKKAAAAGVGVGKCRRRFVPSVTSALIVGAFLGLLQAVFLVAAGKPLLRIMGVKPGSPMMIPALRYLVVRSLGAPAVLLSLAMQGVFRGFKDTKTPLYATVTGDLANIALDPILIFTCRFGVVGAAIAHVISQYLITLIMLCKLVRKVDVIPSSLKSLKFRRFLGCGFLLLARVVAVTFCVTLAASLAARHGATAMAAFQICAQVWLASSLLADGLAVAGQALLASAFAKKDHYKVAVTTARVLQLAVVLGVGLTAFLAAGMWFGAGVFTSDAAVISTIHRGVPVGVAAVTIPCLVLLSSHGGFVGIWIALAIYMSVRAFASTWRMGAARGPWKFLRK
5	Os02g02980	MSAHLRLLSAAPLPALLPTRRLPAVPTPALAARAARLVLSRPLTEPQPPRLPRGAAARCRGVAVAGADGDEPAAAAAGTAGLWEQVRDIVVFAGPALGLWICGPLMSLIDTMVIGQTSSLQLAALGPGTVFCDYLCYIFMFLSIATSNMVATSLAKKDEELAQHQVSMLLFVALTCGLGMFLFTKLFGTQVLTVFTGSGNYDIISAANTYAQIRGFAWPAVLVGLVAQSASLGMKDSWGPLKALAAASVINGVGDLLLCSVCGYGIAGAAWATMVSQIVAAFMMMQNLNKRGFRAFSFTIPSSSELLQIFEIAAPVFITMTSKVAFYALLTYSATSMGAITLAAHQVMVNVLCMCTVWGEPLSQTAQSFMPELIYGAKCNLMKARMLLKSLVMIGAITGTTVGAVGTLVPWLFPSLFTNDFMVVQQMHKVLIPYFCALLVTPSVHSLEGTLLAGRDLRFLSQSMGACFGIGTFLLMIIRNKFGSLPGCWWILVLFQWGRFGSALQRLLSPTGMLYNENFNNHHDEYVKVKAT
6	Os02g45380	MSSPRRDGRGAVDDLTASLLHKGDGGEAVFVVVVVPPVAEEEEPPPVLTCKPPGRFARAVKEAWSVPFPMMPSMSAGAAGAEARSILGLALPMILTGLLLYLRSMISMLFLGRLGGLALAGGSLAIGFANITGYSVLSGLAMGMEPICGQAFGAGHYDLLGVTMQRTVLLLVAASVPIAGLWVHMRPLLLLCGQDAAIAAVAETYILASLPDLLLQAFLHPVRIYLRTQSINLPLTVCAALAIALHLPINYVAVSVLGLGIKGVALASVLANLNLVLFLFGYIWFKGVHKRTGGFALSADCLRGWGELVSLALPSCISVCLEWWWYEIMILLCGLLANPQATVASMGILIQTTSLIYIFPSSLGFGVSTRVSNELGANRPERACRAATVGLMLGFAFGGVASAFACHVRGAWATMFTADPAIVALTASVLPILGACELGNCPQTTGCGVLRGSARPKDAASINLRSFYLVGTPVALILAFWYHYDFRGLWLGLLAAQATCVVRMLLVIGETDWTAEAKRAQQLTGAADIKDCGGKGDHVAVIEQPDEQC

7	Os02g57570	MAYTEPLLLSARHTTQTSPRHHLLRSRHAAAAAADGRMVVAVQDDETGALVAAVGKGDEDDDDDDAVAGEEDEDEDDAPVVRTARGAWEVFAAESRRLWAIGAPIAFNVICLYGTNSTTQIFVGHIGNRELSAVAIGLSVVSNFSFGFLLGMGSALETLCGQAFGAGQVAMLGIYMQRSWIILAASAALLSPLYVFAGPILRLLGQEESIAAAAGEFTVRIIPQMFALAINFPTQKFLQAQSKVTVLAWIGFAALLAHVGLLALFVSALGWGIAGAAAAYDVSSWLTALAQVAYVVGWCRDGWTGLSRKAFNELWAFVKLSLASAVMLCLEIWYMMVLVVLTGHLDDAEIAVDSISIWYSLLP
8	Os03g08900	MGDGRGDEEECRVALLNGGGAAKEGWQVVSGGDGKLRRRVWEESRKLWVIVAPAIFSRVVTYSMNVITQAFAGHLGDLELAAISIANTVVVGFNFGLMLGMASALETLCGQAFGAKKYHMMGVYMQRSWIVLLACAVLLLPMYIYAEDVLLLTGQPPELSAMAGRVSVWFIPLHLSFAFLFPLQRFLQCQMKNFASAAASGVALCVHVAISWLLVSRFRFGLVGIALTLNFSWWATAAMLFAYVACGGCPETWNGLSLEAFAGCHAMLLTEFVCLICSLENWYYRILILLTGNLKNAAIAVDALSICMTINAWELMIPLAFFAGTGVRVANELGAGNGKGARFATIVSSVTSLVIGLFFWVLIVGLHDKFALIFTSSDVVLDAVDNLSVLLAFTILLNSIQPVLSGVAVGSGWQSMVAYVNIGTYYLIGIPMGILLGWLFKLGVLGIWAGMIGGTAVQTLILAIITIRCDWDKEAMIASTRMDKWSQVR
9	Os03g11734	MAGLKKMEEVTAAAAAVAASSTAEKRAAAVVVPDAALTMNGAAGAEEKTAAAAAAPEDLPAPAALSGWPRRVGLYLFVMNIRSVFKLDELGSEVLRIAVPASLALAADPLASLVDTAFIGRLGSVEIAAVGVSIAIFNQVSKVCIYPLVSVTTSFVAEEDAIISKCIEENSSQDLEKASPVDSETNNLPVSGPDKVECVNSCIPTECTNPSDQGCKRKYIPSVTSAVIVGSFLGLLQAVFLVFSAKFVLNIMGVKNDSPMLRPAVRYLTIRSLGAPAVLLSLAMQGVFRGFKDTKTPLYATVVGDAANIILDPILMFVCHMGVTGAAVAHVISQYLITMILLCRLIRQVDVIPPSLKSLKFGRFLGCGFLLLARVVAVTFCVTLASSLAARHGPTIMAAFQICCQLWLATSLLADGLAVAGQAVLASAFAKNDKGKVVVATSRVLQLSIVLGMGLTVVLGVGMKFGAGIFTKDIDVIDVIHKGIPFVAGTQTINSLAFVFDGINFGASDYTYSAYSMVGVAAISIPCLVYLSAHNGFIGIWIALTIYMSLRTIASTWRMGAARGPWVFLRK

10	Os03g12790	MCNSGTSSSPSAPAPPPPPLTSFKHSSHLLRLVDDDADDGHALLLSKVAGEAQAIGRVSVPMAVTGLVMYSRALISMLFLGRLGELALAGGSLALGFANITGYSVLSGLALGMEPICGQAFGARRGKLLALALHRTVLLLLAVALPISLLWVTSTGYILKQLGQDEGVADAAQTFAAYASADLAVLAVLHPLRVYLRSQNLTLPITACSLFSVLLHGPINYLLVVRLRMGVAGVALAVALTDLNLLLALLCFLAISGAHRDSWVGPTSDCLRGWPALLRLAVPTATAVCLEWWWYELMIVLSGLLANPRATVASMGILIQATSLVYVFPSSLGQGASTRVSHQLGAGRPAGARRAAGAALSIGLVVGAAAATFMVSVRSHWGRMFTSDGEILRLTAVALPIAGLCELGNCPQTAGCGVLRGSARPASGARINLASFYLVGMPVGVALAFGARLGFAGLWLGLLAAQAACAVWMARAVAATDWDVEVARAKELTKASTTGSGTNHQHECNNSNTNTANAKANTKTTTSPAANNINAGGGGSSDNRGYVPISESGHNDGSDDLEKLEEGLMVATSGGCCGCGDALGVDTKAGDKQQCSNGGAGTAEGNAGQRRGSASSERAPLISVGDDEEAGEENDGDGGGGGHV
11	Os03g37411	MAGGDQRGDSPSSHELSGRLEGILADGEAPWARRACKAAALEVRLLAPIAAPAIVVYVPNNVLSISTQIFCGHLGNLELAASSLGNNGIQIFAYGLMLGMGSAVETLCGQAYGVHKYDMLGVYMQRSTVLLMATGVPLAVIYAFSRPILVLLGESPEIASAAAVFVYGLVPQIFAYAANFPIQKFLQAQSIVAPSAYTSAATLVLHLVVGWLVVYQLGMGLLGASLVLSLSWWVIVAAQFVYIAASKRCRRTWTGFSWMAFSGLPEFLKLSTASAVMLCLETWYFQILILLAGLLDDPQLALDSLTVCMTLAGWVMMISIGFNAAASVRVGNELGAGHPRAAAFSVVVVTAVSFVITVVMAVVFLMFRDYISYIFTEGETVARAVSDLCPFLAATLILNGIQPVLSGVAVGCGWQKIVAYINVGCYYFVGIPLGFLLGFKFHLGAKGIWTGMLGGTCMQTLILFWITFRTDWNKEVEEAKKRLNQWEDKKQPLLAGTVDY
12	Os03g37470	MATTAASPEIAGAARLYVVGLIPQIFAYAANFPIQKFLQAQSIVAPSAYISAATLAAHVALSWFAVYKLGLGLLGASLILSLSWWVIVLAQFAYIVVSDRCRLTWAGFSSKAFSGLPEFLQLSAASAVMLCLETWYFQVTVLIAGLLKDPEIALDSLAVCMSISGWVFMVSVGFNAAASVRVSNELGAGNPRAAAFSVKVVTSLSLIVAAIIAAIVMCLREYLSYVFTQGEEVARAVSSMTPLLAVTIVLNGIQPVLSGVAVGCGWQAFVAYVNIGCYYIIGVPFGCVLGFHFDLGAMGIYGGMIVGLFVQTLILVYVTFRTDWNREVGEAKKRLNKWGDIAKPLLANED

13	Os03g37490	MGSSVKDAGGGKEEQQQQLESPLLEAAVSSGGGDGGGGHGVSGELESILGDETVPWARRMWAATGVEMRLMLRLAAPAVLVYMINYLMSMSTQIFSGHLGTLELAAASLGNTGIQVFAYGLMLGMGSAVETLCGQAYGAHKYDMLGVYLQRSTVLLMATGVPLAVIYAFSRPILVLLGESPEIASAAAVFVYGLVPQIFAYAANFPIQKFMQAQSIMAPSAYISAATLAFHLVLSYLVVYQFGLGLLGASLMLSISWWVIVVAQFIYIVTSRRCRLTWTGFSMLAFSGLPDFFKLSLASAVMLCLETWYFQILVLIAGLLKDPEMALASLSVCMTISGWVFMISVGFNAAASVRVSNELGAGNPKSAAFSVVVVTVLSFFLSVVISLVILLCRDYISYIFTDGEDVATAVSKLTPLLALTLILNGIQPVLSGVAVGCGWQAFVAYVNVGCYYIVGIPLGCLLGFYFDLGAAGIWSGMIGGTLMQTLILMWVTFRTNWNREVEEAMKRLNKWEDKTPLLSE
14	Os03g37640	MAGGVSDGGAAHGASGRLESILSDSSMPLARRAWAATTIELGLLTRIAAPAVVMYMINYLMSMSTQIFSGHLGNLELAAASLGNNGIQMFAYGLMLGMGSAVETLCGQAFGAHKYDMLGVYLQRSAVLLTITGVPLAVIYGFSEPILVFMGQSPEIARAAAIFVYGLIPQIFAYAINFPIQKYMQAQSIVLPSAYISAATLALHVLLSWVVVYKVGLGLLGASLVLSISWWVIVAAQFAYIVTSPTCRHTWTGFTWQAFAGLWDFLKLSAASAVMLCLESWYFQVLVLIAGLLPNPELALDALSVCMTISGWVFMISVGFNAAASVRVSNELGAGNPKAAYFSVWVVTISCAIISAILAVVILCLRNYISYLFTEGEVVSNAVADLCPLLAITLILNGIQPVLSGVAVGCGWQQFVAYVNIGCYYIVGVPLGVLLGFVFKLGVKGIWGGMLGGTCMQTAILVWVTLRTDWNNEVEEAQKRLNKWEDKKKEPLLTGIRDNN
15	Os03g42830	MGKLVSKSWQESKLLWHIAFPAILTAVFQFSIGFVTVGFVGHIGQVELAAVTVVENVIEGFAYGVLLGMGSALETLCGQAVGAGQVSMLGVYIQRSWIICGATAVILTPTYVFTAGILIGLRQPTDIAAVAGTYTRWVIPQLFAYAANFPLQKFFQSQSKVWAMTAISGIALALHVVLNYIFLTRLGHGLVAAALIGNVTWWLIILAQFIYLVSGCFPEAWKGFSMLAFKNLAAFVKLSLASAIMLCLELWYYTAVLILVGLLKDAKLQVDVMSVCINYQLWTLMVALGFNAAVSVRVSNELGANRPKAAKFAVAMAVSTSAIVGAVFMAVFFIWRTQLPRFFSDDADVVRESAKLGYLLAATIFLNSIQPVLSGVAIGAGWQSLVAFINIGCYYLVGIPLGVLFGFKLKLDAMGIWVGMSLGTLLQTAILAFISFRTKWERQAMMAEERIREWGGRNDDALPSTTTPTADDHNVDR

16	Os03g62270	MAIPLQGKAQQQQGEGGKGDGAVDDDGDDQPSVASELRELWGMAAPITALNCVVYLRAMVSVLCLGRLGPLDLAGGALAIGLTNITGHSVLFGLASGLEPLCAQAFGSKNYDLLTLSLQRAVLLLTLAALPIALLWLHVGPILVALGQDPTISASAAAYAAYALPDLAASAVLQPLRVYLRSQGITKPMAACSAIAVALHVPLNVLLVFGLGFGVRGVAAAQALTNTNMVLFLLAYIRWSRACDATWKGWARPAAVASGLAGLVRLAVPSCVGVCLEWWWYEVVTVLAGYLPDPAAAVGAAGVLIQTTSLMYTVPMALAACVSTRVGNELGGGKPRRARMAAMVALGCAVVIGVVHVAWTAAFSREWVELFTREAAVVRLAAAAMPILGLCELGNCPQTTGCGVLRGTARPAVGARINLLSFYLVGTPVAVTLAFGARVGFGGLWYGLLSAQAACVALVLLAVVWRTDWHLEALRAKKLTGLEMIAAAAEGDDDECKRLIAPLPPPDGHDVAVDVV
17	Os03g64150	MTPPPPSPPHERKTWAESVASEFRAQRGIAFPLIAMNLTWFAKLAVTTAFLGRLGDLQLAAGTLGFSFANVTGFAVLTGLCAAMDPICGQAHGASNGKLLRKTLVMATILLLGASIPIAFLWLHVDAVLLRFGQQADMSSNARSYVVCLLPDLAVTSFVNPLKSYLSAQGVTLPTLFASALALALHVPLTMWMARTRGIQGVATAVWVSDLAVAVMLAGYVLVSERRRKAGGGGGWVEQTRGEWVRLLRLAVPSCLNTCLEWWCYEILVLLTGRLPDARRTVAVMAVTLNFDYLLFAGMLSLSVSASVRVSNELGAGEAWAARRAGMVSIVGGAVGGVGGGVAMVAARRAWGSIYSSDAGVREGVGRAMEVMAVLEVVNFPLNVCGGIVRGTARPAVGMYAVVAGFYVLALPLGVALAFKARLGIQGLLLGFLVGAAASLAVLLTFIARMDWPAEAQKARTRTTATVAQFHQHDEVVQP
18	Os04g30490	MAAPPSMEEPLLGGGNGEEKKGGSSRLAVVAEVRKQLYLAGPLIAGWLLQNVVQMISVMFVGHLGELELSSASIATSFAGVTGFSLLAGMASSLDTLCGQAFGAKQHRLVGVYKQRAMVVLGLASVCVAAVWAYTGELLLLFGQDPEIAAAAGSYIRWMIPALLAYGPLQCHVRFLQTQNAVMPVMLSSGAAAACHLPVCWLLVYGAGLGSKGAALANAVAYLANAAALAAYVRLSPACRSTWTGFSSEAFHDLVGFMRLAVPSALMVCLEWWSFELLVLLSGLLPNPKLEASVLSICLNSGSLAFMIPFGLGSAISTRVSNELGAGRPEAARLASRVVMALGLVVGVAIGLAMILVRHLWGYAYSNEEEVVQYVAKMMPILAVSFLFDDLQCVLSGVARGCGWQKIGAIVNLGAYYLVGIPAALCFAFVYHLGGMGLWLGIMCALIVQMLLLLAITVCTNWEKEALKAKERVFSSSLPADMT

19	Os04g48290	MTTCADDQTGCAFFAPLLSSKGAEVVILVAGDEAEEQQPAPVLTSKPPGRLAKAVNEAWSVSLGVAFPVTPSMFTCSARGEARSILGLAFPMILTGLLLYLRSMISMLFLGHLGGLALAGGSLAIGFANITGYSVLSGLAMGMEPICGQAFGAGNYALLGVTMQRTVLLLIAAAIPIGGLWVQMRPLLLFCGQDAAIAAVAETYIFASLPDLVLQAFLHPVRIYLRTQSINLPLTVCAGLAIAIHLPINYVLVVVLGLGVKAVALASVLANLNLVLFLLAYIFLKGVHKRTGGFLLSAESFRGWGELISLALPSCVSVCLEWWWYEIMILLCGLLLNPQATVASMGILIQTTSLIYIFPSSLSFGVSTRVSNELGAGQPEEASRAATVGLVLGFGFGAFASAFAFLVRNVWASMFTADPAIVALTASVLPILGLCELGNCPQTTGCGVLRGSARPKDAASINLRSFYLVGTPVALVMAFWFHLDFRGLWFGLLAAQATCTVRMLLVIGRTDWAAEAKRSKQLTGAGAANMESDDRVAADEKSRLPVDTDVERSSDHTDRC
20	Os05g48040	MEERIPLLSKRFPADGTAGVGGGREEEGGDRWWSGLAREAGKVGSMALPMAAMSVAQNAVQVASNMMVGHLPGVLPLSASAIATSLASVSGFSLLVGMASGLETLCGQAYGAKQYDKLGVQTYRAIVTLTVVTIPISLLWVFIGKLLTLIGQDPVISHEAGRYIVWLIPGLFAYAVCQPLTKFLQSQSLIFPMLWSSIATLLLHIPLSWLLVFKTSMGFTGAALAISISYWLNTFMLAAYIRFSCSCKVTRSPPTIEAFRGVGLFLRIALPSALMLCFEWWSFEILVLLSGLLPNPELESSVLSICLTTTSLMYTIPYGLGGAASTRVANELGAGNPEGARSAVHLVMSIAGTEAVLVTGMLFAAQRILGYAYSSDEEVVTYFTSMVPFVCISVAADSLQGVLSGIARGCGWQHLGAYVNLGSFYLVGIPVALLLGFGFKMEGKGLWLGIACGSVLQFLLLAVIAFFSNWQKMAEKARERIFGETPSEKQHLVLDATNSV
21	Os06g29844	MAAKGSPEEEALLAGVGGDHQLVESDELAPAAAVVREEVKKQLWLAVPLVAGALLQNVIQMISVMFVGHLGELPLAGASMASSFASVTGLSLLLGMASALDTLCGQAFGSRQYHLLGVYKQRAMLLLTAVSVPLVVVWFYTGDILVAFGQDADIAAEAGAYARWMIPALFAYGPLQCHVRFLQTQNVVLPVMASAGAAALCHLVVCWALVYAAGMGSKGAALSNAVSYWINVAILAVYVRVSSSCKKTWTGFSMEAFHDPLSFFRLAIPSALMVCLEMWSFELIVLLSGILPNPKLETSVLSISLNTAAFVWMIPFGLGSAISTRVSNELGAGRPRAARLAVRVVVFMAVSEGLVIGLVLVGVRYIWGHAYSDEEEVVTYVAKMMLVIAVSNFFDGIQCVLSGVARGCGWQKIGACVNLGAYYIVGIPSAYLIAFVLHVGGMGLWLGIICGLLVQVLLLMAITLCTNWDKEAANAKDRVFSSSLPSDLAT

