>AFZ51979

MEAKNKIFSIIQGFWGSQCLYIATCLGIPNLLEEYGAQSVESLAEKTETHTETLYVVLRGLAHLEILEEKPDRVFAPTEASSLLVTNAGPSIGHFALHITEPCQWDGWKELYDAVHTGEVAFERANGKGVYEFTRDNPWSGDVFINAMSFLTDHATEALMAVYDFGQYETVMDVGGGQGGLIAEIVKTYNCKGMLFDVPYVIETAPSFLESRGVPKDAIALHTGDVFEKVPTGADAIVMKYFLSAWNDEDAGKILARCREALPDHGKIVLLQSIVPDVGEPTVCPDGIMPGLFAVQIRSAVPGGVWRTLKQYQEIFANSGFKLDRVVHTSTNLSAMEFSLA

>maker-Fvb5-3-augustus-gene-182.54|maker-Fvb5-3-augustus-gene-182.54-mRNA-1|Fx\_ananassa\_v1.0.a1

MLGFADSMALKSAVELRIPDIINSHGQALSLSEIVSNIDSKSPSPDITCLSRIMRLLVHRNIFAAHHDDGDSGETLYGLTPSSRWLLQDSELTLAPMVLLQTDPILMAPMQYFSQCVKQGGTHAFSKAHGRDIWQFFSENLEANQLFNDAMACSANIIMKVILARCKGAFDDVTTLVDVGGGTGRAAAEIVKAYPSIKAINFDLPYVVATAPAYHGVSHVGGDMFDEGNIPNADAIFMKWIMHDWSNGDCIKILKNCRKAIPERSGKVIIVDAVLEPNGDGLFDDTGLVFDLLMITHSSGGKERSESEWKQMLEQAGFPRYNIINIPAVVSIIEAYPV\*

>maker-Fvb6-2-augustus-gene-322.43|maker-Fvb6-2-augustus-gene-322.43-mRNA-1|Fx\_ananassa\_v1.0.a1

MEAAAELDEASLRGQADVWKYMLGFADSMALRSAVELRIPDIIHSHGRALTLSEIASSFDSASPSPDISCLARIMRLLVRRNIFTAHHDGEDSEKTGLYGLTHSSRWLLHDSELTLTPMVLMETNPTLLAPWHYFSQCVKQRGPYAFERAHGSDIWQFFSENLKFNRLFNDGMACTAKITMKAILAGYKGGFEDVATLVDVGGGTGSAVAEIVKAYPSVKGINFDLPHVVATAPLYHGVSHVGGDMFDEGSIPKADAIFMKWVMHDWSDSDCVKIFKNCRNVIPERTGKVIIVDVILEPNGVGMFDDTGLVFDLLMIAHTSGGKERTESEWKKMLEQAGFPRLKIIKIPALMLIIEAYRV\*

>maker-Fvb6-3-augustus-gene-174.48|maker-Fvb6-3-augustus-gene-174.48-mRNA-1|Fx\_ananassa\_v1.0.a1

MERLNSFRHVNQKWSNGDNSNELLHAQAHIWNHIFNFINSMSLKSAIQLGIPDIINKHGRPMTLSELTSALPINPTKSHSIYRLMRILIHSGFFAKKKLSKSDEEGYVLTDASQLLLKDHPLSMTPFLNAMLDPVLTKPWHYLSTWFQNDDPTPFDTAHGMTFWDYGYHQPSIAHFFNDAMASDARLVTSVIVDECRGVFEGLDSLVDVGGGTGTVAKAIADAFPHIECTVLDLPHVVADLQGSKNLKYTGGDMFEAVPPADAVLLKWILHDWNDEECVKILERSKEAITSKDKKGKVIIIDMMMENQKGDEESMETQLFFDMLMMALLTGKERNEKEWSKLFTDAGFGDYKITPILGLRSLIEVYPK\*

>maker-Fvb6-3-augustus-gene-47.29|maker-Fvb6-3-augustus-gene-47.29-mRNA-1|Fx\_ananassa\_v1.0.a1