22	Os06g29950	MASALDTLCGQAFGAQQYHLLGIYKQRAMLLLTAVSVPLAVVWFYTGDILRLFGQEADIAAEAGTYARWMIPALFAYGLLHCQIRFLQTQNVVLPVMAAAGATALCHLLVCWVLVYAAGMGNRGAALSNAVSYWINVAILAVYVRVSSSCKKTWTGFSTEAFRDALGFFRLAVPSALMVWSSSQPKAADVRAINQPQHCFLGVDDPLWPRLCHKSKQEIERDGRWTPILRRPKGSGWIGAAIAIITTGNHRLVTATISTTHAIFTIRGDENIGGFTWQLGVIFDKYGERFINRDNHHEVFILGVQTFEHVVGRLIEVSVELAITFNRRTRVSNELGAGRPHAACLAVRVSVFMAISEGLVIGLVLISVRNIWGHAYSNEEEVVKYVGKVLLVISVSNFFDGIQCVLSGVARGCGWQKIGACVNLGAYYIVGIPSAYLIAFILHLSGMGLWLGITCGILVQVVLLMAFTLCTNWDKEAANAKHRALNSSLPSDTAT
23	Os06g29994	MEKASCLEEALLLPESCKEEEITASDEVKRQLRLAGPLIAGSLLQNLIQMISVMFVGHLGELPLAGASMASSFAAVTGFSLLLGLASALDTLCGQAFGARQYHLLGVYKQRAMLLLTAVSVPLAVAWYYTGDILLLFGQDADIAAEAGAYARWMIPALFAYGPLQCHVRFLQTQNMVVPVMAAAGAAALCHLGVCWALVHAAGMGSRGAALGNAVSYWINVGVLAVYVRVSRSCKKTWTGFSMEAFRDPLSFFRLAIPSALMVCLEWWSFELLVLLSGLLPNPKLETSVLSITLNTANCLFMIPFGLGAAISTRVSNELGAGRPRAARLAVRVVTLLATLEGLGMALVLACVRYVWGHAYSNEEEVVAYVAKMMLVLAVSNFLDGIQCVLSGVARGCGWQKIGACINLGAFYVVGVPAAYLAAFVLRAGGLGLWMGIICGVAVQTLLFLAITSRTDWQKEAKMAKDRVFSSSLPTDLAT
24	Os06g36330	MCTTTSAPSVPEVATPADGGGHHVYVSLPQCTDGGDVEGGHCRPVVHQVKCRGGDDDGGGGGRGGGVVMPAAGETVREAAALCRLACPIALTALMLYSRSALSMLFLGSLGDLPLAAGSLAVAFANITGYSVLSGLSLGMDPLCSQAFGARQPRLLGLTLYRSVLFLLCCSLPLSALWLNMAKILLFLGQDRDITAMAQDYLLFSLPDLFSFSLIHPLRVYLRSQGITQPLAVAAAAAVVFHVPANYVLVGRLRLGAPGVAAAASASNFVLLAVLLAYVARRDEALREAGGPTAEWLAGWGPLARLAAPSCVSVCLEWWWYEVMILLCGLLPEPRPAVASMGVLMQTTALVYVFPSSLGFGVSTRVGNELGANRPGRARAAAHVAVAGAAAMGLAAMAFATGMRHAWGRLFTADADILRLTAAALPVVGLCELGNCPQTVGCGVLRGTARPARAAHVNLGAFYLVGMPVAVVLAFGLGVGFVGLWVGLLAAQVCCAGLMLCVVGSTDWEAQARRAQALTSSAAVSGKADAAEGGGRWPEKGEHQEWEKRRHVALISSEEADPETAEVL

25	Os06g49310	MSGGGGEVEAAAEAAPLLVPHDPQPAVGAEVRRQVGLAAPLVACSLLQYSLQVVSVMFAGHLGELSLSGASVASSFANVTGFSVLLGMGSALDTFCGQSYGAKQYDMLGTHAQRAIFVLMLMGVPLAFVLAFAGQILIALGQNPEISSEAGLYAVWLIPGLFAYGLLQCLTKFLQTQNIVHPLVVCSGATLVIHILLCWVMVHCFDLGNRGAALSISLSYWFNVILLAIYVKVSEVGRRSWPGWSREALKLKDVNMYLRLAIPSTFMTCLEYWAFEMVVLLAGFLPNPKLETSILSISLNTMWMVYTIPSGLSSAISIRVSNELGARNPQAARLSVFVSGIMCLTEGILVAIITVLVRDIWGYLYSNEEEVVKYVAAMMPILALSDFMDGIQCTLSGAARGCGWQKVCSVINLCAYYTIGIPSAVTFAFVLKIDGKGLWLGIICAMTVQILALVVMLLRTSWNEEAEKARARVQGSDGRITLA
26	Os07g01750	MQDQRAGPAKSKEKKRVSRHKQAKLTTVIIKAVPLTTKELRQKKSELRVERRRVKMGGDERAVAAPLLQQQQDGGGGDGERRRRRWWWGWWDGEEAAGQLAFAAPMVATSMAYYAIPLVSVMYAGRLGELELAGATLGNSWGTVTGIALMPWLNIRGVLAAKGLQKDKLDTGLSGSLETLCGQGYGAKMYHMMGVYLQASIITSAFFSVLVSLLWFYSEPVLIFLRQDPEVTRTATLFLRYSIPAQFAYGFIQCTLRFLQTQSVVTPLVVFALLPLVLHFGITHAFVHYLGFGYAGAGMSTSVSLWLSFLMLAAYVCLSERFKHTWEGFSTEAFRHVLPGLKLAIPSAVMVCFEYWAFEVLVLVAGLMPNSHMSTSIIAMCENTEAISYMITYGFAAAISTRVSNELGAGNVAKAKKALAVTLVLSLLLGVAFLLLLGLGHDLWAGLFSKSDAVISEFASMTPLLIGSVVLDSTQGVLSGVSRGCGWQHLAAWTNLVAFYIVGLPLSILFGFKLGLQTKDQMGKIRADNERQRRRFCLLRLERSELTSLAAAYASLVESNIEVKSFRA
27	Os07g31884	MSHFRQVRGAHAASSLLPFSHRPPRATTTTTPPRPNRCRRLHIHSSASHHHIHNQLRHRRASHHRRREIVVVVVRCSGRDDDGVMASTDPLLGGKEEEEGGGEVRRARRWWVGRVVDTEEAWAQTRFAVPMVLTNMSYYAIPLVSVMFSGHLGDVHLAGATLGNSWATVTGYAFVTGMSGALETLCGQAYGARMYRMLGLYLQSSLLMSAAVSVLVSALWCFTEPLLLLLRQDPAVSAAASAFVRAQVPGLFAFSFLQCLLRYLQTQSVVAPLVACSLAPFLLHVALAHLLVNALGLGLAGAGAAVSITFWASCLMLLAYVLRSERFAETWNGFSAEAFRFVVPTIKLATPSAVMVCLEYWAFELLVLIAGLLPNPTVSTSLIAMCSSTEAIAYMITYGFSAAVSTRVSNEIGAGNVEGAKNAVAVTLKLSVFLAAAFVLLLGFGHGLWAGLFSGSAIIAAEFAAVAPLMMASILLDSAQGVLSGVARGCGWQHLAAVTNLVAFYVIGMPLSIFFAFKLKWYTKGLWMGLICGLTCQTCTLMVITARTKWSKIVDAMQEKKASYVA

28	Os07g33310	MGHAVDGRLEALLSGGGGGGEAAAPWARRMAAAAALELRLLAPLAAPAVVVYMLIIVMSSATQIFCGQLGNVQLAASSLGNNGIQVFAYGLMLGMGSAVETLCGQAYGAGRHEMLGVYLQRSAVLLTAAGVPLAALYACSERVLLLLGQSPEISRAAAGFARGLIPQIFAYAANFPIQKFLQAQSIVAPSAAVLAASFALHLPLSWAAVRVLGLGLPGAALALSATWWVLVAGQFAYIVRSPRCAATWTGFTWAAFHDLAAFARLSAASAVMLALEVWYFQVLILLAGMLPDPQIALDALTVCTSIQSWVFMISVGFNAAASVRVGNELGAGNPRSAAFSTWMVTALSAIIAAIAGVVVILLRDKLSYIFTQGEAVSRAVSDLCPLLVGTIVLCGIQPVLSGVAVGCGWQALVAYINIGCYYLIGLPLGVLLGFKFDYGIKGLWGGMIGGTLIQTLILIWITFRTDWNKEVEDARRRLDKWDDTKQPLLVNRQ
29	Os08g37432	MEDEATSVAAPLLRPRGGVDAEAVKQQLWPAGARVAGEWWVESKKLWRVVGPAIFQRIALYGINVVSQAFIGHMGDLELAAFSIASTVVAGFNFGFLLGMASALETLCGQAFGAKKYHMLGVYLQRSWLVLLMFAVALTPTYVLMEDLLLLIGQPADLASLAGKMSVWLLPQHFAMAMLLPLTRFLQSQLKNWVTAVTAGVALALHLVITYLLVNTLHLGLLGAVAAANVAWWIVVLGQLVYVVGGWCPLSWKGFSMEAFADFWEFIKLSSASGVMLCLENWYYRVLVLLTGYLNNAEIAVDALSICLTINGWEMMIPFGFLAATGVRVANELGAGSGKGARFAIVVSVTTSVAIGLVFWCLIIAYNDKIALLFSSSKVVLDAVSDLSVLLAFTVLLNSVQPVLSGVAIGSGWQALVAYVNVGSYYLVGVPIGAILGWPLHFGVGGIWSGLIGGTAVQTLILAYLTISCDWDEEAKKASTRMEVWASSK
30	Os08g43250	MCHCSSKVVAVAQCHQPLLPPPEACPALHDRPRSARGGGGAIAEVASIVRLAMPMVGAGLLMYMRSLVSMLFLGRLGRLPLAGGSLALGFANITGYSVLSGLAAGMDPVCGQAFGAGRTSVLAAALRRTVVLLLAASVPIAALWLAMHRVLVAAGQDPDIAACAYEFILCSLPDLAVQSFLHPLRVYLRAQSITLPLTYAAAAALALHVPVNVLLVHGLGLGIRGVALAAVWTNLNFLLFLVAYAYFSGLIRGDDDDDGGNGKAGEEGATTTTTTMEWGWLVKLSVHSCMSVCLEWWWYEIMVLLCGVLADPKAAVAAMGILIQTTSLLYIFPHSLSCAVSTRVGHELGAGRPERARLAARVGLACGAALGVVACAFAASLRGVWARMFTADATILRLASSALPILGAAELGNCPQTVGCGVLRGSARPGRAARINVSAFYGVGMPAALALAFWPARLDFRGMWAGMLAAQLVCAALMLLAVRRTDWDEQAARAREITGAVAGVVVGDGDVVVKGDHADAAKVKADSGLLVVTVLS

31	Os08g43654	MSSTSGSAWDHSNNGGGGSPELREALLLGDGGSSPESREIKGIAVKKQDDLEEIRSVGELMRLAAEENRRLWYLAGPAIFTSLAQYSLGAVTQVFAGHLTTLELDAVSTENMVIAGLAFGIMYGMGSALETLCGQAFGAKQHHMLGIYLQRSWVILTAMSVILLPIYLFATPILRFFHQDDEIAVLASRFSLYMIPQLFAYALNFPIQKFLQAQSKVMAMAAVSAAVLLFHVALTWLLLVPLRMGLVGLAVALNVSWWLVVLGQLAYIVMGYCPGAWNGFDWLAFTDLLSFARLSLGSAIMICLEFWFYMFLIVIVGNLPNAQVAVAAVSICTNLFGWQIMVFFGFNAAISVRVSNELGAGRPRAARLAIAVVLVSSVAIGVAFFAAVLLLRDVYGAPFTGSPEVVRAVASLGVVFAFSLLLNSVQPVLSGVAVGAGWQWLVAYINLGCYYCVGIPVGYAIAFPLRRGVQGMWGGMLTGVGLQTAILVAITARTNWNKEASEAHARIQHWGGTAKLAVDDPI
33	Os08g44870	MGSVSPPAPEEDAAAVESAGAAARMFWHETKRLWAIGTPIAIGTITNYAISSVTTMFIGHLGNLPLAAASVGLSVFATFALGFLLGMGSALETLCGQAFGAGQVSMLGVYLQRSWIILLGATVLMVPVYVLAEPLLLLVGQDPEVARAAGRFTLYILPGAFAFAVNFPSGKFLQAQSKVGVLAWIGVAGLAFHVGITYLAVSVLGWGLPGAAAAYDVSQWASSLAQVAYIMGWCREGWRGWSMAAFHDLAAFLRLSIESAVMLCLEIWYLGLITVLTGDLDDAQMAVDSLGICMNINGYEGMIFIGLNAAISVRVSNELGSGRPRAAMHAVVVVVAESLLIGLLCMALVLAFSDKLALVYTSDAHLLRAVSRIAGLLGVTMVLNSVQPVLSGVAVGGGWQGLVAYINLACYYLFGLPVGYLLGYYFNLGVGGVWGGMLCGVALQTLILLFVVWRTDWKAEAAQASARVHKWGGTDETKPLLQGDHSDRD
34	Os09g29284	MASVPLLAEWPAGKEKEEGRVRRRLPALAREAWEESKKLWEIVGPAVFLRLVLYSFNIISQAFAGHIGDLELAAFSIANNVITGLNFGFLLGMASALETLCGQAYGAKQCSMLGIYLQRSWIILFVFAVLLVPTYVFTAPLLEALGQPAALARKAGMVSVYMLPSHFQYAVLLPLNKFLQSQRKNWVTVVTAAAAFPVHIAVSWLLVSRLRFGVLGAAMSLGVSGWLVTLLQLAYVVGGGCPVTWSGFSPLAFVDLWGFVKLSVSSGVMVCLETWYYKILILLTGHLKNSELAVNALSICMSFQSWEMMIPVGFLAGTGVRVANELGAGNGKGAKFATIVSTTTSFLIGLFFSALALAFHDKIALVFSSSNAVIDAVDNISFLLAVTILLNGVQPVLSGVAIGSGWQAAVAYVNIGCYYFIGVPIGVLLGWSFNLGVFGIWAGMIAGTAIQTIILAHMTIQCDWNKEVLQASERVQRWGNPK

35	Os09g35600	MASRHSDEATQCHQQLLVMPAATASYPKLHDRPRLAGAAAGVLGEVASILCLAGPMVGAGILLYLRSLVSMVFLGRLGQLPLAGGSLALGFANITGYSVLSGLAGGMDPVCGQAFGAGRTDLLRAALRRTVVLLLAASVPISALWVAMHRVLVATGQDPDIAATAYAYILCSLPDLAVQCFLHPIRIYLRAQSVTLPLTYAAAAALLLHVPINVVLVDRLGLGIRGVALGAVCTNLNCLLFLAAYVCLSGMYGGRAKACASAAAPAAGEEDDDGGVREWWSLVRLSVHSCMSVCLEWWWYEIMVLLCGVLADPKAAVAAMGVLIQTTSLIYIFPHSLGCAVSTRVGHELGAGRPERARLVARVGVGLGAALGIVAFGFAVSVRAAWARMFTAEDAILRLAAAALPLLGAAELGNCPQTAGCGVLRGSARPERAARINVAAFYGVGMPVALALAFWPAGLDFRGMWGGMLAAQLVCAWLMLRAVLGTDWAEQAERARELTGGGDGYAAVAAVIVDDDKAKQHAEMDKPQQVDNTLLMAIDCV
36	Os09g37610	MELAGGGTGVVRQRAEPLGAGLLLRGGGRSVGGGGIGCARRATLRGLALSPLARRAVSAAGGHFLPRRAVRAAAAAGDGGFYGEEDAASDQPFPARASPSDDANDSTAVRSLGGDHPGEIKKELLNLALPAIVGQAIDPVAQLLETAYIGRLGPVELASAAVGVSVFNIISKLFNIPLLSITTSFVAEDVARHDSDQFTSEGNMSSESGGRKRLPSISSAILLAAAIGVIEASALILGSEILLSIMGVSHASTMHSPAKLFLSLRALGAPAVVVSLAIQGIFRGLKDTKTPLLYSGLGNISAVLLLPFLVYSLNLGLNGAALATIASQYLGMFLLLWSLSKRAVLLPPKIEDLDFVGYIKSGGMLLGRTLSVLITMTLGTAMAARQGTIAMAAHQICLQVWLAVSLLSDALAVSAQALIASSFAKLDYEKVKEVTYYVLKIGLLVGAALALLLFASFGRIAELFSKDPMVLQIVGSGVLFVSASQPINALAFIFDGLHFGVSDFSYSASSMITVGAISSLFLLYAPKVFGLPGVWAGLALFMGLRMTAGFLRLGSRAGPWWFLHQKEPTYKLHSSTC
37	Os10g11354	MKAAAMEEPLIAGSSGGAAEKNGGEEEGLVVTEIKKQLYLAGPLVVGMLLQNVVQMISVMFVGHLGELALSSASMATSFAGVTGFSLLAGMASSLDTLCGQAFGAKQHHMLGVYKQRAMLVLALVSVPIAAVWAFTGEILLVVGQDPEIAAGAGSYIRWMIPTLFVYGPLQCHVRFLQTQSAVVPVMLSAGATAANHVLVCWLLVHRLGLGAKGAALANAVSFLTNLSVLAIYVRLSPACRRTWTGFSGEAFRDVLGFLRLAVPSALMVCMEWWSFELLVLLSGLLANPKLETAVLSICLNTNSFAFMVPLGLGAAISTRVSNELGAGRPQAARLATRVVMLLAFLVGTSEGLVMVIVRNLWGYAYSNEEEVADYIAKMMPILAVSILFDAIQCVLSGVVRGCGRQQIGAFINLGAYYLAGIPVAFFFAFVCHLGGMGLWFGILCGLVVQMLLLLTITLCTNWDKEALKAKDRVCSSSLPKDLAT

38	Os10g11860	MEGQGLVSRSWQESKLLWRVAFPAVLVELLQFSIGFVTASFVGHLGVVELAAVTAVESILEGFAYGVLFGMGCALDTLCGQAVGAGRLDVLGLYVQQSWIVCGATAVALTPTYAFAEPILRSLLRQPADVAAVAGPYALWSLPRLFAHAANFPLQKFFQTQSRVWALAAISAAVLAVHAALTYAAVVRLRYGLRGAAVAGNLSYWLIDAAQFVYLVSGRFPDAWKGFTMTAFSNLAAFVKLSLVSAIMICLEFWYYAALLILVGLLKNARLQLDIMSICINYQFWTMMVAMGFSEAISVRVSNELGARRPKEAKFSVAVASLTSAMIGAIFMSIFFIWRTSLPSLFSDDKEVVDGAARLGYLLAVTVFFGNIGPVLSGVAVGAGWQILVAFVNIGCYYLVGIPFGVLFGFKLKLGALGIWMGMLTGTLLQMAILFFIIMRTKWEAQAILAEKRISELGETTAND
39	Os10g13940	MNGESLLDRSSSADAAMNDAVPGHRHHHPLSVFLRDARLAFRWDELGREIMGIAVPGALALMADPVASLVDTAFIGHIGPVELAAVGVSIAVFNQVSRIAIFPLVSVTTSFVAEEDATSSDREKYEINGENEFNVSDSEMEELVSHEEASAAPSKSSFETDSSDVKIEHKRKNIPSVSTALLLGGVLGLLQALLLVICAKPLLGYMGVKQGSAMLMPALKYLVVRSLGAPAVLLSLAMQGVFRGLKDTKTPLYATVAGDATNIVLDPIFMFVFQYGVSGAAIAHVISQYFIASILLWRLRLHVDLLPPSFKHMQFSRFLKNGFLLLARVIAATCCVTLSASMAARLGSVPMAAFQICLQIWLASSLLADGLAFAGQAILASAFARQDHSKAAATASRILQLGLVLGLLLSIFLGIGLRLGSRLFTDDQDVLHHIYLGIPFVSLTQPINALAFVFDGINYGASDFGYAAYSMILVAIVSIIFIVTLASYNGFVGIWIALTVYMSLRMLAGFLRIGTARGPWTFYAAQRMHSHEVVGLC
40	Os10g20350	MSSALDTLCGQAYGAGQHRLLGVYAQRAMLVLAAAAVPIALVWASAGEILLLFGQDPAIAAEAGAYARWMIPSLAAYVPLACALRFLQAQGIVVPVMASSGVAAVGHVAVCWALVHKAGMGSKGAALSGAVTYWTNLAVLALYVRLSGACETTWTGFSIDAFRELRRFTELAVPSAMMVCLEWWSFEILVLLSGILPNPQLETSVLSICLSTSSLLFMVPRGIGSSLSTRVSNELGGGHPRAARMAARVAIAMTVLVCLVLVIAMIFLRNVWGNAYSSEEEVVAYIASMLPVLAVSFFIDGINGALSGVLTGCGKQNIGAHVNLAAFYLVGIPTAVLLAFVLHLNGEGLWLGLVCGSISKVGMLLFITLRTDWGKEAIMAKERVFSSSLPTR

41	Os10g20390	MASTAAEVKRLLRLAGPLMAGFVLRNSVQMVSVMFVGHLGELQLAGSSLAASLASVTGFSLLSGMSSALDTLCGQAYGAGQHRLLGVYAQRAMLVLAAAAVPIALVWASAGEILLLFGQDPAIAAEAGAYARWMIPSLAAYVPLACALRFLQAQGIVVPVMASSGVAAVAHVAVCWALVHKAGMGSKGAALSGAVTYWTNFAVLAFYARLSGACKTTWTGFSMNAFRELRRFTELAVPSAMMVCLEWSSFEILVLLSGILPNPQLETAVLSISLSTASLLIMVPRGIGSSLRVRTPHMTPYIISDVTHQYFISPGSKGLSQCST
42	Os10g20450	MEKPAASVEEPLLVGAGEKKGESAAAAELKRLLRLAGPLVASGVLRNVVQMVSVMFVGHLGELPLAGASLATSLANVTGFSLLFGMASALDTLCGQAYGARQHHLLGVYKQRAMLVLAVAAVPIALVWASAGEILLLFGQDPAIAAEAGAYARWLIPSLVPFVPLVCHIRFLQAQSAVLPVMASCGVTAASHVAVCWALVRKAGMGSRGAALANAVSYGVNLTIMSLYVRLSRSCEKTWTGFSMEAFRELRQYAELAIPAAMMVCLEWWSFEFLVMLSGLLPNPKLETSVLSICLNTGALLVMVPIGLSTAISTRVWNELGAGNPQAAKLATRVVICMAMTEGSVVAFTMILLRNSWGHMYSDEAEVVTYIARMIPVLAISFFIDGMHSALSGVLTGCGKQKIGARVNLGAFYLAGIPMAVFLAFVLHLNGMGLWLGIVCGSLSKLILLFWITMSINWEKESTRAKELVFSSSLPVA
43	Os10g20470	MAAAAVHEPLLAAAPPTPGKAADGDGPEEGRRLASAEAKRLLRLAGPIVASCILQCVVNMVSVMFVGHLGELPLAGASLATSLANVTGYSLLTGMATAMDTLCGQAYGARQYHLLGVYKQRAMVVLAAACVPIALVWASAGRILLLLGQDAGIAAEAGAYARWMLPSLAAYVPLQCHIRFLQTQTVVLPVTASSAATALLHPLVCWLLVFRAGMGSKGAALANAISYAVNLAILAVYVRASNTCKGRWSGFSGEAFKELRQFAALAMPSAMMICLEWWSFEILVLLSGLLPNPQLETSVLSICLNTGALLYMVPLGLCSSISTRVSNEIGAGQPQAAKRATRVVMYMALSEGLVISFTMFLLRNVWGYMYSNEQEVVTYIARMLPILDISFFIDGLHSSLSGVLTGCGKQKIGAAVNLGAFYLVGIPVAVLLAFYLHLNGMGLWLGIVCGSIIKLLVLIIVSCCIDWEKEAILAKDRVFSSSLPVA
44	Os10g37920	MCEALVDRQLLPPCGCNGGGDVVVVVVPKTSAAPVLEDRPKTSAAAVSKGGEAASILRLSLPMIMTGLILYIRPMISMLFLGRLGELALAGGSLAIGFANITGYSVLSGLAMGMEPVCGQAVGAGNLPLVGATMQRMVLLLLAVSVPVAFLWAWMEPLLLLCGQDAAIAAAAQRYILFCLPDLLFLSLLHPLRIYLRVQSINLPLTACAALAVAAHLPINHLLVSVLGLGIEGVALASAWANLNLVIFLLAFVYVSGVHRDTGGFSLPRKMFKDVDGWVRLVRLAAESCASVCLEWWWYEIMILLCGLLANPRATVASMGILIQTTSLLYIFPSSLSFGVSTRVSNELGANRPSAARAAARAGLALSAVQGLASLAFAVSVRGAWARMFTPDADILALTASVLPILGLCELGNCPQTTGCGVLRGSARPRDGAHINLGAFYGVGTPVAVGLAFWAGMDFRGLWLGLLAAQAACVAVMLVVIQRTDWDV

		QAKLAQVLAGAAASGGDHGVNEAGGNDAVAHVKVAAPHGDEDSSLLITVST
45	Os11g03240	MERTTEDDERPTVPLLEPKPASNEEEEEVGSVRRRVVEENKKLWVVAGPSICARFSSFGVTVISQAFIGHIGATELAAYALVSTVLMRFSNGILLGMASALETLCGQSYGAKQYHMLGVYLQRSWLVLFCCAVILLPVYIFTTPLLIALGQDPEISAVAGTISLWYIPVMFSYIWAFMLQMYLQAQSKNMIVTYLAFLNLGIHLFLSWLLTVKFQLGLAGVMGSMVISFWIPVFGQLAFVFFGGCPLTWTGFSSSAFTDLGAIMKLSLSSGVMLCLELWYNTILVLLTGYMKNAEVALDALSICLNINGWEMMISIGFLSAIGVRVANELGAGSARRAKFAIFNVVTTSFLIGFVLFVLFLFFRGSLAYIFTESKAVADEVADLAPLLAFSILLNSVQPVLSGVAIGSGWQSVVAYVNVTSYYLIGIPLGAILGYVLGFQAKGIWIGMLLGTLVQTLVLLFITLRTNWKKQVEITRERLNRWYMDENGRSQNSIGNA
46	Os11g03484	MEKPGDDEKLTVPLLEPKPATYKHQEDDDAEEDEVGSVRRRVVEENKKLWVVAGPSICARFSSFGVTVISQAFIGHIGATELAAYALVSTVLMRFSNGILIGMASALETLCGQSYGAKQYHMLGIYLQRSWIVLFCCAVILLPIYLFTTPLLIALGQDPDISVVAGTISLWYIPIMFSYVWGLTIQMYLQSQSKNMIVTYLSLLNFGLNLFLSWLMVVKFHLGLAGVMGSMVIACWIPIFGQLAYVFFGGCPQTWTGFSSSAFTDLGAIIKLSISSGVMLCVELWYNTILVLLTGYMKNAEVALDALSICLNINGWEMMIAIGFLAATG
47	Os11g03500	MERPGDEHDDCRTVPLLEPKHAHGEGSNNKQEEDEEEVGSLGRRVLVESKKLWVVAGPSICARFSTFGVTVISQAFIGHVGATELAGYALVSTVLMRFSGGILLGMASALETLCGQSYGAKQYHMLGIYLQRSWIVLLCCAVLLLPIYLFTTPLLIFLGQDPKIAAMAGTISLWYIPVMISNVGNFTLQMYLQAQSKNMIVTYLAMLNLGLHLFLSWLLTVQFYLGLAGVMGSMLAFVFFGGCPLTWTGFSFAAFTELGAIVKLSLSSGVMLCVELWYNTILVLLTGYMKNAEIALDALSICLNINGWEMMISIGFLSAKGVRVANELGAGSARRAKFAIFNVVTTSFSIGFMLFVLFLIFRGRLVYIFTESTVVADAVAELSPLLAFSNLLNSIQPVLSGVAVGSGWQSVVAYVNVTSYYLFGIPIGVILGYVLGFQVKGIWIGMLLGTLVQTIVLLFITLRTDWEKQVEIARQRLNRWSMDENGRQQNPGENP

48	Os12g01580	MTATSPPMRSVAAAALVLTPTPTLNRLSFPFAHRHCPSTAAPRWRPARCRGKPAVEDVVHDDEEETWRREANPERKDGGEEMLGRGWFMVDEIGMEILTIALPAVLALAADPITALIDTAFVGHVGSTELAAVGVSISIFNLVSKLLNVPLLNVTTSFVAEQQAVDADYNSSVENSHIGEEISISQEKAGEQRKFLPAVSTSLALAAGIGLMETVALILGSGTLLDIVGVPVDSPMRIPAEQFLTLRAYGAPPVIVALAAQGAFRGFMDTKTPLFAVVAGNLVNALLDAIFIFPLGLGVSGAALATVTSEYLTAFILLWKLNSKIVLFSWNIVSGDIIRYLKSGALLIARTIAVVLTFTVSTSLAAREGSVPMAGYEICLQVWLTISLLNDALALAGQALLASEYAKGNYKKARIVLYRVLQIGGVTGAALSTTLLLGFGYLSMLFTDDAAVLDVAQTGVWFVTVSQPINAVAFVMDGLYYGVSDFAFVAYSTLFAGAISSAVLLVAAPKFGLGGVWAGLTLFMSLRAIAGFWRLGSKGGPWKIIWSETE
49	Os12g03200	MERTTEDDERLTDPLLEPKPAINGGGGGSNEEEEEVGSLGRRLVEENKKLWVVAGPSICARATSFGATVVSQAFIGHIGATELAAYALVSTVLMRLSVGILIGMASALETLCGQSYGAKQYHMLGIYLQRSWIVLFCCAVILLPIYLFTTPLLIALGQDPDISVVAGTISLWYIPIMFSYVWGLTIQMYLQSQSKNMIVTYLSLLNFGLHLFLSWLMVVKFHLGLAGVMGSTVIACWIPIFGQLAYVFFGGCPQTWTGFSSSAFTDLGAIIKLSISSGVMLCVELWYNTILVLLTGYMKNAEVALDALSIW
50	Os12g03230	MGSMVISFWIPVFGQLAFVFFGGCPLTWTGFSSSAFTDLGAIMKLSLSSGVMLCLELWYNTILVLLTSYMKNAEVALDALSICLNINGWEMMISIGFLSAIGVRVANELGAGSARRAKFAIFNVVTTSFLIGFVLFVLFLFFRGSLAYIFTESKAVADEVADLAPLLAFSILLNSVQPVLSGVAIGSGWQSIVAYVNVTSYYLIGIPLGAILGYVLGFQVKGIWIGMLLGTLVQTLVLLFITLRTDWKKQVEITRERLNRWYMDENGRSQNSIGNA
51	Os12g03260	MERPGDEHDDCRTAPLLEPKHAHGEGSNNDKQEEDEEEVGSLGPRVLVESKKLWVVAGPSICARFSTFGVTVISQAFIGHIGATELAGYALVSTVLMRFSGGILLGMASALETLCGQSYGAKQYHMLGIYLQRSWIVLLCCAVLLLPIYLFTTPLLIFLGQDPKIAAMAGTISLWYIPVMISNVGNFTLQMYLQAQSKNMIVTYLAMLNLGLHLFLSWLLTVQFHLGLAGVMGSMVIAYWIPVFGQLAFVFFGGCPLTWTGFSSAAFTELGAIVKLSLSSGVMLCVELWYNTILVLLTGYMKNAEIALDALSICLNINGWEMMISIGFLSATGVRVANELGAGSARRAKFAIFNVVTTSFSIGFMLFVLFLIFRGRLAYIFTESKVVADAVAELSPLLAFSILLNSIQPVLSGVAVGSGWQSVVAYVNVTSYYLFGIPIGVILGYVLGFQVKGIWIGMLLGTLVQTIVLLFITLRTDWEKQVEIARQRLNRWSMDE

		NGRQQNPGENP
52	Os12g36660	MEELKLMRRLCLPISALNLLHYVKSMVTVLCLGRLGRAELAGGALAVGLTNVTGYSVLSGLALGLEPLAGQAFGSGTGRTRSRPRRALRRAVLLLLAASFPVAALWACAGPAARAARQDAAVARAAGSYCRYAIPDLAAASVLLPARVYLRSKGETRRLASCAALAVALVHAPATAYLGARLRVPGVAMAACMTSFATLAFLWISLTWAPAQNEPDEPADLEEWAGVGQWAEWADLLRLSLPSCLSVCLEWWWYELMTIAAGYLRDPHTALATAAIVIQTTSLLYTIPVTLSSAVSTRVANELGAGRPRSAQVSFVVAMGIAMMGSCVGLTWTTFGRGLWVQVFTTDPTIQSLTTSVLPVIGLCELANCPQTTGCGVLRGSARPAVGAAINLYSFYLVGAPVALVLAFGLDMGFLGLCLGLLSAQVKIVNL
53	Os12g42130	MAETSSARSPLLDVDESSGASEELLRREPVPRSVLSRLAAWEAGNLWRISWASILITLLSFTLSLVTQMFVGHLGELELAGASITNIGIQGLAYGIMIGMASAVQTVCGQAYGARKFRAMGIVCQRALVLQFATAIVIAFLYWYAGPFLRLIGQAADVAAAGQLYARGLVPQLLAFALFCPMQRFLQAQNIVNPVAYITMAVLIFHILISWLTVFVLGFGLLGAALTLSFSWWVLVALTWGLMVWTPACKETWTGLSVLAFRGLWGYAKLAFASAVMLALEIWYVQGFVLLTGFLPDPEIALDSLSICINYWNWDFQIMLGLSYAASIRVGNELGAGHPNVARFSVFVVITASVAFSILATILVLVLRYPLSTLYTSSTTVIEAVIKLTPLLSISIFLNGIQPILSGVAVGSGWQVVVAYVNVGAYYLIGLPIGCVLGYKTSLGAAGIWWGLIIGVSVQTVALIIITARTNWDNEVMKAIQRLRQTAVDDGTVPIVDDIE
54	AT4G29140	MCNPSTTTTTTGSENQESRTGLFLDLFSINSFEPTKRNLRHCENRGSPLMAEAVTEAKSLFTLAFPIAVTALVLYLRSAVSMFFLGQLGDLELAAGSLAIAFANITGYSVLSGLALGMEPLCSQAFGAHRFKLLSLTLHRTVVFLLVCCVPISVLWFNVGKISVYLHQDPDIAKLAQTYLIFSLPDLLTNTLLHPIRIYLRAQGIIHPVTLASLSGAVFHLPANLFLVSYLRLGLTGVAVASSITNIFVVAFLVCYVWASGLHAPTWTDPTRDCFRGWAPLLRLAGPSCVSVCLEWWWYEIMIVLCGLLVNPRSTVAAMGVLIQTTSFLYVFPSSLSFAVSTRVGNELGANRPKTAKLTATVAIVFAAVTGIIAAAFAYSVRNAWGRIFTGDKEILQLTAAALPILGLCEIGNCPQTVGCGVVRGTARPSTAANVNLGAFYLVGMPVAVGLGFWAGIGFNGLWVGLLAAQISCAGLMMYVVGTTDWESEAKKAQT