MLGFADSMALRSAVELRIPDIIHSHGRALTLSEIASSFDSASPSPDISCLARVMRLLVRRNIFTAHHDGEDSEKTFLYGLTHSSRWLLHDSELTLAPMVLMETNPTLMAPWHCFSQCVKQRGPCTFKRAHGLDIWQFFYENLKFNRLFNDGMACTAKITIKAILAGYKGGFEDVATLVDVGGGTGSAVAEIVKAYPSIKGINFDLPHVVATAPVYHGVSHVGGDMFDEGSIPNADAIFMKWVMHDWSDSDCVKILKNCRNAIPERTGKVIIVDVILETNGVGMLDDTGLVFDLLMIARTSGGKERTESEWKKMLEQAGFPRLKIIKIPALMLIIEAYPV\*

>maker-Fvb6-4-augustus-gene-323.29|maker-Fvb6-4-augustus-gene-323.29-mRNA-1|Fx\_ananassa\_v1.0.a1

MEAAAELEEASLRGQADVWKYMLGFADSMALRSAVELRIPDIIHSHGRALTLSEIASSFDSASPSPDISCLARIMRLLVRRNIFTAHHDGEDSEKTVLYGLTHSSRWILHDSELTLAPMVLMETNPTLMAPWHCFSQCVKQRGPCAFKRTHGHDIWQFFSENLKFNRLFNDGMACTAKITMKAILAGYKGGFEDVATLVDVGGGTGSAVAEIVKAYPSIKGINFDLPHVVATAPVYHGVSHVGGDMFDEGSIPNADAIFMKWVMHDWSDSDCVKILKNCRNVIPERTGKVIIVDVILEPNGVGMFDDTGLVFDLLMIAHTSGGKERTESEWKKMLEQAGFPRLKIIKIPALMLIIEAYPV\*

>maker-Fvb6-1-augustus-gene-179.34|maker-Fvb6-1-augustus-gene-179.34-mRNA-1|Fx\_ananassa\_v1.0.a1

MFSQVYKGIKDSDKPSLIKQALMSSLANNGVASATASSTDELIVQSQLHVRNHILQLMNSMVLNCAIQLGIPDIIHNHAQPITLSDLTSALNVHPSKSRFLYRLMCILVQQGFFTKHNDVQHGIVYSLTPSSKLLLKDGLMTTFLLLLLDPLLTSPWHLLGTWFQNCASTPFEMAHGMSFFDLVAHEPVFGNMFNEAMVADSKLVSRAVVKECQGVFEGLKSLVDVGGGKGTMASAIADAFPQIKCTVLDLPHVIENLKGSNNLDFIGGNMFEQIPPANAILLKWILHDWNDEESVEILKRCRDAIPSKSDGGKVIIIEMVVTVDDDKKMNNKSTETQLFWDMLMMVCLTGRERTEKDWEKLFLAAGFSHYKITHTLGIRSFIEVYP\*

>maker-Fvb6-1-augustus-gene-179.41|maker-Fvb6-1-augustus-gene-179.41-mRNA-1|Fx\_ananassa\_v1.0.a1

MERLNSFRHLNQKWSNGEHSNELLHAQAHIWNHIFSFINSMSLKSAIQLGIPDIINKHGRPMTLSELTSALPINPTKSHSIYRLMRILIHSGFFAKKKLSKSDEEGYVLTDSSQLLLKDHPLSITPFLNAMLDPVLTKPWHYFSTWFQNDDPTPFDTAHGMTFWDYGNHQPSIAHFFNDAMASDARLVTSVIVDECRGVFEGIDSLVDVGGGTGTVAKAIADAFPHIKCTVLDLPHVVADLQGSKNLKYTGGDMFEAVPPADAVLLKWILHDWNDEECVKILERSKEAITGKDKKGKVIIIDMMMENQKGDEESMETQLFFDMLMMALVTGKERNEKEWSKLFTDAGFSDYKITPILGLRSLIEVYP\*