		LTCAETVENDIIKAVVASTIDGECDEAEPLIRITVLY
55	AT5G19700	METPNIISHTNLLSKIDLEKQNPAPIFPTITELKSEARSLFSLAFPTILAALILYARSAISMLFLGHIGELELAGGSLAIAFANITGYSVLAGLALGMDPLCSQAFGAGRPKLLSLTLQRTVLFLLTSSVVIVALWLNLGKIMIYLHQDPSISSLAQTYILCSIPDLLTNSFLHPLRIYLRAQGITSPLTLATLAGTIFHIPMNFFLVSYLGWGFMGVSMAAAASNLLVVIFLVAHVWIAGLHQPTWTRPSSECFKDWGPVVTLAIPSCIGVCLEWWWYEIMTVLCGLLIDPSTPVASMGILIQTTSLLYIFPSSLGLAVSTRVGNELGSNRPNKARLSAIVAVSFAGVMGLTASAFAWGVSDVWGWIFTNDVAIIKLTAAALPILGLCELGNCPQTVGCGVVRGTARPSMAANINLGAFYLVGTPVAVGLTFWAAYGFCGLWVGLLAAQICCAAMMLYVVATTDWEKEAIRARKLTCTEGVDVVITTTQTNGDLSEPLIYVVTVATD
56	AT1G58340	MCNSKPSSASSSLLSCKDKTHISKLETCDTDNPHYSEFRDTDSLDLKRWPSFLEGLEEVKAIGKISGPTAMTGLLMYSRAMISMLFLGYLGELELAGGSLSIGFANITGYSVISGLSMGMEPICGQAYGAKQMKLLGLTLQRTVLLLLSCSVPISFSWLNMRRILLWCGQDEEISSVAQQFLLFAIPDLFLLSLLHPLRIYLRTQNITLPVTYSTAVSVLLHVPLNYLLVVKLEMGVAGVAIAMVLTNLNLVVLLSSFVYFTSVHSDTWVPITIDSLKGWSALLSLAIPTCVSVCLEWWWYEFMIILCGLLANPRATVASMGILIQTTALVYVFPSSLSLGVSTRISNELGAKRPAKARVSMIISLFCAIALGLMAMVFAVLVRHHWGRLFTTDAEILQLTSIALPIVGLCELGNCPQTTGCGVLRGCARPTLGANINLGSFYFVGMPVAILFGFVFKQGFPGLWFGLLAAQATCASLMLCALLRTDWKVQAERAEELTSQTPGKSPPLLPIASSKSRSTSGTEDMMRTMLV

57	AT4G23030	MAAPLLMIIKNQTDHRQDPNPNPTHLSSSIQEAKSIAKISLPLILTGLLLYSRSMISMLFLGRLNDLSALSGGSLALGFANITGYSLLSGLSIGMEPICVQAFGAKRFKLLGLALQRTTLLLLLCSLPISILWLNIKKILLFFGQDEEISNQAEIFILFSLPDLILQSFLHPIRIYLRSQSITLPLTYSAFFAVLLHIPINYLLVSSLGLGLKGVALGAIWTNVNLLGFLIIYIVFSGVYQKTWGGFSMDCFKGWRSLMKLAIPSCVSVCLEWWWYEIMILLCGLLLNPQATVASMGILIQTTALIYIFPSSLSISVSTRVGNELGANQPDKARIAARTGLSLSLGLGLLAMFFALMVRNCWARLFTDEEEIVKLTSMVLPIIGLCELGNCPQTTLCGVLRGSARPKLGANINLCCFYFVGMPVAVWLSFFSGFDFKGLWLGLFAAQGSCLISMLVVLARTDWEVEVHRAKELMTRSCDGDEDDGNTPFLLDSLDIEENLVF
58	AT5G52050	MSQSNRVRDEVTLPLLQKTSHLKNHSSVLSVFLNEAISICKISYPLVLTGLFLYVRSFVSLSFLGGLGDATLAGGSLAAAFANITGYSLFSGLTMGVESICSQAFGARRYNYVCASVKRGIILLLVTSLPVTLLWMNMEKILLILKQDKKLASEAHIFLLYSVPDLVAQSFLHPLRVYLRTQSKTLPLSICTVIASFLHLPITFFLVSYLGLGIKGIALSGVVSNFNLVAFLFLYICFFEDKLSVNEDEKITEETCEDSVREWKKLLCLAIPSCISVCLEWWCYEIMILLCGFLLDPKASVASMGILIQITSLVYIFPHSLSLGVSTRVGNELGSNQPKRARRAAIVGLGLSIALGFTAFAFTVSVRNTWAMFFTDDKEIMKLTAMALPIVGLCELGNCPQTTGCGVLRGSARPKIGANINGVAFYAVGIPVGAVLAFWFGFGFKGLWLGMLAAQITCVIGMMAATCRTDWELEAERAKVLTTAVDCGSSDDDAKEDMEAGMVDK
59	AT2G38510	MQVGEEMASLTKIACPIVMTSLLIFSRSIISMWFLSHLGKVELAGGALAMGFGNITGVSVLKGLSVGMDPICGQAFGAKRWTVLSHTFQKMFCLLIVVSVPIAVTWLNIEPIFLRLGQDPDITKVAKTYMLFFVPELLAQAMLHPLRTFLRTQGLTSPLTISAIVSILLHPLFNYVFVVRMRLGVKGVAIAMAFNTMNIDVGLLVYTCFSDSLIKPWEGLALRSLFRGWWPLLSLAAPSAISVCLEYWWYEIMLFLCGLLGNPKASVAAMGILIQTTGILYVVPFAISSAIATRVGHALGGGQPTRAQCTTVIGLILAVAYGLAAAVFVTALRSVWGKMFTDEPEILGLISAALPILGLCEIGNSPQTAACGVLTGTARPKDGARVNLCAFYIVGLPVAVTTTFGFKVGFRGLWFGLLSAQMTCLVMMLYTLIRTDWSHQVKRAEELTSAAADKSHSEDETVHAEVQDDDDVSSNDLEIGLLQNTN

60	AT1G71870	MEDKIQSDDFTSHKNPTLPQVIEELKELWAMVLPITAMNCLVYVRAVVSVLFLGRLGSLELAGGALSIGFTNITGYSVMVGLASGLEPVCSQAYGSKNWDLLTLSLHRMVVILLMASLPISLLWINLGPIMLFMGQNPEITATAAEYCLYALPDLLTNTLLQPLRVYLRSQRVTKPMMWCTLAAVAFHVPLNYWLVMVKHWGVPGVAIASVVTNLIMVVLLVGYVWVSGMLQKRVSGDGDGGSTTMVAVVAQSSSVMELVGGLGPLMRVAVPSCLGICLEWWWYEIVIVMGGYLENPKLAVAATGILIQTTSLMYTVPMALAGCVSARVGNELGAGRPYKARLAANVALACAFVVGALNVAWTVILKERWAGLFTGYEPLKVLVASVMPIVGLCELGNCPQTTGCGILRGTGRPAVGAHVNLGSFYFVGTPVAVGLAFWLKIGFSGLWFGLLSAQAACVVSILYAVLARTDWEGEAVKAMRLTSLEMRKVGQDEESSLLLLDDEKLGDVL
61	AT5G49130	MVVEEDSRLINLQHKYNPTMPEVVEELKRIWDISFPVAAMSILNYLKNMTSVVCMGRLGSLELAGGALAIGFTNITGYSVLSGLATGMEPLCGQAIGSKNPSLASLTLKRTIFLLLLASLPISLLWLNLAPLMLMLRQQHDITRVASLYCSFSLPDLLANSFLHPLRIYLRCKGTTWPLMWCTLVSVLLHLPITAFFTFYISLGVPGVAVSSFLTNFISLSLLLCYIYLENNNNDKTTSKSLCLDTPLMLYGSRDSGENDVWSTLVKFAVPSCIAVCLEWWWYEFMTVLAGYLPEPKVALAAAAIVIQTTSLMYTIPTALSAAVSTRVSNELGAGRPEKAKTAATVAVGAAVAVSVFGLVGTTVGREAWGKVFTADKVVLELTAAVIPVIGACELANCPQTISCGILRGSARPGIGAKINFYAFYVVGAPVAVVLAFVWGLGFMGLCYGLLGAQLACAISILTVVYNTDWNKESLKAHDLVGKNVISPNVDQIIVKCEEGLH
62	AT4G22790	MSETSKSESLDPEVSEGLCSKTLMQSIVHELKLQMRIGLPLVVMNLLWFGKMTTTSVFLGRQGELNLAGGSLGFSFANVTGFSVLYGISAAMEPICGQAFGAKNFKLLHKTLFMAVLLLLLISVPISFLWLNVHKILTGFGQREDISFIAKKYLLYLLPELPILSFLCPLKAYLSSQGVTLPIMFTTAAATSLHIPINIVLSKARGIEGVAMAVWITDFIVVILLTGYVIVVERMKENKWKQGGWLNQSAQDWLTLIKLSGPCCLTVCLEWWCYEILVLLTGRLPNPVQAVSILIIVFNFDYLLYAVMLSLGTCVATRVSNELGANNPKGAYRAAYTTLIVGIISGCIGALVMIAFRGFWGSLYTHHDQLILNGVKKMMLIMAVIEVVNFPLMVCGEIVRGTAKPSLGMYANLSGFYLLALPLGATLAFKAKQGLQGFLIGLFVGISLCLSILLIFIARIDWEKEAGKAQILTCNTEDEQTSQGSGQDSHS

63	AT1G33560	MASFIDLFAGDITTQLLKLLALVANTVYSCKGIAERLITMIRDVQPTIREIQYSGAELSNHHQTQLGVFYEILEKARKLCEKVLRCNRWNLKHVYHANKMKDLEKQISRFLNSQILLFVLAEVCHLRVNGDRIERNMDRLLTERNDSLSFPETMMEIETVSDPEIQTVLELGKKKVKEMMFKFTDTHLFGISGMSGSGKTTLAIELSKDDDVRGLFKNKVLFLTVSRSPNFENLESCIREFLYDGVHQRKLVILDDVWTRESLDRLMSKIRGSTTLVVSRSKLADPRTTYNVELLKKDEAMSLLCLCAFEQKSPPSPFNKYLVKQVVDECKGLPLSLKVLGASLKNKPERYWEGVVKRLLRGEAADETHESRVFAHMEESLENLDPKIRDCFLDMGAFPEDKKIPLDLLTSVWVERHDIDEETAFSFVLRLADKNLLTIVNNPRFGDVHIGYYDVFVTQHDVLRDLALHMSNRVDVNRRERLLMPKTEPVLPREWEKNKDEPFDAKIVSLHTGEMDEMNWFDMDLPKAEVLILNFSSDNYVLPPFIGKMSRLRVLVIINNGMSPARLHGFSIFANLAKLRSLWLKRVHVPELTSCTIPLKNLHKIHLIFCKVKNSFVQTSFDISKIFPSLSDLTIDHCDDLLELKSIFGITSLNSLSITNCPRILELPKNLSNVQSLERLRLYACPELISLPVEVCELPCLKYVDISQCVSLVSLPEKFGKLGSLEKIDMRECSLLGLPSSVAALVSLRHVICDEETSSMWEMVKKVVPELCIEVAKKCFTVDWLDD
64	AT3G08040	MTETGDDLATVKKPIPFLVIFKDLRHVFSRDTTGREILGIAFPAALALAADPIASLIDTAFVGRLGAVQLAAVGVSIAIFNQASRITIFPLVSLTTSFVAEEDTMEKMKEEANKANLVHAETILVQDSLEKGISSPTSNDTNQPQQPPAPDTKSNSGNKSNKKEKRTIRTASTAMILGLILGLVQAIFLIFSSKLLLGVMGVKPNSPMLSPAHKYLSIRALGAPALLLSLAMQGIFRGFKDTKTPLFATVVADVINIVLDPIFIFVLRLGIIGAAIAHVISQYFMTLILFVFLAKKVNLIPPNFGDLQFGRFLKNGLLLLARTIAVTFCQTLAAAMAARLGTTPMAAFQICLQVWLTSSLLNDGLAVAGQAILACSFAEKDYNKVTAVASRVLQMGFVLGLGLSVFVGLGLYFGAGVFSKDPAVIHLMAIGIPFIAATQPINSLAFVLDGVNFGASDFAYTAYSMVGVAAISIAAVIYMAKTNGFIGIWIALTIYMALRAITGIARMATGTGPWRFLRGRSSSSSS
65	AT1G51340	MMSEDGYNTDFPRNPLYIFFSDFRSVLKFDELGLEIARIALPAALALTADPIASLVDTAFIGQIGPVELAAVGVSIALFNQVSRIAIFPLVSITTSFVAEEDACSSQQDTVRDHKECIEIGINNPTEETIELIPEKHKDSLSDEFKTSSSIFSISKPPAKKRNIPSASSALIIGGVLGLFQAVFLISAAKPLLSFMGVKHDSPMMRPSQRYLSLRSLGAPAVLLSLAAQGVFRGFKDTTTPLFATVIGDVTNIILDPIFIFVFRLGVTGAATAHVISQYLMCGILLWKLMGQVDIFNMSTKHLQFCRFMKNGFLLLMRVIAVTFCVTLSASLAAREGSTSMAAFQVCLQVWLATSLLADGYAVAGQAILASAFAKKDYKRAAATASRVLQLGLVLGFVLAVILGAGLHFGARVFTKDDKVLHLISIGLPFVAGTQPINALAFVFDGVNFGASDFGYAAASLVMVAIVSILCLLFLSSTHGFIGLWFGLTIYMSLRAAVGFWRIGTGTGPWSFLRS

66	AT2G38330	MAAVATSFCFSPHRSPSRFGNPNSSIRRTIVCKSSPRDESPAVSTSSQRPEKQQNPLTSQNKPDHDHKPDPGIGKIGMEIMSIALPAALALAADPITSLVDTAFVGHIGSAELAAVGVSVSVFNLVSKLFNVPLLNVTTSFVAEEQAIAAKDDNDSIETSKKVLPSVSTSLVLAAGVGIAEAIALSLGSDFLMDVMAIPFDSPMRIPAEQFLRLRAYGAPPIVVALAAQGAFRGFKDTTTPLYAVVAGNVLNAVLDPILIFVLGFGISGAAAATVISEYLIAFILLWKLNENVVLLSPQIKVGRANQYLKSGGLLIGRTVALLVPFTLATSLAAQNGPTQMAGHQIVLEIWLAVSLLTDALAIAAQSLLATTYSQGEYKQAREVLFGVLQVGLATGTGLAAVLFITFEPFSSLFTTDSEVLKIALSGTLFVAGSQPVNALAFVLDGLYYGVSDFGFAAYSMVIVGFISSLFMLVAAPTFGLAGIWTGLFLFMALRLVAGAWRLGTRTGPWKMLWSAPEKPE
67	AT4G39030	MLIKSQRLTLFSPLLSKTRRIPVNSHQTLVAESVITRRTLGAITATPSFHKNPVVIRRRIKLERVTRNCVRIDREIDEEEEEEEKERGDLVKQSIWEQMKEIVKFTGPAMGMWICGPLMSLIDTVVIGQGSSIELAALGPGTVLCDHMSYVFMFLSVATSNMVATSLAKQDKKEAQHQISVLLFIGLVCGLMMLLLTRLFGPWAVTAFTRGKNIEIVPAANKYIQIRGLAWPFILVGLVAQSASLGMKNSWGPLKALAAATIINGLGDTILCLFLGQGIAGAAWATTASQIVSAYMMMDSLNKEGYNAYSFAIPSPQELWKISALAAPVFISIFSKIAFYSFIIYCATSMGTHVLAAHQVMAQTYRMCNVWGEPLSQTAQSFMPEMLYGANRNLPKARTLLKSLMIIGATLGLVLGVIGTAVPGLFPGVYTHDKVIISEMHRLLIPFFMALSALPMTVSLEGTLLAGRDLKFVSSVMSSSFIIGCLTLMFVTRSGYGLLGCWFVLVGFQWGRFGLYLRRLLSPGGILNSDGPSPYTVEKIKSI
68	AT2G21340	MQIQCKTLTFTVSSIPCNPKLPFPSSLTLRSWNPSFPSFRSSAVSGPKSSLKLNRFLRNCASTNQELVVDGETGNGSISELQGDAANGSISPVEVEAEVEEVKVDDLATQSIWGQMKEIVMFTGPAAGLWLCGPLMSLIDTAVIGQGSSLELAALGPATVICDYLCYTFMFLSVATSNLVATSLARQDKDEVQHQISILLFIGLACGVTMMVLTRLFGSWALTAFTGVKNADIVPAANKYVQIRGLAWPAVLIGWVAQSASLGMKDSWGPLKALAVASAINGVGDVVLCTFLGYGIAGAAWATMVSQVVAAYMMMDALNKKGYSAFSFCVPSPSELLTIFGLAAPVFITMMSKVLFYTLLVYFATSMGTNIIAAHQVMLQIYTMSTVWGEPLSQTAQSFMPELLFGINRNLPKARVLLKSLVIIGATLGIVVGTIGTAVPWLFPGIFTRDKVVTSEMHKVIIPYFLALSITPSTHSLEGTLLAGRDLRYISLSMTGCLAVAGLLLMLLSNGGFGLRGCWYALVGFQWARFSLSLFRLLSRDGVLYSEDTSRYAEKVKAA

69	AT5G65380	MRGGDGEEGSESRVALLKSPHTAEEDGEGLKDRILVETKKLWQIVGPAIFSRVTTYSMLVITQAFAGHLGDLELAAISIVNNVTVGFNFGLLLGMASALETLCGQAFGAKKYHMLGVYMQRSWIVLFFCCVLLLPTYIFTTPVLKFLGQPDDIAELSGVVAIWVIPLHFAFTLSFPLQRFLQCQLKNRVTAYAAAVALVVHILVCWLFVDGLKLGVVGTVATISISWWVNVLILLVYSTCGGCPLTWTGLSSEALTGLWEFLKLSASSGVMLCLENWYYRILIIMTGNLQNARIAVDSLSICMAINGWEMMIPLAFFAGTGVRVANELGAGNGKGARFATIVSVTQSLIIGLFFWVLIMLLHNQIAWIFSSSVAVLDAVNKLSLLLAFTVLLNSVQPVLSGVAVGSGWQSYVAYINLGCYYCIGVPLGFLMGWGFKLGVMGIWGGMIFGGTAVQTMILSFITMRCDWEKEAQKASARINKWSNTIK
70	AT5G10420	MDKKSGGTKAIEEATVPLLECHNAAEEGGGMKREIWIETKKIWYIVGPSIFTGLATYSILIITQAFAGHLGDLELAAISIINNFTLGFNYGLLLGMASALETLCGQAFGAREYYMLGVYMQRYWIILFLCCILLLPMYLFATPILKFIGQSDDIAELTGTIALWVIPVHFAFAFFFPLNRFLQCQLKNKVIAISAGVSLAVHILVCWFFVYGYKLGIIGTMASVNVPWWLNIFILFLYSTRGGCTLTWTGFSSEAFTGLLELTKLSASSGIMLCLENWYYKILMLMTGNLVNAKIAVDSLSICMSVNGWEMMIPLAFFAGTGVRVANELGAGNGKGARFATIVSITLSLMIGLFFTVIIVIFHDQIGSIFSSSEAVLNAVDNLSVLLAFTVLLNSVQPVLSGVAVGSGWQSYVAYINLGCYYLIGLPFGLTMGWIFKFGVKGIWAGMIFGGTAIQTLILIIITTRCDWDNEAHKSSVRIKKWLVSDAGN
71	AT5G44050	MGERDDEAEGILEKAKIPLLKDQNVAEEENGEIKKEIWLETKKLWRIVGPAIFTRVTTNLIFVITQAFAGHLGELELAAISIVNNVIIGFNYSLFIGMATALETLCGQAFGAKKYDMFGVYLQRSWIVLFLFSILLLPMYIFATPILKFMGQPDDIAELSGIISVWAIPTHFSFAFFFPINRFLQCQLKNSVIAISSGVSLVVHIFVCWLFVYVLELGVIGTIATANVSWWLNVFILFTYTTCGGCPLTWTGFSMESFTRLWEFTKLSASSGIMVCLENWYYRMLIVMTGNLEDARIDVDSMSICMSINGLEMMVPLAFFAGTSVRVANELGAGNGKRARFAMIISVTQSLIIGIIISVLIYFLLDQIGWMFSSSETVLKAVNNLSILLSFAILLNSVQPVLSGVAVGSGWQSLVAFINLGCYYFIGLPLGIVMGWMFKFGVKGIWAGMIFGGTMVQTLILIFITMRCDWEKEAQNAKVRVNKWSVSDARK

72	AT1G33100	MAGRGGELTEALVKKTGREEEDELGMKEKVWIESKKLWVVAAPAIFTRYSTFGVSMVTQAFIGHLGPTELAAYSITFTILLRFSNGILLGMAGALGTLCGQAYGAKQYQMLGIYLQRSWIVLTGGTICLMPVFIFAGPILLALGQEERIVRVARVLALWVIGINFSFVPSFTCQMFLQAQSKNKIISYVTAVSLGLHVFFSWLLVAHFNFGITGAMTSMLIAFWLPIIVQLLYVTCGGCKDTWRGFSMLAFKDLWPVLKLSLSSGGMLCLELWYNSVLVLLTGNLKNAEVALDALAICISINALEMMIALGFLAAVSVRVSNELGSGNPKGAKFATLIAVFTSLSIGIVLFFVFLFLRGRISYIFTTSEAVAAEVADLSPLLAFSILLNSVQPVLSGVAIGAGWQGYVAYVNLACYYLVGIPIGVILGYVVGLQVKGVWIGMLFGIFVQTCVLTVMTLRTDWDQQVSTSLRNINRWVVPESRDANQISSEE
73	AT1G33110	MAGGGGELTAALLKKTAENGGEEKDELGLKQKVWIESKKLWIVAAPAIFTRFSTFGVSIISQSFIGHLGPIELAAYSITFTVLLRFSNGILLGMASALETLCGQAYGAKQNHMLGIYLQRSWIVLTGCTICLTPVYIFSGPILLALGQEERIVRVARIIALWVIGINFSFVPSFTCQMFLQAQSKNKIIAYVAAVSLGVHVFLSWLLMVHFNFGITGAMTSTLVAFWLPNIAQLLFVTCGGCKDTWRGFSMMAFKDLWPVFKLSMSSGGMLCLELWYNSILVLLTGNLKNAEVALDALAICLNINGLEMMIALGFLAAASVRVSNELGSGNPKGAKFATLTAVFTSLSLGIVLFFVFLFLRGRVSYIFTTSEAVAAEVADLSPLLAFSILMNSVQPVLSGVAVGAGWQGYVTYVNLACYYLVGIPIGIILGYVVGLQVKGVWIGMLFGIFVQTCVLTVMTLRTDWDQQVSTSLRRLNRWVVPESRDVNQVSSEE
74	AT1G33900	MAGLEDTTDLRLPSASEPIKNIVLVGRTGNGKSATGNSLIGKQVFRSETRATGVTMKCETCVAVTPCGTGINVIDTPGLFDLSVSAEYLSQEIINCLVLAEDGLHAVVLVLSVRTRISQEEEATLNTLQVIFGSQIIDYLVVLFTGGDELEANNMTLDDYLSKGCPEFLKTVLRLCGGRRILFDNRTTDEGKKVKQVQELLAHVAAIEKSTSGIPFTDEMHRKIQKEAETLREQQKEVESKDLAAAEIEKWKKHYQTEHDKNMNMMAEMLGNRLREDSERQEKMLLALRDNLEISQRQNKLNELTDNEPDLIHCGVSLRRMPCNML
75	AT1G33080	MARREGEVTETLLKKSTENRGEDRDGLGMKEKVWRESKKLWVVAGPAIFTRFSTSGLSLISQAFIGHLGSTELAAYSITLTVLLRFSNGILLGMASALETLCGQAYGAKQYHMLGIYLQRSWIVLTGCTICLMPIYIFAGPILLALGQEERLVRVARIIALWVIGINISFVPSFTCQMFLQAQSKNKIIAYVAAVSLGVHVFLSWLLVVHFDFGIAGAMTSSLVAHWLPNIAQVLFVTCGGCTETWRGFSWLAFKDLWPVFKLSVSSGGMICLELWYNSILILLTGNLKNAEVALNALAICININALEMMVAFGFMAAASVRVSNEIGSGNSNGAKFATMVVVSTSLSIGIIFFFIFLFLRERVSYIFTTSEAVATQVADLSPLLAFSILLNSIQPVLSGVAVGAGWQKYVTVVNLACYYLVGIPSGLFLGYVVGLQVKGVWLGMIFGIF

		VQTCVLTVMTMRTDWDQQVSSSLKRLNRWVEPESPSRNQTLQNE
76	AT5G17700	MSGGGGEMEERLLNGSETEQRRESLYLRKKIWSEVRKMWRIALPSTLFRVMSFGCVVVAQAFIGHSSETGLAAYALLQSTFIRFIYGIMAGMSSATETLCGQAYGAEQYHMMGIYLQRSWIVDTFIATLFVPFIVLAGPILRLLGQNVVISETVDEIYPWVIPYLYSIVFTMTMQMYLQAQMKNAIIGILSTLALVLDIAATWWCVSVMGMGIHGALLGLNISSWSVAIAEFVYVFGGWCPHTWTGFSTAAFLDLIPMLKLSISSGFMLCLEYWYMSIIVLMSGYAKDANIAISAFSICQYIYSWEMNICFGLMGAACVRVANELGKGDADAVRFSIKVVLVVSAVIGVICSALCLAFGGQISYLFSDSQAVSDAVADLSIVLSISILFNIIQPILSGVAIGAGMQSMVALVNLASYYAIGVPLGVLLVYVFNFGIKGLWSGMLAGVGIQTLILCYVIYKTDWELEVKKTNERMKTWTLNLPAVQSTTISTRDEERK
77	AT3G03620	MSTQEEMEERLLREGSDAEGQSNNRESIYLRTKVWSEVNKMWRIALPSSLFRMTSFGSIIVAQAFIGHSSELGLAAYALLQSTFIRFLYGLMGGMSSATETLCGQAYGAEQYHTMGIYLQRSWIVDMAVTTLFLPFIVLAGPILRLLGQNVEITKTVDEIYPWMIPYVYSLIFTMTIQMYLQAQMRNAIVGVLSTLSLALDLVVTWWCVSVMGMGIGGALLGLNVGSWAMVLAEFVYIFGGWCPFTWTGFSIAAFVDLIPMLKLSISSGFMICLEYWYMSILVLMAGYTKDAKIAISAFSICQYIYTWELNICLGFLGAACVRVANELGKGDAHAVRFSIKVILTISTLMGVIFSALCLAFCGRISYLFSNSDEVSDAVNDLSVILAVSILLNSIQPILSGVAVGAGMQSIVAVVNLASYYAIGIPLGLILTYVFHLGVKGLWSGMLAGIAIQTIILCYIIYKTDWELEVKRTCERMKVWSLKPSNEESNPIIREESRSK
78	AT5G38030	MEEDKILTETLLSAAEEPPALPFSSVEDIPPITTVGGFVKEFNVEVKKLWYLAGPAIFMSITQYSLGAATQVFAGHISTIALAAVSVENSVIAGFSFGVMLGMGSALETLCGQAFGAGKLSMLGVYLQRSWVILNVTAVILSLLYIFAAPILAFIGQTPAISSATGIFSIYMIPQIFAYAVNYPTAKFLQSQSKIMVMAAISAVALVLHVLLTWFVIEGLQWGTAGLAVVLNASWWFIVVAQLVYIFSGTCGEAWSGFSWEAFHNLWSFVRLSLASAVMLCLEVWYLMAVILFAGYLKNAEISVAALSICMNILGWTAMIAIGMNAAVSVRVSNELGAKHPRTAKFSLLVAVITSTVIGLAISIALLIFRDKYPSLFVGDEEVIIVVKDLTPILAVSIVINNVQPVLSGVAVGAGWQAVVAYVNIVCYYVFGIPFGLLLGYKLNFGVMGIWCGMLTGTVVQTIVLTWMICRTNWDTEAAMAEGRIREWGGEVSDQLL

		N
79	AT3G26590	MAKDKDITETLLTAAEERSDLPFLSVDDIPPITTVGGFVREFNVETKKLWYLAGPAIFTSVNQYSLGAITQVFAGHISTIALAAVSVENSVVAGFSFGIMLGMGSALETLCGQAFGAGKLSMLGVYLQRSWVILNVTALILSLLYIFAAPILASIGQTAAISSAAGIFSIYMIPQIFAYAINFPTAKFLQSQSKIMVMAVISAVALVIHVPLTWFVIVKLQWGMPGLAVVLNASWCFIDMAQLVYIFSGTCGEAWSGFSWEAFHNLWSFVRLSLASAVMLCLEVWYFMAIILFAGYLKNAEISVAALSICMNILGWTAMIAIGMNTAVSVRVSNELGANHPRTAKFSLLVAVITSTLIGFIVSMILLIFRDQYPSLFVKDEKVIILVKELTPILALSIVINNVQPVLSGVAVGAGWQAVVAYVNIACYYVFGIPFGLLLGYKLNYGVMGIWCGMLTGTVVQTIVLTWMICKTNWDTEASMAEDRIREWGGEVSEIKQLIN
80	AT1G12950	MEKDNDFKDPFLASTEEEELDPATQKALMEYLGVGSRASSLVSFSSTAVDIPPISGVGDFVREFRIESRKLWKLAGPAIFTTMSQYSLGAVTQVFAGHISTLALAAVSIENSVIAGFSFGIMLGMGSALETLCGQAFGAGKVSMLGVYLQRSWVILSVTALFLSLIYIFAAPILTFIGQTAAISAMAGIFSIYMIPQIFAYAINFPTAKFLQSQSKIMVMAGISGVVLVIHSFFTWLVMSRLHWGLPGLALVLNTSWWVIVVAQLVYIFNCTCGEAWSGFTWEAFHNLWGFVKLSLASAAMLCLEIWYFMALVLFAGYLKNAEVSVAALSICMNILGWAAMVAFGTNAAVSVRVSNELGASHPRTAKFSLVVAVILSTAIGMFIAAGLLFFRNEYPVLFVEDEEVRNVVRELTPMLAFCIVINNVQPVLSGVAVGAGWQAVVAYVNIACYYLFGVPFGLLLGFKLEYGVMGIWWGMVTGTFVQSIVLTWMICKTNWEKEASMAEERIKEWGGVPAEKETLLN

81	AT1G23300	METLNVDHEDTISSEQEHRAHTKSDTDMPPISGGRDFIRQFAAESKKLWWLAGPAIFTSFCQYSLGAVTQILAGHVNTLALAAVSIQNSVISGFSVGIMLGMGSALATLCGQAYGAGQLEMMGIYLQRSWIILNSCALLLCLFYVFATPLLSLLGQSPEISKAAGKFSLWMIPQLFAYAVNFATAKFLQAQSKVIAMAVIAATVLLQHTLLSWLLMLKLRWGMAGGAVVLNMSWWLIDVTQIVYICGGSSGRAWSGLSWMAFKNLRGFARLSLASAVMVCLEVWYFMALILFAGYLKNPQVSVAALSICMNILGWPIMVAFGFNAAVSVRESNELGAEHPRRAKFLLIVAMITSVSIGIVISVTLIVLRDKYPAMFSDDEEVRVLVKQLTPLLALTIVINNIQPVLSGVAVGAGWQGIVAYVNIGCYYLCGIPIGLVLGYKMELGVKGIWTGMLTGTVVQTSVLLFIIYRTNWKKEASLAEARIKKWGDQSNKREEIDLCEEDENNSNGENNHRK
82	AT1G47530	MGKDKTLPLLDPREPPELTGTKSASKVWAKEFGEESKRLWELAGPAIFTAISQYSLGALTQTFSGRLGELELAAVSVENSVISGLAFGVMLGMGSALETLCGQAYGAGQIRMMGIYMQRSWVILFTTALFLLPVYIWAPPILSFFGEAPHISKAAGKFALWMIPQLFAYAANFPIQKFLQSQRKVLVMAWISGVVLVIHAVFSWLFILYFKWGLVGAAITLNTSWWLIVIGQLLYILITKSDGAWTGFSMLAFRDLYGFVKLSLASALMLCLEFWYLMVLVVVTGLLPNPLIPVDAISICMNIEGWTAMISIGFNAAISVRVSNELGAGNAALAKFSVIVVSITSTLIGIVCMIVVLATKDSFPYLFTSSEAVAAETTRIAVLLGFTVLLNSLQPVLSGVAVGAGWQALVAYVNIACYYIIGLPAGLVLGFTLDLGVQGIWGGMVAGICLQTLILIGIIYFTNWNKEAEQAESRVQRWGGTAQE
83	AT4G25640	MDPTAPLLTHGGEVEEDYAPARSWTDVKRVLSTESAKLWMIAAPVGFNIICQYGVSSVTNIFVGHIGEVELSAVSISLSVIGTFSFGFLLGMGSALETLCGQAYGAGQVNMLGVYMQRSWIILFVSCFFLLPIYIFATPVLRLLGQAEEIAVPAGQFTLLTIPQLFSLAFNFPTSKFLQAQSKVVAIAWIGFVALSLHVIMLWLFIIEFGWGTNGAALAFNITNWGTAIAQIVYVIGWCNEGWTGLSWLAFKEIWAFVRLSIASAVMLCLEIWYMMSIIVLTGRLDNAVIAVDSLSICMNINGLEAMLFIGINAAISVRVSNELGLGRPRAAKYSVYVTVFQSLLIGLVFMVAIIIARDHFAIIFTSSKVLQRAVSKLAYLLGITMVLNSVQPVVSGVAVGGGWQGLVAYINLGCYYIFGLPFGYLLGYIANFGVMGLWSGMIAGTALQTLLLLIVLYKTNWNKEVEETMERMKKWGGSETTSKDILASGWPSGLRRQTQVLVFVRGRGFKPHF

84	AT4G00350	MEIPVREERRSSSSSAGPLQQTISLAADDAIDSGPSSPLVVKVSVFETEHETTKLIHAPSTLLGETTGDADFPPIQSFRDAKLVCVVETSKLWEIAAPIAFNILCNYGVNSFTSIFVGHIGDLELSAVAIALSVVSNFSFGFLLGMASALETLCGQAFGAGQMDMLGVYMQRSWLILLGTSVCLLPLYIYATPLLILLGQEPEIAEISGKFTTQIIPQMFALAINFPTQKFLQSQSKVGIMAWIGFFALTLHIFILYLFINVFKWGLNGAAAAFDVSAWGIAIAQVVYVVGWCKDGWKGLSWLAFQDVWPFLKLSFASAVMLCLEIWYFMTIIVLTGHLEDPVIAVGSLSICMNINGWEGMLFIGINAAISVRVSNELGSGHPRAAKYSVIVTVIESLVIGVVCAIVILITRDDFAVIFTESEEMRKAVADLAYLLGITMILNSLQPVISGVAVGGGWQAPVAYINLFCYYAFGLPLGFLLGYKTSLGVQGIWIGMICGTSLQTLILLYMIYITNWNKEVEQASERMKQWGAGYEKLEKIAT
85	AT1G61890	MNSESLENLHRPLIESSKSFVDYRLETVLTDRELPYFRRIYLAMMIEMKFLFHLAAPAIFVYVINNGMSILTRIFAGHVGSFELAAASLGNSGFNMFTYGLLLGMGSAVETLCGQAHGAHRYEMLGVYLQRSTVVLILTCLPMSFLFLFSNPILTALGEPEQVATLASVFVYGMIPVIFAYAVNFPIQKFLQSQSIVTPSAYISAATLVIHLILSWIAVYRLGYGLLALSLIHSFSWWIIVVAQIVYIKMSPRCRRTWEGFSWKAFEGLWDFFRLSAASAVMLCLESWYSQILVLLAGLLKNPELALDSLAICMSISAISFMVSVGFNAAASVRVSNELGAGNPRAAAFSTVVTTGVSFLLSVFEAIVVLSWRHVISYAFTDSPAVAEAVADLSPFLAITIVLNGIQPVLSGVAVGCGWQAFVAYVNIGCYYVVGIPVGFVLGFTYDMGAKGIWTGMIGGTLMQTIILVIVTLRTDWDKEVEKASSRLDQWEESREPLLKQ
86	AT1G11670	MGSEATTAVNNLQQPLLESTKSEADFRMESVLTDTHLSYFRRIYLASLIEMKYLFHLAAPAIFVYVINNGMSMLTRIFAGRLGSMQLAAASLGNSGFNMFTLGLMLGMGSAVETLCGQAHGAHRYDMLGVYLQRSTIVLVITGLPMTLLFIFSKPLLISLGEPADVASVASVFVYGMIPMIFAYAVNFPIQKFLQSQSIVTPSAYISAATLVIHLILSWLSVFKFGWGLLGLSVVHSLSWWIIVLAQIIYIKISPRCRRTWDGFSWKAFDGLWDFFQLSAASAVMLCLESWYSQILVLLAGLLKDPELALDSLAICMSISAMSFMVSVGFNAAASVRVSNELGAGNPRSAAFSTAVTTGVSFLLSLFEAIVILSWRHVISYIFTDSPAVAEAVAELSPFLAITIVLNGVQPVLSGVAVGCGWQAYVAYVNIGCYYIVGIPIGYVLGFTYDMGARGIWTGMIGGTLMQTIILVIVTFRTDWDKEVEKASRRLDQWEDTSPLLKQ