>maker-Fvb2-2-augustus-gene-106.22|maker-Fvb2-2-augustus-gene-106.22-mRNA-1|Fx\_ananassa\_v1.0.a1

MEHTQKELILEQKEEELAKVEMWKYVLGFSKIAVVKCAIELGIADAIESHGSAMTLSEIAATLKCDPSSLYRIMRFLVHHQIFKEVQPKIQLGPRSYAQTPLSRCLLKSGKTSMAALILLEASPVMLEPWHGLSAGVQGDGMSTPAFEAVHGEDVWSFAAANPGHSELINEAMACDARLAVPAVIESCIEVFHGIESIVDVGGGDGTTLSLLVKACPWITRGINFDLPHVVSVAKESDRVENVGGDMFDCIPKADAAIIKSVLHDWGDEECICILRNCREAIPKDKGKVIILEAIIEEDELEEDELTHVRLMLDMVMMAHTNTGKERTLKEWGYVLQEAGFSRHTVTPISAVQSVIQAFL\*

>maker-Fvb2-2-augustus-gene-105.52|maker-Fvb2-2-augustus-gene-105.52-mRNA-1|Fx\_ananassa\_v1.0.a1

MEHTQRELILEQKEEELAKVEVWKYVFGFSKIAVVKCAIELGIADAIESHGSAMTLSELAATLKCDPSSLYRIMRFLVHHQIFKEVQPKIQLGPRSYAQTPLSRCLLKSGKNSMAAFILLETSPVMLEPWHGLSARVQGNGMSTPAFEAVHGEDVWSFAAANPGHSELINEAMACDARLAVPAVIESCIEVFHGIESIVDVGGGDGTTLSLLVKACPWITRGINFDLPHVVSVAKESDRVENVGGDMFDCIPKADAAIIKWVLHDWGDEECICILRNCREAIPKDKGKVIILEAIIEEDELEEDELTHVRLMLDMVMMAHTNTGKERTLKEWGYVLQEAGFSRHTVTPISAVQSVIQAFL\*

>maker-Fvb5-2-augustus-gene-98.40|maker-Fvb5-2-augustus-gene-98.40-mRNA-1|Fx\_ananassa\_v1.0.a1

MEAVTELDEVTLRGQADVWKYMLGFADSMALKSAVELRIPDIINSHGQALSLSEIVSNIDSKSPSPDITCLSRIMRLLVRRNIFAAHHDDGDSGETLYGLTPSSRWLLQDSELTLAPMVLLQTDPILMAPMQYFSQCVKQGGTHAFSKAHGRDIWQFFSENLEANQLFNDAMACSTNIIMKVILARCKGAFDDVTTLVDVGGGTGRAAAEIVKAYPSIKAINFDLPYVVATAPAYHGVSHVGGDMFDEGNIPNADAIFMKWIMHDWSDGDCIKILKNCRKAIPERSGKVIIVDAVLEPNGDGLFDDTGLVFDLLMITHSSGGKERSESEWKQMLEQAGFPRYNIINIPAVVSIIEAYPV\*

>Gohir.A03G158200|Gohir.A03G158200.2|Ghirsutum\_v2.1

MSSQESGREKEIIELDEARLQGQAEIWRYMFSFADSMALKSAVELRIADIIHSHGVAITLSQIASCINGCLTSPDITTLARIMRLLVRRKIFTVHHPLDGGDPLYDLTHSSRWLLHDFEQTLAPMVLMENHPWLIAPWHCFSQCVKEGGIAFKKAHGREIWDLTSGNPEFNKLFNDGLASTSKVVTSAILSGYKQGLSSIESLVDVGGGIGGLISEIVKAYPHIKGVNFDLPHVILAAPAYNEISHVGGDMFHVIPNANAVIMKWVLHDWGDEDCIKILKNCRKAIPRENGKVIIVEVVVKAEGSGVFDDMGFIFDLLMIAHSSGGKERTEVEWKKILEEGGFSRYKIIDIPALPSIIEAYPDDQ\*