87	AT4G21910	MEVPSETTNLADLRRPLVVPVVSERKPPADVGLGLESVLTERSLPYRRRVYLGACIEMKLLFRLALPAILVYLVNSGMGISARIFAGHLGKNELAAASIGNSCFSLVYGLMLGMGSAVETLCGQAYGAHRYEMLGIYLQRATIVLALVGLPMTLLYTFSYPILILLGEPKTVSYMGSKYIAGLIPQIFAYAVNFTAQKFLQAQSVVAPSAFISAAALILQILLTWITVYVMDMGFMGIAYVLTISWWVIVGSQCFYIAVSPKFRHTWTGLSWRSLQGLWSFFKLSAGSAVMICLEMWYSQILVLLAGLLENPARSLDSLSICMSISALSFMVSVGFNAAVSVRTSNELGAGNPKSAWFSTWTATFVSFVISVTEALAVIWFRDYVSYIFTEDADVAKAVSDLCPFLAITIILNGIQPVLSGVAVGCGWQTYVAYVNVGCYYVVGIPVGCILGFTFDFQAKGIWTGMIGGTLMQTLILLYVTYRTDWDKEVMLHEIKWKKRGNVWICGTTRRSLSKTSYNKFGGVIDNKEKEISVVCAGDFNVRSFSWLLCLFYGNRTIKIYFCLMDYSLFTKSCS
88	AT3G21690	MDSSPNDGVHQPLLHPQPSPSPPESTNGELETVLSDVETPLFLRLRKATIIESKLLFNLAAPAVIVYMINYLMSMSTQIFSGHLGNLELAAASLGNTGIQVFAYGLMLGMGSAVETLCGQAYGGRKYEMLGVYLQRSTVLLTLTGLLLTLIYVFSEPILLFLGESPAIASAASLFVYGLIPQIFAYAANFPIQKFLQSQSIVAPSAYISTATLFVHLLLSWLAVYKLGMGLLGASLVLSLSWWIIVVAQFVYIVTSERCRETWRGFSVQAFSGLWSFFKLSAASAVMLCLETWYFQILVLLAGLLENPELALDSLSICMTISGWVFMISVGFNAAISVRVSNELGAGNPKSAAFSVIIVNIYSLITCVILAIVILACRDVLSYAFTEGKEVSDAVSDLCPLLAVTLVLNGIQPVLSGVAVGCGWQTFVAKVNVGCYYIIGIPLGALFGFYFNFGAKGIWTGMIGGTVIQTFILAWVTFRTDWTKEVEEASKRLDKWSNKKQEVVPE
89	AT3G59030	MSSTETYEPLLTRLHSDSQITERSSPEIEEFLRRRGSTVTPRWWLKLAVWESKLLWTLSGASIVVSVLNYMLSFVTVMFTGHLGSLQLAGASIATVGIQGLAYGIMLGMASAVQTVCGQAYGARQYSSMGIICQRAMVLHLAAAVFLTFLYWYSGPILKTMGQSVAIAHEGQIFARGMIPQIYAFALACPMQRFLQAQNIVNPLAYMSLGVFLLHTLLTWLVTNVLDFGLLGAALILSFSWWLLVAVNGMYILMSPNCKETWTGFSTRAFRGIWPYFKLTVASAVMLCLEIWYNQGLVIISGLLSNPTISLDAISICMYYLNWDMQFMLGLSAAISVRVSNELGAGNPRVAMLSVVVVNITTVLISSVLCVIVLVFRVGLSKAFTSDAEVIAAVSDLFPLLAVSIFLNGIQPILSGVAIGSGWQAVVAYVNLVTYYVIGLPIGCVLGFKTSLGVAGIWWGMIAGVILQTLTLIVLTLKTNWTSEVENAAQRVKTSATENQEMANAGV

90	AT3G23560	MADPATSSPLLDDHVGGEDERGRRSRSSTLVQKVIDVEEAKAQMIYSLPMILTNVFYYCIPITSVMFASHLGQLELAGATLANSWATVSGFAFMVGLSGSLETLCGQGFGAKRYRMLGVHLQSSCIVSLVFSILITIFWFFTESIFGLLRQDPSISKQAALYMKYQAPGLLAYGFLQNILRFCQTQSIIAPLVIFSFVPLVINIATAYVLVYVAGLGFIGAPIATSISLWIAFLSLGTYVMCSEKFKETWTGFSLESFRYIVINLTLSLPSAAMVCLEYWAFEILVFLAGVMPNPEINTSLVAICVNTEAISYMLTYGLSAAASTRVSNELGAGNVKGAKKATSVSVKLSLVLALGVVIVLLVGHDGWVGLFSDSYVIKEEFASLRFFLAASITLDSIQGVLSGVARGCGWQRLVTVINLATFYLIGMPIAAFCGFKLKFYAKGLWIGLICGIFCQSSSLLLMTIFRKWTKLNVATV
91	AT3G23550	MADPTSKDDHDGEGGRDKSSTFVQKLIDVEEAKTQIIYSLPMIFTNLFYYCIPLTSVMFASQLGQLELAGATLANSWATVTGFAFMTGLSGALETLCGQGFGAKSYRMLGIHLQSSCIVSLVFTILITILWFFTESVFLLLRQDPSISKQAALYMKYLAPGLLAYGFLQNILRFCQTQCIVTPLVLFSFLPLVINIGTTYALVHLAGLGFIGAPIATSISLWIAFVSLGFYVICSDKFKETWTGFSMESFHHVVLNLTLSIPSAAMVCLEYWAFEILVFLAGLMRNPEITTSLVAICVNTESISYMLTCGLSAATSTRVSNELGAGNVKGAKKATSVSVKLSLVLALGVVIAILVGHDAWVGLFSNSHVIKEGFASLRFFLAASITLDSIQGVLSGVARGCGWQRLATVINLGTFYLIGMPISVLCGFKLKLHAKGLWIGLICGMFCQSASLLLMTIFRKWTKLTAATV
92	AT2G04070	MEEPFLPQDEQIVPCKATWKSGQLNVELKKVSRLAVPMATVTIAQYLLPVISVMVAGHNGELQLSGVALATSFTNVSGFSIMFGLVGSLETLSGQAYGAKQYEKMGTYTYSAISSNIPICVLISILWIYMEKLLISLGQDPDISRVAGSYALRLIPTLFAHAIVLPLTRFLLAQGLVLPLLYFALTTLLFHIAVCWTLVSALGLGSNGAALAISVSFWFFAMTLSCYVRFSSSCEKTRRFVSQDFLSSVKQFFRYGVPSAAMLCLEWWLFELLILCSGLLQNPKLETSVLSICLTTATLHYVIPVGVAAAVSTRVSNKLGAGIPQVARVSVLAGLCLWLVESSFFSILLFAFRNIIGYAFSNSKEVVDYVADLSPLLCLSFVLDGFTAVLNGVARGCGWQHIGALNNVVAYYLVGAPVGIYLAFSCELNGKGLWCGVVVGSAVQAIILAIVTASMNWKEQAKKARKRLISSENGLA

93	AT2G04050	MEEPFLLQDEHLVPCKDTWKSGQVTVELKKVSSLAAPMAAVTIAQYLLPVISVMVAGHNGELQLSGVALATSFTNVSGFSILFGLAGALETLCGQAYGAKQYEKIGTYTYSATASNIPICVLISVLWIYIEKLLISLGQDPDISRVAGSYALWLIPALFAHAFFIPLTRFLLAQGLVLPLLYCTLTTLLFHIPVCWAFVYAFGLGSNGAAMAISVSFWFYVVILSCYVRYSSSCDKTRVFVSSDFVSCIKQFFHFGVPSAAMVCLEWWLFELLILCSGLLPNPKLETSVLSICLTTASLHYVIPGGVAAAVSTRVSNKLGAGIPQVARVSVLAGLCLWLVESAFFSTLLFTCRNIIGYAFSNSKEVVDYVANLTPLLCLSFILDGFTAVLNGVARGSGWQHIGALNNVVAYYLVGAPVGVYLAFNRELNGKGLWCGVVVGSAVQAIILAFVTASINWKEQAEKARKRMVSSENRLA
94	AT2G04080	MEEPFLPRDEQLVSCKSTWQSGQVTVELKKVSRLAAPMATVTIAQYLLPVISVMVAGHIGELELAGVALATSFTNVSGFSIMFGLVGALETLCGQAYGAEQYEKIGTYTYSAMASNIPICFIISILWIYIEKLLITLGQEPDISRVAGSYSLWLVPALFAHAIFLPLTRFLLAQGLVISLLYSAMTTLLFHIAVCWTLVFALGLGSNGAAIAISLSFWFYAVILSCHVRFFSSCEKTRGFVSNDFMSSIKQYFQYGVPSAGLICLEWWLFELLILCSGLLPNPKLETSVLSICLTIGTLHYVIPSGVAAAVSTRVSNKLGAGNPQVARVSVLAGLCLWLVESAFFSTLLFTCRNIIGYTFSNSKEVVDYVADISPLLCLSFILDGLTAVLNGVARGCGWQHIGALINVVAYYLVGAPVGVYLAFSREWNGKGLWCGVMVGSAVQATLLAIVTASMNWKEQAEKARKRIISTENGLV
95	AT2G04040	MEEPFLLRDELLVPSQVTWHTNPLTVELKRVSRLAAPMATVTIAQYLLPVISVMVAGHNGELQLSGVALANSFTNVTGFSIMCGLVGALETLCGQAYGAKQYEKIGTYAYSAIASNIPICFLISILWLYIEKILISLGQDPEISRIAGSYAFWLIPALFGQAIVIPLSRFLLTQGLVIPLLFTAVTTLLFHVLVCWTLVFLFGLGCNGPAMATSVSFWFYAVILSCYVRFSSSCEKTRGFVSRDFVSSIKQFFQYGIPSAAMICLEWWLFEILILCSGLLPNPKLETSVLSICLTIETLHYVISAGVAAAVSTRVSNNLGAGNPQVARVSVLAGLCLWIVESAFFSILLFTCRNIIGYAFSNSKEVLDYVADLTPLLCLSFILDGFTAVLNGVARGSGWQHIGAWNNTVSYYLVGAPVGIYLAFSRELNGKGLWCGVVVGSTVQATILAIVTASINWKEQAEKARKRIVSTENRLA

96	AT2G04100	MEDPLLLGDNQIITGSLKPTPTWRMNFTAELKNLSRMALPMATVTVAQYLLPVISVMVAGHRSELQLSGVALATSFTNVSGFSVMFGLAGALETLCGQAYGAKQYAKIGTYTFSAIVSNVPIVVLISILWFYMDKLFVSLGQDPDISKVAGSYAVCLIPALLAQAVQQPLTRFLQTQGLVLPLLYCAITTLLFHIPVCLILVYAFGLGSNGAALAIGLSYWFNVLILALYVRFSSSCEKTRGFVSDDFVLSVKQFFQYGIPSAAMTTIEWSLFEFLILSSGLLPNPKLETSVLSICLTTSSLHYVIPMGIGAAGSIRVSNELGAGNPEVARLAVFAGIFLWFLEATICSTLLFICRDIFGYAFSNSKEVVDYVTELSPLLCISFLVDGFSAVLGGVARGSGWQHIGAWANVVAYYLLGAPVGLFLGFWCHMNGKGLWIGVVVGSTAQGIILAIVTACMSWNEQAAKARQRIVVRTSSFGNGLA
97	AT2G04090	MEDPLLLGDDQLITRNLKSTPTWWMNFTAELKNVSSMAAPMATVTVSQYLLPVISVMVAGHCGELQLSGVTLATAFANVSGFGIMYGLVGALETLCGQAYGAKQYTKIGTYTFSAIVSNVPIVVLISILWFYMDKLFVSLGQDPDISKVAGSYAVCLIPALLAQAVQQPLTRFLQTQGLVLPLLYCAITTLLFHIPVCLILVYAFGLGSNGAALAIGLSYWFNVLILALYVRFSSACEKTRGFVSDDFVLSVKQFFQYGIPSAAMTTIEWSLFELLILSSGLLPNPKLETSVLSICLTTSSLHCVIPMGIGAAGSTRISNELGAGNPEVARLAVFAGIFLWFLEATICSTLLFTCKNIFGYAFSNSKEVVDYVTELSSLLCLSFMVDGFSSVLDGVARGSGWQNIGAWANVVAYYLLGAPVGFFLGFWGHMNGKGLWIGVIVGSTAQGIILAIVTACLSWEEQAAKARERIVGRTLE
98	AT1G66780	MENGFSLVPKEEEEEEDYSNEKSEDQTSYYLSTEMMKKVSFMAAPMVAVAASQYLLQVISIVMAGHLDELSLSAVAIATSLTNVTGFSLIFGLAGALETLCGQAFGAGQFRNISAYTYGSMLCLLLVCFPISLLWVFMDKLLELFHQDPLISQLACRYSIWLIPALFGYSVLQSMTRFFQSQGLVLPLFLSSLGALFFHVPFSWLLVYKLRFGIVGAALSIGFSYWLNVGLLWAFMRDSALYRKNWNLRAQEIFLSMKQFITLAIPTAMMTCLEWWSFELLILMSGLLPNSKLETSVLSICLTMSSLHYVIVNAIGAAASTHVSNKLGAGNPKAARSAANSAIFLGMIDAAIVSISLYSYRRNWAYIFSNESEVADYVTQITPFLCLSIGVDSFLAVLSGVARGTGWQHIGAYANIGSYYLVGIPVGSILCFVVKLRGKGLWIGILVGSTLQTIVLALVTFFTNWEQEVAKARDRVIEMIPQEII

99	AT1G64820	METDFSLVRKEEEEEEEDNRNGMSYLSMEMMKKVSSMAAPMVAVSVSQFLLQVISMVMAGHLDELSLSAVAIATSLTNVTGFSLIVGFAGALDTLCGQAFGAEQFGKIGAYTYSSMLCLLVFCFSISIVWFFMDKLLEIFHQDPLISQLACRYSIWLIPALFGFTLLQPMTRYFQSQGITLPLFVSSLGALCFHIPFCWLLVYKLKFGIVGAALSIGFSYWLNVFLLWIFMRYSALHREMKNLGLQELISSMKQFIALAIPSAMMICLEWWSFEILLLMSGLLPNSKLETSVISICLTTSAVHFVLVNAIGASASTHVSNELGAGNHRAARAAVNSAIFLGGVGALITTITLYSYRKSWGYVFSNEREVVRYATQITPILCLSIFVNSFLAVLSGVARGSGWQRIGGYASLGSYYLVGIPLGWFLCFVMKLRGKGLWIGILIASTIQLIVFALVTFFTNWEQEATKARDRVFEMTPQVKGNQKTQIIVEEDTQVLLNHIAETV
100	AT1G66760	MKKSIETPLLLNTKQSQDEDKEKIRWEKMKKVASMAAPMVAVNMSQYLLQATSTMIVGHRSELALAGIALGSSFANVTGFGVLFGLSGSLETLCGQAYGAKQYHKLGSYTFTSIVFLLIISVPISILWMFMNQILLLLHQDPQIAELAGVYCLWLVPALFGYSVLESLVRYFQSQSLIYPMVLSSLAALSFHVPLCWLMVHKFDFGAKGAAASIGISYWLNAVFLWVYMKRSSRCVETRIYMSKDVFVHTNIFFQFAIPSAMMCCLEWLAFEVITLLSGLLPNSKLETSVISICLTTSSLHYNLVNGIGDAASTNVANELGAGNPRGARDSAAAAIIIAAVESVIVSSSLFLSRSVWPYAYSNVEEVISYVTDITPILCISILMDSFLTVLSGIVRGTGWQKIGAYVNITSYYVIGIPVGLLLCFHLHFNGKGLWAGLVTGSTLQTLILFLVIGFTNWSKEAIKARERIGDEKVWRHDSLLN
101	AT1G15170	MGDAESTKDRLLLPVERVENVTWSDLRDGSFTVELKRLIFFAAPMAAVVIAQFMLQIVSMMMVGHLGNLSLASASLASSFCNVTGFSFIIGLSCALDTLSGQAYGAKLYRKLGVQTYTAMFCLALVCLPLSLIWFNMEKLLLILGQDPSIAHEAGKYATWLIPGLFAYAVLQPLTRYFQNQSLITPLLITSYVVFCIHVPLCWFLVYNSGLGNLGGALAISLSNWLYAIFLGSFMYYSSACSETRAPLSMEIFDGIGEFFKYALPSAAMICLEWWSYELIILLSGLLPNPQLETSVLSVCLQTISTMYSIPLAIAAAASTRISNELGAGNSRAAHIVVYAAMSLAVIDALIVSMSLLIGRNLFGHIFSSDKETIDYVAKMAPLVSISLMLDALQGVLSGIARGCGWQHIGAYINLGAFYLWGIPIAASLAFWIHLKGVGLWIGIQAGAVLQTLLLALVTGCTNWESQADKARNRMALAYGT

102	AT1G15180	MGDAESTSKTSLLLPVERVENVTWRDLRDGLFTAELKRLICFAAPMAAVVIAQFMLQIISMVMVGHLGNLSLASASLASSFCNVTGFSFIVGLSCALDTLSGQAYGAKLYRKVGVQTYTAMFCLALVCLPLTLIWLNMETLLVFLGQDPSIAHEAGRYAACLIPGLFAYAVLQPLTRYFQNQSMITPLLITSCFVFCLHVPLCWLLVYKSGLGNLGGALALSFSNCLYTIILGSLMCFSSACSETRAPLSMEIFDGIGEFFRYALPSAAMICLEWWSYELIILLSGLLPNPQLETSVLSVCLQTTATVYSIHLAIAAAASTRISNELGAGNSRAANIVVYAAMSLAVVEILILSTSLLVGRNVFGHVFSSDKETIDYVAKMAPLVSISLILDGLQGVLSGIARGCGWQHIGAYINLGAFYLWGIPIAASLAFWIHLKGVGLWIGIQAGAVLQTLLLTLVTGCTNWESQADKARNRMALAYGT
103	AT1G71160	MESSFHFINEALLITQTFITFHQFLVASACVLIAVFGYYFFKPRCIIYLIDFSCYQPPDFLRAPVSNFIEHLTISGVFDQESLDLQQKILERSGISDDASVPATVHEIPPNASISAAREETHEILFAIVQDLFSKHEIDPKSIDILVSNCSLFCPSPSITSMIINKFGMRSDIKSFSLSGMGCSAGILSVNLVKDLMKIHGDSLALVLSMEAVSPNGYRGKCKSMLIANTIFRMGGAAILLSNRKQDSHKAKYKLQHIIRTHVGSDTESYESVMQQVDEEGKVGVALSKQLVRVASKALKINVVQLGPRVLPYSEQLKYIISFIQRKWGMHKEIYTPNFKKAFEHFCIHAGGRAIIEGVEKHLKLDKEDVEASRSTLYRYGNTSSSSLWYELQYLEAKGRMKMGDKVWQIGFGSGFKANSAVWKCISEIDSRGRNAWSDRIHLYPVCGDTSSALKTELLS
104	AT1G71150	MAKPNIDELNQILTSYQNTINDTLQLFEQVPSPTQDKLYWNDVLQISDHLSKQATIVGMLWITGEPPKAEAMKETMEAYFNALQGFLLHCHGSMVGAGTTLSSTIHASVKQIVDSSFRLLQGSVSLYEGSYEKGRKPTIPQLAGAVWEACSNLKNVPETNIKAIGRAMAHVAVSMKDVLREMKELKPASSSPDHNVSTNSDDDDLGDELSPEEFEVAKMVADIVSETLVVIKELIRAITCMIKLENPKDNSEFVDSFEKLLKLCQGIGVQIDELGACVYPPQEFGLMKQTVENMRESIGEIESDVKSSKNSSSEALSGSCRRLQSLIEHMVTELDTRIEAEVVYKMQNVTL
105	AT1G71140	MDSAEKGLLVVSDREEVNKKDGFLRETKKLSYIAGPMIAVNSSMYVLQVISIMMVGHLGELFLSSTAIAVSFCSVTGFSVVFGLASALETLCGQANGAKQYEKLGVHTYTGIVSLFLVCIPLSLLWTYIGDILSLIGQDAMVAQEAGKFATWLIPALFGYATLQPLVRFFQAQSLILPLVMSSVSSLCIHIVLCWSLVFKFGLGSLGAAIAIGVSYWLNVTVLGLYMTFSSSCSKSRATISMSLFEGMGEFFRFGIPSASMICLEWWSFEFLVLLSGILPNPKLEASVLSVCLSTQSSLYQIPESLGAAASTRVANELGAGNPKQARMAVYTAMVITGVESIMVGAIVFGARNVFGYLFSSETEVVDYVKSMAPLLSLSVIFDALHAALSGVARGSGRQDIGAYVNLAAYYLFGIPTAILLAFGFKMRGRGLWIGITVGSCVQAVLLGL

		IVILTNWKKQARKARERVMGDEYEEKESEEEHEYIS
106	AT2G34560	MATDEPSQTRWSFLEFKTFYDAKFGRKKLPEEDVSNKDQPEDGSSNGNNGDVNNNSSPVTNQDGNTALANGNVIREKPKKSMFPPFESAETRTLAESLSRDIIRGNPNIKWESIKGLENAKKLLKEAVVMPIKYPTYFNGLLTPWKGILLFGPPGTGKTMLAKAVATECNTTFFNISASSVVSKWRGDSEKLIRVLFDLARHHAPSTIFLDEIDAIISQRGGEGRSEHEASRRLKTELLIQMDGLQKTNELVFVLAATNLPWELDAAMLRRLEKRILVPLPDPEARRGMFEMLIPSQPGDEPLPHDVLVEKSEGYSGSDIRILCKEAAMQPLRRTLAILEDREDVVPEDELPKIGPILPEDIDRALSNTRPSAHLHAHLYDKFNDDYGSQILK
107	AT5G52450	MRDDRERGEGDLSWPLIGEKSSVKEEVKKQLWLSGPLIAVSLLQFCLQVISVMFVGHLGSLPLSAASIATSFASVTGFSFLMGTASALDTLCGQAYGAKKYGMLGIQMQRAMFVLTLASIPLSIIWANTEHLLVFFGQNKSIATLAGSYAKFMIPSIFAYGLLQCFNRFLQAQNNVFPVVFCSGVTTSLHVLLCWVLVFKSGLGFQGAALANSISYWLNVVLLFCYVKFSPSCSLTWTGFSKEALRDILPFLRLAVPSALMVCLEMWSFELLVLLSGLLPNPVLETSVLSICLNTSGTMWMIPFGLSGAASTRISNELGAGNPKVAKLAVRVVICIAVAESIVIGSVLILIRNIWGLAYSSELEVVSYVASMMPILALGNFLDSLQCVLSGVARGCGWQKIGAIINLGSYYLVGVPSGLLLAFHFHVGGRGLWLGIICALVVQVFGLGLVTIFTNWDEEAKKATNRIESSSSVKDFAVDDRSVVVF
108	AT1G73700	MEDGVTPPLLITEKDTTMIRVKEEVKKQLWLSAPLIGVSLLQYSLQVISVMFVGHLGSLPLSAASIATSFASVTGFTFLLGTASALETLCGQAYGAKLYGKLGIQMQRAMFVLLILSVPLSIIWANTEQILVLVHQDKSIASVAGSYAKYMIPSLFAYGLLQCINRFLQAQNNVFPVFVCSGITTCLHLLLCWLFVLKTGLGYRGAALAISVSYWFNVILLSCYVKFSPSCSHSWTGFSKEAFQELYDFSKIAFPSAVMVCLELWSFELLVLASGLLPNPVLETSVLSICLNTSLTIWQISVGLGGAASIRVSNELGAGNPQVAKLAVYVIVGIAVAEGIVVVTVLLSIRKILGHAFSSDPKIIAYAASMIPIVACGNFLDGLQCVLSGVARGCGWQKIGACVNLGSYYLVGVPLGLLLGFHFHIGGRGLWLGIVTALSVQVLCLSLVTIFTNWDKEAKKATNRVGSSDDKDGDVQ

109	*Pt*XP002307572	MGEESEYQTPLLELDSHSRIRDLSSVTIEEFLEHGPVAVRWWPRLVAWESRLLWILSGSSIIVSVSTFMLSFVTQMFSGHLGALELAGASIANVGIQGLAYGIMLGMASAVQTVCGQAYGAKKYSSMGIICQRAIILHLGAAFLLTFLYWFSGPVLRAIGQTESIAEQGEIFARGLIPQLYAFAFSCPMQRFLQAQNIVNPLAYMSVAVFLLHILLTWIVVYVLQYGLLGAALTLSFSWWLFVILNGLYIILSPSCKETWTGLSASAFTGIWPYFKLTVSSAVMLCLEIWYSQGLVLISGLLTDPTVALDSISICMNYLNWDMQFMLGLSASTSVRVGNELGAGHPKVAKLSVMVVNGTSIVISIIFSAIVLIFRVGLSKLFTTDYEVIDAVSDLTPLLAISVFLNGIQPILSGVAIGSGWQATVAYVNLATYYVIGLPIGCVLAFKTSLGVAGIWWGMVAGVLLQTITLIILTARTNWDTEVQNAAERVKKSANEDFSGLVEAI
110	*Vv*XP002282932	MGSEEYQPLLLGLNSHARIPDLSSFAVEEFLAHKPVAVRWWPRLFGWESRLLWLLSGSSIVASIFNYMLSFVTLMFTGHLGALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKKYKAMGIICQRAIILHLGAAVLLTFLYWFSGPFLRAIGQSDSISAQGQIFARGLILQLYAFAISCPMQRFLQAQNIVNPLAYMAVGVFFLHVLLTWLVVYVLDYGLLGAALTLSFSWWILVVVIALYILLSPSCKETWTGFSSKAFKGMWPYFKLTVASAVMLCLEIWYNQGLVLISGLLSNPTISLDSISICMNYLNWDMQFMLGLSAATSVRVSNELGASHPKVAKLSVLVVNTNSIIISIFFSAIILIFKVGLSKLFTNDAEVIEAVSNLTPLLAISVFLNGIQPILSGVAIGSGWQAIVAYVNLATYYLIGLPIGCVLGFKTSLGVAGIWWGMIIGVLLQTVTLIILTARTDWNAEVSKAAERLRNSANVENLNLLEDV
111	***Vv***CAO69962	MASAAEDGEPLLLGHSSAGIHELSSSAVEELLLHKPVPGRWWPRLFGWESRLLWVLSGSAIVSSVFNYMLSFITLMFAGQLGALELAGASIASVGIQGLAYGLMLGMASAVQTVCGQAYGAKKYAAMGIICQRAIVLHLGAAILLTFLYWYSGAFLKAIGQSESIAVQGQIFARGLILQVYAFALSCPMQRFLQAQNIVNPLAYIAVGVTLLHILLTWLVVNVLDSGLLGIALTLSLSWWLLVFSIALYILLSPSCKETWTGFSLKAFQGIWPYFKLTVASAVMLCLEIWYSQGLVLISGLLPNPTVSLDSISICMNYLNWDITFMLGLSAGASVRISNELGAAHPLVAKFSVLVVNANSIIISIFFSAIVLIFKIGLSKLFTSDTEVINAVSNLTPLLAISVFLNGIQPILSGVAIGSGWQAIVAYVNLATYYLIGLPIGCVLGFKTSLGVVGIWWGMIIGVLLQTVTLIVLTARTNWDAEVILWVD

112	*Md*GU064953	MGSQEEYQPLLIRLDSYSQIPNLSSSAIEEFLEHKPVAVRWWPKLVAWESRLLWILSGSSIAVSIFNYMLSFVTLMFCGHLGALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKQLPAMGIICQRAIILHLGAAVLLTFVYWWSGPILIAIGQTEDIAEQGQVFARGIIPQLYAFAINCPQQRFLQAQNIVNPLAYMSFGVFLVHILLTWVVVYVVDYGLMGAALTLSLSWWLLVITYGIYILVSPMCKETWTGFSWKAFRGIWPYFKLTLASAIMLCLEIWYNQGLVLISGLLSNPTISLDSISICMNYLNWDMQFMLGLSAAASVRVSNELGAGHPKVAKFSVFVVNGTSILISIVFSAIILIFRVGLSKLFTSDAEVIAAVSDLTSLLAISVFLNGIQPILSGVAIGSGWQAVVAYVNLTCYYIIGLPIGCVLGFKTSMGVAGIWWGMIIGVFLQTVTLIVLTARTNWDSEVVKAAERLKKSASAERLDLVTDI
113	*Md*GU064955	MGTAEEYQPLLNGLDSHSRIPDLSSTAVEEFLEHKPVAVRWWLRLVAWESRLLWTLSGSSIIVSIFNYMLSFTTLMFCGHLSALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGARQYPAMGIICQRAIVLHLGAAVLLTFLYWWSGPILIAIGQTEEIAEQGQVFARGIVPQLYAFAINCPQQRFLQAQNIVNPLAFMSFGVFLVHILLSWVVVYVADYGLTGAALTLSFSWWLLVIVYGIYIVVSPKCKETWTGFSGKALWGIWPYFKLTVASAIMLCLEIWYSQGLVLISGLLANPTIALDSISICMNYLNDMQFMLGLAAAASVRVSNELGAGHAKVAKFSVFVVNGTSILISIIFTAIILIFRVALSKLFTSDDEVVTAVSNLTPLLAISVFLNGIQPILSGVAIGSGWQAVVAYVNLTCYYIIGLPIGCVLGFKTSMGVAGIWWGLIIGVFLQTVTLIVLTARTNWTAEVEKAAERLKRSASAERLKRSASAERLDLVTDI
114	*Bn*ACJ36209	MSSTETYEPLLRRLHSDSQITERSSPEIEEFLGRGRSTVTTRWWLRLFVWESKLLWKLSGASIVVSVLNYMLSFVTVMFTGHLGSLELAGASIATVGIQGLAYGIMLGMASAVQTVCGQAYGARQYSSMGIICQRAMVLHLAAAVLLTFLYWYSGPILKAMGQTVAIAHEGQVFARGMIPQIYAFALACPMQRFLQAQNIVNPLAYMSLGVFLLHTLLTWLVTNVLDFGLLGAALILSLSWWLLAAVNGLYIVMSPSCRETWTGFSARALTGIWPYLKLTVASAVMLCLEIWYNQGLVIISGLLTNPTISLDAISICMYYLNWDMQFMLGLSAAISVRVSNELGAGNPRVAKLSVVVVNITTVLISLLLCIVVLVFRVGLSKAFTSDKEVIVAVSDLFPLLAVSIFLNGIQPILSGVAIGSGWQAVVAYVNLVTYYVIGLPIGCVLGFKTSLGVAGIWWGMIAGVILQTITLIVLTLRTNWTSEVENAAHRLKASANESQEMATEGV

115	*Bn*ACJ36211	MSSTETYEPLLRRLHSDSQITERSSPEIEEFLGRGRSTVTPRWWLRLFVWESKLLWKLSGASIVVSVLNYMLSFVTVMFTGHLGSLELAGASIATVGIQGLAYGIMLGMASAVQTVCGQAYGARQYSSMGIICQRAMVLHLAAAVLLTFLYWYSGPILKAMGQTVAIAHEGQVFARGMIPQIYAFALACPMQRFLQAQNIVNPLAYMSLGVFLLHTLLTWLVTNVLDFGLLGAALILSFSWWLLAAVNGLYIVMSPSCRETWTGFSARALTGIWPYLKLTVASAVMLCLEIWYNQGLVIISGLLTNPTISLDAISICMYYLNWDMQFMLGLSAAISVRVSNELGAGNPRVAKLSVVVVNITTVLISLFLCVVVLVFRVGLSKAFTSDKEVIVAVSDLFPLLAVSIFLNGIQPILSGVAIGSGWQAVVAYVNLVTYYVIGLPIGCVLGFKTSLGVAGIWWGMIAGVILQTITLIVLTLRTNWTSEVENAAHRLKASANESQEMATEGV
116	*Br*ACJ36214	MSSTETYEPLLRRLHSDSQITERSSPEIEEFLGRGRSTVTPRWWLRLFVWESKLLWKLSGASIVVSVLNYMLSFVTVMFTGHLGSLELAGASIATVGIQGLAYGIMLGMASAVQTVCGQAYGARQYSSMGIICQRAMVLHLAAAVLLTFLYWYSGPILKAMGQTVAIAHEGQVFARGMIPQIYAFALACPMQRFLQAQNIVNPLAYMSLGVFLLHTLLTWLVTNVLDFGLLGAALILSFSWWLLAAVNGLYIVMSPNCRETWTGFSARALTGIWPYLKLTVASAVMLCLEIWYNQGLVIISGLLTNPTISLDAISICMYYLNWDMQFMLGLSAAISVRVSNELGAGNPRVAKLSVVVVNITTVLISLLLCIVVLVFRVGLSKAFTSDKEVIVAVSDLFPLLAVSIFLNGIQPILSGVAIGSGWQAVVAYVNLVTYYVIGLPIGCVLGFKTSLGVAGIWWGMIAGVILQTITLIVLTLRTNWTSEVENAAHRLKASANESQEMATEGV
117	*Bo*ACJ36215	MSSTETYEPLLRRLHSESQITERSSPEIEEFLGRGRSTVTPRWWLRLFVWESKLLWKLSGASIVVSVLNYMLSFVTVMFTGHLGSLELAGASIATVGIQGLAYGIMLGMASAVQTVCGQAYGARQYSSMGIICQRAMVLHLAAAVLLTFLYWYSGPILKAMGQTVAIAHEGQVFARGMIPQIYAFALACPMQRFLQAQNIVNPLAYMSLGVFLLHTLLTWLVTNVLDFGLLGAALILSLSWWLLAAVNGLYIVMSPSCRETWTGFSARALTGIWPYLKLTVASAVMLCLEIWYNQGLVIISGLLTNPTISLDAISICMYYLNWDMQFMLGLSAAISVRVSNELGAGNPRVAKLSVVVVNITTVLISLFLCVVVLVFRVGLSKAFTSDKEVIVAVSDLFPLLAVSIFLNGIQPILSGVAIGSGWQAVVAYVNLVTYYVIGLPIGCVLGFKTSLGVAGIWWGMIAGVILQTITLIVLTLRTNWTSEVENAAHRLKASANESQEMATEGV

118	*Vv*CAO69963	MGSEEYQPLLLGLNSHARIPDLSSFAVEEFLAHKPVAVRWWPRLFGWESRLLWLLSGSSIVASIFNYMLSFVTLMFTGHLGALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKKYKAMGIICQRAIILHLGAAVLLTFLYWFSGPFLRAIGQSDSISAQGQIFARGLILQLYAFAISCPMQRFLQAQNIVNPLAYMAVGVFFLHVLLTWLVVYVLDYGLLGAALTLSFSWWILVVVIALYILLSPSCKETWTGFSSKAFKGMWPYFKLTVASAVMLCLEIWYNQGLVLISGLLSNPTISLDSISICMNYLNWDMQFMLGLSAATSVRVSNELGASHPKVAKLSVLVVNTNSIIISIFFSAIILIFKVGLSKLFTNDAEVIEAVSNLTPLLAISVFLNGIQPILSGVAIGSGWQAIVAYVNLATYYLIGLPIGCVLGFKTSLGVAGIWWGMIIGVLLQTVTLIILTARTDWNAEVSKAAERLRNSANVENLNLLEDV
119	*Vv*ACN91542	METPLLNSGAEEGYSGPDGDYQPLRSWREVRSMVWKETVKLWRVAGPLAFQILCQFGTNSMTSVFVGHIGNLQLSAVSISLSVIGTFSFGFMLGMGSALETLCGQAYGAGQVHLLGVYLQRSWIILLVTCVILSPVYVFATPILKVLGQEDAIADLAGQFTIETIPQLFSLAIIFPTQKFLQAQSKVNVQATIAFVALILHIGMLSVFIFVFGWGTTGAAIAYDISNWVIAVSQVVYAIGWCKEGWTGLTWSAFREIWAFVRLSIASAVMLCLEIWYFTIIVLLTGHLQNAVIAVGSLSICMTFNGWEGMLFIGMNAALSIRVSNELGYGHPRAAKFSVYVAVSQSLLIGILCMVVVLLARDYIAFIFTSNKEMQEAVSNLAYLLGATMLLNSMQPVLSGVAVGSGWQALVAYINLGCYYIIGVPLGCLLGYLAKFGVKGLWGGMICGTALQTLILLFIVYRTNWNKEVEQTTERMQKWGGVQIETKKTSDDV
120	*Vv*ACN88706	METPLLKSGAERGYGGEGGDYPPLTTWREVRSMLWRETVKVWRVAGPLAFQILCQFGTNLVTTVFVGHIGNLELSAVSISVSVIGTFSFGFMLGMGSALETLCGQAYGAGQVQLLGVYLQRSWIILLVSCIILLPIYIFATPILKALGQEDEIADLAGQFTLETIPQLFSLAIIFPTQKFLQAQSKVNVQATICFVALILDIGMLAVFIFVFGWGTTGAAIAYDISSWVTAVAQVVYAISWCKEGWTGLTWSAFREIWAFVRLSLASAVMLCLEIWYFMIIILLTGHLQNAVIAVGSLSICMTFGGLEVVMFMGMNAAVSIRVSNELGYGHPRAAKYSVFVAVSQSLLIGIFCMVVVLLARDYIAIIFTTNKEMQEAVSHLAYLLGVTMLLNSLQPVFSGVAVGGGWQAMVAYINLGCYYIIGIPLGYLLGYKAKLGVQGLWGGMICGTALQTLVLLFIVYRTNWNREVEQTTERMQKWGGQRIEADDV