>Gohir.A03G158100|Gohir.A03G158100.1|Ghirsutum\_v2.1

MERTELDEARLQGQAEIWRYMFSFADSMALKSAVELRIADIIYSYGGAATLSQIASCINDGLTSPDITTLARIMRLLVRRKIFTIHHPSDGRDSLYNLTHSSRWLLHDSEQSLAPMVLMENHPWQMAPWRYFSQCVKEGGDAFKKAHGCEIWDLASRNPDFNKLFNDGLACTSKVVTSAILSGYKQGFNSIGSLVDVGGGTGGLISEIIKVYPHIKCVNFDLPHVVSTAPAYNGVSHIGGDMFHAIPNTDAIIMKWILHDWDDEDCIKILKNCKKAIPKENGKVIIIEIILKEDGSGVFDEIGFILDLAMIAHTNGKERTEVEWKKILEGGGFFHYKIINIPSLLSIIEAYPDDK\*

>Gohir.A03G158000|Gohir.A03G158000.1|Ghirsutum\_v2.1

MERIELDEAMLQGQAEIWRYMYSFADSMALKSAVELRIADIIHSNGGPVTLSQIASCINGGLASPDITTLARIMRLLIRRKIFTVHPSDGGDLLYDLTHSSRWLLHDSEQTLAPMVLMNTHPWQMTPWHYFSQCVKEGGIAFKKAYGCELWDLASRDPDLNKLFNNGLACSSKVITSVILSSYKQGLSSIGSLVDVGGGIGGLISEIVKAYPHIKGVNFDLPHVVSTAPTYNAVSHIGGDMFHDAIPNADAVIMKWILHDWTDEECIKILRNCKKAIPRENGKVILVEIILKEDGSGVFDDIGFVMDLVMIAHTNGKERTEAEWKKILGGGGFSHYKIINIPALFSIIEAYPDAQ\*

>Gohir.A11G293300|Gohir.A11G293300.1|Ghirsutum\_v2.1

MERIELDEAMLQGQAEIWRYLYSFADSMALKCAVELRIADIIHSNGGPLTLSQIASCINGGLTSPDITTLARIMRLLIRRKIFTVHHPSDGGDLLYDLTHSSRWLLHDSEQTLVPMVLMENHPLQMAPWHYFSQCVKEGGFAFKKAHGCEIWDLASRNPDFNKLFNDGLACTSKFLTSVILSSYKQGLSSIGSLVDVGGGTGGLISEIVKKHPHIKGINFDFPHVVSTAPTYDGVSHIGGDLFHAIPNADAVILKWILHCWGDEDCIKILRNCRKAIPRENGKVIIVEIILKEDGSGVFDEIGFLLDLVMIAHANGKERTEAEWKKILEGGGFSHYKIINIPALASIIEAYPDA\*

>Gohir.A04G132406|Gohir.A04G132406.1|Ghirsutum\_v2.1

MEVSGIEEEEARPEVDIWNYVFGYAKIAVVKCAIELGIADVIENYGSPMPLSELATALRCDPSRLHRIMRFMVHYRIFKREPINQHTVGFSSTPLSRCLIKGGEKSMAAFILFMSSPPWLASWHCLNSRVLETSNNISPFEAANGKDLWSYTETNPYHNEVFNEAMACVARLTVQAIIKGCPEVFDGVKSLVDVGGGINFDLPHVVAVAPKFGSIENVGGDMFMSIPNVDAAFLMWILHDWDDEECIKILKKCREASLEDKGKVIIVEAVLEKDKEVDELGYLGLMLDMAMMAHTDKGKERTLKEWSYVLRQSGFTRFNVKPIRAVQFIIEAYP\*