121	*Le*AAQ55183	METPLLNGYSGSGERNDLIGADGDYRPAKSTKDWWAIFCVETLKLWRIGGPIAFNIICQYGVNSLTNIFVGHLGNVELSAISIAQTVISTFSFGFMMGMGSALETLCGQAYGAGQVHMLGVYMQRSIIILLATCVFLLPIYLFTTPLLVLLGQETAIADLSGRYTMLLIPQLFSLAINFPTSKFLQAQSKVDVLAGIGFAAVLVHALFLWLFIYTLEWGTNGAAIAFDLTNWLTAMAQLAYVVGWCKDGWKGLSWSAFNEIWAFVRLSIASAVMLCLEIWYMMSIILLVGHLNNAVIAVGSISICMNINGWESMLFIGINAAISIRVSNELGQGHPRATKYSVYITVFQSLLIGILCMVIVLVARDHLAIIFSNSKEMQEAVADLAYLLGITMVLNSVQPVISGVAVGGGWQALVAYINLGCYYVFGLPLGYLLGYVAKLGTKGLWLGMIAGAALQTLLLLIILYKTNWNKEVNDTTERMRKWGGQDFETQKSADGQLTIENGGVA
122	*Mp*BAB71817	MAKHSLKQPLLDKEDQPPVLPPSSYNGSESQGLAEEPKGEFKTWLVEELTHQFWLAGPMILVNLLQYLLNVVSVMFVGHLGELALASSSIATSLAGVTGYHVMMGLASALETLCGQAFGAKEYRLSGIFLQRAIFVLTLCAFPISFVWWHMGTILKFIGQDPSISDGAMEYARFLIPSLFAYAFLQPLVKFLQTQSAVNSMAVFSGITLLFHAPLCYMLVFYFGIGFRGAAIANSISQWINVIFLALYVRFSPTCKRTWTGFSREALHDIFYFLKLAVPSTVMVCLEYWCFESIVLLSGLLPNPKLETSALAICLNTIALMYMVPFGLSAAVSTRVSNELGAGRPYAAKAAVKLTVSLALLEGCLMSILLISVRGVWPYLYSGDAEVVNYVSKMVPFLATLAILDGFQGTLCGVARGCGWQHLGAYTNLGAFYVIGIPTALLMAFHFHLNGYGLWIGIICGLVTQAFLLAVITLTLNWQKLADEATDRVHHSYVEGDVLPKHGQKVDHSQLTQ
123	*Nt*CAQ51477	MVEELPQSLKEKKWQINWDAVSQELKKTSRFMAPMVAVTVFQYLLQVVSVMMVGHLGELALSSVAIATSLTNVTGFSLLTGLVGGMETLCGQAYGAQQYHKLSTYTYTAIISLFLVCIPICVLWCFMDKLLILTGQDHSISVEARKYSLWVIPAIFGGAISKPLSRYSQAQSLILPMLLSSFAVLCFHLPISWALIFKLELGNIGAAIAFSISSWLYVLFLASYVKLSSSCEKTRAPFSMEAFLCIRQFFRLAVPSAVMVCLKWWSFEVLALVSGLLPNPKLETSVMSICITISQLHFSIPYGFGAAASTRVSNELGAGNPQKARMAVQVVMFLTVVETLVFNTSLFGSRHVLGKAFSNEKQVVDYIAAMTPFLCLSIVTDSLQIVITGIARGSGWQHIGAYINLVVFYVIAIPLAVVLGFVLHLKAKGLWIGIVVGCAIQSIVLSIVTGFTDWEKQAKKARERVHEGRS
124	*Hv*BAF75822	MEEGAAASMMTGDKKWVAVVDVPADADAATAANGHGPEEKAAEDLPAALSGCPRTTGLYLFVMNIRSVFKLDELGSEVLRIAVPASLALAADPLASLVDTAFIGRLGSVEIAAVGVSIAIFNQVSKVCIYPLVSVTTSFVAEEDAIIS

		KYLEENSSQDLEKASHVHSDACNVPASGPDTPVCANSCIPTECTDLSNQGCKKRYIPSVTSALIVGSFLGLVQAVFLIFSAKFVLGIMGVKHDSPMLEPAVRYLTIRSLGAPAVLLSLAMQGVFRGFKDTKTPLYATVVGDATNIILDPILMFVCHMGVTGAAVAHVISQYLITMILICRLVQQVDVIPPSLKSLKFGRFLGCGFLLLARVVAVTFCVTLASSLAARDGPTIMAAFQICCQLWLATSLLADGLAVAGQAVLASAFAKNDHKKVIAATSRVLQLSIVLGMGLTVVLGLFMKFGAGVFTRDADVINVIHKGIPFVAGTQTINALAFVFDGINFGAQDYTYSAYSMVGVASISIPCLVYLSAHKGFIGIWVALTIYMSLRTVASTWRMGAARGPWVFLRK
125	*Sbi*ABS89149	MEEHRSPAHAKPEAEQPPQQQVPAAMAVAVAVDVAAPAALQNSTAAPAENGDVAAAGAAENGTAASAANGDGGGSELLGGPRWTGLHLFVMNIRSVFKLDELGAEVLGIAVPASLALTADPLASLIDTAFIGRLGSVEIAAVGVAIAVFNQVMKVCIYPLVSVTTSFVAEEDAVLSKGGAKVIDNGEEEEELEAGQVGPEKHTAAAGADPEKQQQPADEEAAKNGGEGCAPAVVAGRSSGKKSGNRRFVPSVTSALIVGALLGLFQTVFLVAAGKPLLRLMGVKPGSPMVMPALRYLTLRALGAPAVLLSLAMQGVFRGFKDAKTPLYAIVAGDAANIVLDPILIFGCRLGVIGAAIAHVLSQYLITLIMLSKLVRKVDVVPPSLKCLKFRRFLGCGFLLLARVVAVTFCVTLAASLAARHGPTAMAAFQICTQVWLATSLLADGLAVAGQAMIASAFAKEDRYKVAATAARVLQLGVVLGAALTALLGLGLQFGAGVFTSDAAVIKTIRKGVPFVAGTQTLNTLAFVFDGINFGASDYAFSAYSMIGVAAVSIPSLIFLSSHGGFVGIWVALTIYMGVRALASTWRMAAAQGPWKFLRQ
126	*Mt*HM856605	MDSHTPLLNTTAATSSSSELLELDGGDYLEVKGFKQARKVFAIETLRIWKIALPIVFNILCQYGVNSITNIFVGHLGDIQLSAISLINSVIGTFAFGFMLGMGSATETLCGQAFGAGQVHMLGVYMQRSWIILFVTSIILLPIYIFAAPILKLLGQQEDMADLAGSFALLVIPQFLSLSFNFPTQKFLQSQSKVNVIAWIGLVALIVHIGLLWLLIYVLDLGLTGAAIAFDVTSWGITLAQLVYVVIWCKDCWNGLSWLALKDIWAFVRLSVASAVMLCLEIWYMMSLIVLAGHLDNAVIAVDSISICMNFNGWEGMIFIGVNAAISVRVSNELGLRHPRAAKYSVYVTVFQSLFMGIFFMGVILVTKDYFAIVFTNSKTLQVAVADLGNLLAVTMVLNSVQPVISGVAVGGGWQALVAYINVGCYYLFGLPLGYILGNVAELGVKGLWGGMICGILLQTLLLSGILYKTNWNKEVDNTSARVQQWGGQTVEVDSNGVDKP

127	*Mt*ACX37118	MENQPFLVGLDSHSHTHIADLSSDAIEEFLEHRPIGLRWWLKLVAWESRLLWILSGASIVVYLCNFMLSFVTMMFCGHLGSLELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKKHAAMCITLQRAIILHFGAAVILTFLYWFSGDFLKVIGQTESIAVQGQVFARGLIPQLYAFAFSCPMQRFLQAQNIVNPLAYMAVGVLLLHALLSWLVVVVLGYGLLGAALTLSFSWWILVFLNALYIIFSPKCKETWTGFTMKAFIGIWPYFKLTVASAVMLCLEIWYNQGLVLISGLLSNPTVALDSISICMNYLNWDMQVMLGLGAAASVRISNELGAAHPRVAKFAIFVVNGNSILISVVLSAIILIFRDGLRNLFTSDSEVIEAVSDLTPLLAISVLLNGIQPILSGVAIGSGWQALVAYVNLACYYVIGLTVGCVLGFKTSLGVAGIWWGMILGVFIQTVTLIILTARTNWGVEVEKAIVRVKRSAEDDTLDRLVADV

Table S3 List of the cis-regulatory elements present in promoter region of OsMATE1 and OsMATE2

Common elements in OsMATE1 and OsMATE2	**Elements only in OsMATE1**	**Elements only in OsMATE2**
ABRELATERD1	2SSEEDPROTBANAPA	-10PEHVPSBD
ABRERATCAL	AACACOREOSGLUB1	-300ELEMENT
ACGTATERD1	ABREOSRAB21	AMMORESIIUDCRNIA1
ANAERO1CONSENSUS	ACGTABOX	BIHD1OS
ARR1AT	ACGTCBOX	BOXLCOREDCPAL
CAATBOX1	ACGTOSGLUB1	CEREGLUBOX2PSLEGA
CACTFTPPCA1	AMMORESIVDCRNIA1	CPBCSPOR
CATATGGMSAUR	ANAERO3CONSENSUS	ERELEE4
CCAATBOX1	ASF1MOTIFCAMV	GAGA8HVBKN3
CGACGOSAMY3	CANBNNAPA	GAGAGMGSA1
CGCGBOXAT	CARGCW8GAT	GT1GMSCAM4
CURECORECR	CARGNCAT	HEXAMERATH4
DOFCOREZM	CBFHV	INRNTPSADB
EBOXBNNAPA	CCA1ATLHCB1	MARARS
EECCRCAH1	DPBFCOREDCDC3	NODCON1GM
GATABOX	DRECRTCOREAT	NODCON2GM
GCCCORE	E2FCONSENSUS	OSE1ROOTNODULE
GT1CONSENSUS	HEXMOTIFTAH3H4	OSE2ROOTNODULE
GTGANTG10	LTRECOREATCOR15	POLASIG1
LECPLEACS2	MARTBOX	POLASIG2
MYBCORE	MYB1AT	POLASIG3
MYBST1	MYB1LEPR	S1FBOXSORPS1L21
MYCCONSENSUSAT	MYB2AT	SEF3MOTIFGM
P1BS	MYB2CONSENSUSAT	T/GBOXATPIN2
POLLEN1LELAT52	MYBPLANT	TATABOX2
PRECONSCRHSP70A	MYBPZM	TATABOXOSPAL
RAV1AAT	NAPINMOTIFBN	TATCCAOSAMY
ROOTMOTIFTAPOX1	PE2FNTRNR1A	TBOXATGAPB
SEF4MOTIFGM7S	PROXBBNNAPA	WBBOXPCWRKY1
SORLIP1AT	RAV1BAT	WBOXHVISO1
SURECOREATSULTR11	REBETALGLHCB21	
TAAAGSTKST1	RHERPATEXPA7	
TATABOX5	RYREPEATBNNAPA	
WBOXATNPR1	RYREPEATGMGY2	
WBOXNTERF3	RYREPEATLEGUMINBOX	

WRKY71OS	SITEIIATCYTC SORLIP2AT SORLIP5AT SV40COREENHAN TATABOX3 WUSATAg

Table S4 Various cis-elements, sequences, nucleotide position and ID of OsMATE1

Cis- elements	**Nucleotide position**	**Sequence of cis- elements**	**ID**
2SSEEDPROTBANAPA	1179	CAAACAC	S000143
AACACOREOSGLUB1	507	AACAAAC	S000353
ABRELATERD1	588	ACGTG	S000414
ABREOSRAB21	1250	ACGTSSSC	S000012
ABRERATCAL	871	MACGYGB	S000507
ACGTABOX	797	TACGTA	S000130
ACGTATERD1	425	ACGT	S000415
ACGTCBOX	424	GACGTC	S000131
ACGTOSGLUB1	944	GTACGTG	S000278
AMMORESIVDCRNIA1	439	CGAACTT	S000375
ANAERO1CONSENSUS	365	AAACAAA	S000477
ANAERO3CONSENSUS	431	TCATCAC	S000479
ARR1AT	484	NGATT	S000454
ASF1MOTIFCAMV	75	TGACG	S000024
CAATBOX1	158	CAAT	S000028
CACTFTPPCA1	270	YACT	S000449
CANBNNAPA	961	CNAACAC	S000148
CARGCW8GAT	1353	CWWWWWWWWG	S000431
CARGNCAT	1352	CCWWWWWWWWGG	S000446
CATATGGMSAUR	559	CATATG	S000370
CBFHV	584	RYCGAC	S000497
CCA1ATLHCB1	915	AAMAATCT	S000149
CCAATBOX1	167	CCAAT	S000030
CGACGOSAMY3	423	CGACG	S000205
CGCGBOXAT	872	VCGCGB	S000501
CURECORECR	162	GTAC	S000493
DOFCOREZM	82	AAAG	S000265
DPBFCOREDCDC3	870	ACACNNG	S000292
DRECRTCOREAT	584	RCCGAC	S000418
E2FCONSENSUS	975	WTTSSCSS	S000476
EBOXBNNAPA	452	CANNTG	S000144
EECCRCAH1	1210	GANTTNC	S000494
GATABOX	25	GATA	S000039
GCCCORE	1240	GCCGCC	S000430
GT1CONSENSUS	759	GRWAAW	S000198
GTGANTG10	455	GTGA	S000378
HEXMOTIFTAH3H4	425	ACGTCA	S000053
LECPLEACS2	888	TAAAATAT	S000465

LTRECOREATCOR15	422	CCGAC	S000153
MARTBOX	56	TTWTWTTWTT	S000067
MYB1AT	649	WAACCA	S000408
MYB1LEPR	149	GTTAGTT	S000443
MYB2AT	275	TAACTG	S000177
MYB2CONSENSUSAT	275	YAACKG	S000409
MYBCORE	8	CNGTTR	S000176
MYBPLANT	1176	MACCWAMC	S000167
MYBPZM	464	CCWACC	S000179
MYBST1	596	GGATA	S000180
MYCCONSENSUSAT	452	CANNTG	S000407
NAPINMOTIFBN	183	TACACAT	S000070
P1BS	558	GNATATNC	S000459
PE2FNTRNR1A	975	ATTCGCGC	S000455
POLLEN1LELAT52	362	AGAAA	S000245
PRECONSCRHSP70A	1514	SCGAYNRNNNNNNNNNNNNNNNHD	S000506
PROXBBNNAPA	1179	CAAACACC	S000263
RAV1AAT	506	CAACA	S000314
RAV1BAT	1369	CACCTG	S000315
REBETALGLHCB21	595	CGGATA	S000363
RHERPATEXPA7	823	KCACGW	S000512
ROOTMOTIFTAPOX1	265	ATATT	S000098
RYREPEATBNNAPA	719	CATGCA	S000264
RYREPEATGMGY2	719	CATGCAT	S000105
RYREPEATLEGUMINBOX	719	CATGCAY	S000100
SEF4MOTIFGM7S	44	RTTTTTR	S000103
SITEIIATCYTC	412	TGGGCY	S000474
SORLIP1AT	573	GCCAC	S000482
SORLIP2AT	413	GGGCC	S000483
SORLIP5AT	750	GAGTGAG	S000486
SURECOREATSULTR11	91	GAGAC	S000499
SV40COREENHAN	146	GTGGWWHG	S000123
TAAAGSTKST1	521	TAAAG	S000387
TATABOX3	114	TATTAAT	S000110
TATABOX5	48	TTATTT	S000203
WBOXATNPR1	74	TTGAC	S000390
WBOXNTERF3	237	TGACY	S000457
WRKY71OS	75	TGAC	S000447
WUSATAg	116	TTAATGG	S000433

Table S5 Various cis-elements, sequences, nucleotide position and ID of OsMATE2

Cis- elements	**Nucleotide position**	**Sequence of cis- elements**	**ID**
-10PEHVPSBD	693	TATTCT	S000392
-300ELEMENT	663	TGHAAARK	S000122
ABRELATERD1	38	ACGTG	S000414
ABRERATCAL	37	MACGYGB	S000507
ACGTATERD1	38	ACGT	S000415
AMMORESIIUDCRNIA1	212	GGWAGGGT	S000374
ANAERO1CONSENSUS	651	AAACAAA	S000477
ARR1AT	421	NGATT	S000454
BIHD1OS	75	TGTCA	S000498
BOXLCOREDCPAL	1219	ACCWWCC	S000492
CAATBOX1	170	CAAT	S000028
CACTFTPPCA1	1140	YACT	S000449
CATATGGMSAUR	374	CATATG	S000370
CCAATBOX1	432	CCAAT	S000030
CEREGLUBOX2PSLEGA	252	TGAAAACT	S000033
CGACGOSAMY3	1377	CGACG	S000205
CGCGBOXAT	1388	VCGCGB	S000501
CPBCSPOR	736	TATTAG	S000491
CURECORECR	44	GTAC	S000493
DOFCOREZM	247	AAAG	S000265
EBOXBNNAPA	78	CANNTG	S000144
EECCRCAH1	463	GANTTNC	S000494
ERELEE4	1064	AWTTCAAA	S000037
GAGA8HVBKN3	1339	GAGAGAGAGAGAGAGA	S000427
GAGAGMGSA1	1339	GAGAGAGAGAGAGAGAGA	S000405
GATABOX	331	GATA	S000039
GCCCORE	1402	GCCGCC	S000430
GT1CONSENSUS	197	GRWAAW	S000198
GT1GMSCAM4	581	GAAAAA	S000453
GTGANTG10	251	GTGA	S000378
HEXAMERATH4	288	CCGTCG	S000146
INRNTPSADB	487	YTCANTYY	S000395
LECPLEACS2	1079	TAAAATAT	S000465
MARARS	784	WTTTATRTTTW	S000064
MYBCORE	29	CNGTTR	S000176
MYBST1	346	GGATA	S000180
MYCCONSENSUSAT	78	CANNTG	S000407
NODCON1GM	328	AAAGAT	S000461

NODCON2GM	603	CTCTT	S000462
OSE1ROOTNODULE	328	AAAGAT	S000467
OSE2ROOTNODULE	603	CTCTT	S000468
P1BS	546	GNATATNC	S000459
POLASIG1	404	AATAAA	S000080
POLASIG2	997	AATTAAA	S000081
POLASIG3	1035	AATAAT	S000088
POLLEN1LELAT52	580	AGAAA	S000245
PRECONSCRHSP70A	1376	SCGAYNRNNNNNNNNNNNNNNNHD	S000506
RAV1AAT	416	CAACA	S000314
ROOTMOTIFTAPOX1	617	ATATT	S000098
S1FBOXSORPS1L21	272	ATGGTA	S000223
SEF3MOTIFGM	901	AACCCA	S000115
SEF4MOTIFGM7S	501	RTTTTTR	S000103
SORLIP1AT	1193	GCCAC	S000482
SURECOREATSULTR11	111	GAGAC	S000499
T/GBOXATPIN2	37	AACGTG	S000458
TAAAGSTKST1	1006	TAAAG	S000387
TATABOX2	765	TATAAAT	S000109
TATABOX5	782	TTATTT	S000203
TATABOXOSPAL	929	TATTTAA	S000400
TATCCAOSAMY	646	TATCCA	S000403
TBOXATGAPB	257	ACTTTG	S000383
WBBOXPCWRKY1	832	TTTGACY	S000310
WBOXATNPR1	260	TTGAC	S000390
WBOXHVISO1	834	TGACT	S000442
WBOXNTERF3	701	TGACY	S000457
WRKY71OS	261	TGAC	S000447

Table S6 Quercetin (Q) and Kaempferol (K) content in leaves of WT and transgenic lines

		Q[i]	**K**[i]
WT		0.0214	ND
OsMATE1	**L1**	0.0256	0.006
	L2	0.019	0.0071
	L3	0.0174	0.006
OsMATE2	**L1**	0.0227	0.0072
	L2	0.0214	0.0071
	L3	0.0135	0.0066

---

[i] Values are average of 3 biological replicates and expressed as $mg.g^{-1}$ fresh weight of leaves.