>Gohir.A04G132300|Gohir.A04G132300.1|Ghirsutum\_v2.1

MGDMEVTIKEEARAEIKIWNYVFGYAKIAAVKCAIELGIADVIENYGSPMPLSELASALRCEPSRLHRIMRLMVHDRIFKQEPINQHTVGFSSTPLSRCLIKGGEKSMAAFILLMSGPTCLAPWHSLSARVLETDHNISPFEVANGKDIWSYAEANPDFSELFNNAMGCKARLTVQATIEGCPEVFDGVENLVDIGGGNATALSLLVKAFPWIRGINFDLPHVVAVAPKSDSIENVGGDMFMSIPNADAAFLMSVLHDWDDEECIKILKKCREAIPEDKGKVIIVEAVLEEDKEVDEVGVVGLMLDTAMMAITNKGKERTLKEWSYVLRQSGFTRFNVKPIRAVQSVIKAYP\*

>Gohir.A04G132350|Gohir.A04G132350.1|Ghirsutum\_v2.1

MEVTIKEEEARAEVEIWNYVLGYVKIAVVKCAVELGISDVIENYGSPMPLSELATALQCEPSRLHRIMRIMVHYRIFKQEPINQYTVGFSSTPLSRRLIKGGEKSMAAFILLMYSPTCLASWHCLSARVLETGNNISPFEVANGKDIWSYAEANHDFSELFNNAMGCDARLTVQATTEGCPEVFDGVESLVDVGGGNRTALSLLVNAFPWIRGINFDLPHVVTVAPKSDSIENVGGDMFMSIPNVDAAFLMWVLHDWDDEECIKILKKCREAIPEDKGKVIIVEAVLEEDKEGNELGVVGLMLDTTMMAITNKGK\*

>Gohir.A04G132400|Gohir.A04G132400.1|Ghirsutum\_v2.1

MGDKEMGDKEVTIKEEARAEIKIWNYVFGYAKIAAVKCTIELGIADVIENYGSPMPLSELATALRCEPSRLHRIMRLMVHDRIFKQEPINQHTVGFSSTPLSRRLIKGGEKSMAAFILLMSGPTCLAPWHSLSARVLETGNNISPFEVANGKDLWSYTEANPDFRELLNNSMGCKARLTVQATIEGCPEVFDGVESLVDVGGGNGTALSLFVKAFPWIRGINFDLPHVVAVAEKSDGIENVGGDMFMSIPKADAAFLMWVLHDWDDEECIKILKKCREAIPEDKGKVIIVEAVLEEDKEGDELGVARLMLDTAMMVITNKGRERTLKEWSYVLRQSGFKRFNVKPIRAVETVIETVIEAYP\*

>Gohir.A04G132200|Gohir.A04G132200.1|Ghirsutum\_v2.1

MGDMEVTRKEEARAEIKIWNYMLGYVKIAVVKCAIELGIADVIENYGSPMPLSELATALRCEPSHLHRIMRFMVHYRIFKQEHINHHTVGFSSTPLSSLLIKGGEKSMVAFILFVSSPTWLAPWHSLSARVLETGNDISPFEVANGKDLWSYAEANPNFSELFNNAMGCDARLTVQATIEGCPEVFDGVKSLVDVGGGNGTALSLLVKAFPWIRGINFDLPHVVAVAPKSDSIENVGGDMFMSIPNADAAFLMWVLHDWDDEECIKILKKCREAIPEDKGKVIIVEAVLEEDKEGDELGAVGLMLDMVMMAITNKRKERTLKEWSYVLQQSGFTRFNVKPIRAVKFVIEAYP\*

>Gohir.A12G035600|Gohir.A12G035600.1|Ghirsutum\_v2.1

MGDIKVRGKKEDEDEKAEVDIWNYVFGYVKIEVVKCAIELGIADAIDKHGSPMTLSQLTTTLKCEPPRLYRIMRFLVHYQIFKEEPVTQDSFGFALTPLSRRLIRHGERSMAAFILLESSPVMLAPWHSLSARVLDSGNSPFETAHGKDVWSYAEENPRHSKLIDEAMACDARVAVRALIEGCPQVFDGIKSLVDVGGGNGTALSMLVKEFPWMHGINFDLPHVVAVAPKVDGIEYVGGDMFECVPKADAAFFLWVLHDWDDEECIQILKKCREAIPQDKGKVIIVEAVLEEDKNDKLEFVGLMLDMVMMAHTKKGKERTLKEWKYVLGEAGFTRINVKPIHAVQFIIEAYI\*

>Gohir.A12G035700|Gohir.A12G035700.1|Ghirsutum\_v2.1

MGDVKVRGKKEDEDEKAEVDIWNYVFGYVKIAVVKCAIELGIADAIDKHGSPMTLSQLTTTLKCQPSRLYRIMRFLVHYQIFKEEPITKDSIGFALTPLSRRLSRHGERSMAAMILLQSSPVTLATWHSLSARVLDSGNSPFETAHGKDVWSYAEENPRHSKLIDEAMACDARVAVRAIIEGCPQVFDGIKSLVDVGGGNGTALSMLVKAFPWIHGIDFDLPRVVAVAPKVDGIKYVGGDMFECVPKADAAFFMWVLHDWGDEECIQILKKCREAIPQDKGKVIIVESVLEEDENDKLEFVGLMLDMVMMTHTNKGKERTLKEWKYVLGEAGFTRIDVKPIHAVQSVIEAYI\*

>Gohir.D04G169000|Gohir.D04G169000.1|Ghirsutum\_v2.1

MEVSGIEEEEARAEVDIWNYVFGYAKIAVVKCAIELGIANVIENYGSPMSLSELATALRCEPSRLYRIMRFMVHDRIFKQEPINQHTVGFSSTPLSRCLLKGGEKSMAAFILLMSSPTCLAPWHSLSARVLETGNNISPFEVANGKDLWSYTEANPDFRELFNNAMGCDARLTVQATIEGCPEVFNGVESLVDVGGGNGTALSLLVKAFPWIRGINFDLPHVVAVAAKSDSIENVGGDMFMSIPNADAVFLMWVLHDWDDEECIEILKKCREAIPEDKGKVIIVEAVLEEDKEGDELGGVGLMLDTALMAITNKGKERTLKEWSYVLRQSGFTRFNVKPTRAVQFVIEAYP\*

>Gohir.D04G168800|Gohir.D04G168800.1|Ghirsutum\_v2.1

MGDMEVTVKEEARAEIKIWNYVLGYAKIAVVKCAIELGIADTIENYGSPMPLSELATALRCEPSRLHRIMRFMVHDRIFKQEHINHHTVGFSSTPLSRLLIKRGEKSMAALILFVSSPTWLAPWHSLSARVLETGNNISPFEVANGKDLWSYAEANPDFRELFNNAMGCDARLTVQATIEGCPEVFDGVESLVDVGGGNGTALSLLVKAFPWIRGINFDLPHVVAVSAKSDSIENVGGDMFMSIPNADAAFFMWVLHDWDDEECIKILKKCREAIPEDKGKVIIVEAVLEEDKEGDELGAVGLMLDMTMMAITNKGKERTLKEWSYVLRQSGFTRFNVKPIRAVQSVIEAYP\*

>Gohir.D04G169300|Gohir.D04G169300.1|Ghirsutum\_v2.1

MGDMEVTIKEEARAEIKIWNYVLGYVKITVVKCAIELGIADVIENYGSPMPLSELATALRCEPSRLHRIMRFMVHDRIFKQEPINQHTIGFSSTPLSRLLIKGGEKSMAAFILLMSGPACLATWHSLSARVLETGNNISPFEVANGKDLWSYAEANPDFRELFNNAMGCHARLTVHATIEGCPEVFNGVESLVDVGGGNGTALSLLVKAFPWIRGINFDLPHVVAVAATSDSIENVGGDMFMSIPNADAAFLMCVLHDWDDEECIKILKKCREAIPEDKGKVVIVEAVLEEDKEDDEIGGVGLMLDTALMAITNKGKERTLKEWSYVLRQSGFTRFNVKPICAVRSVIEAYP\*

>Gohir.D04G169100|Gohir.D04G169100.1|Ghirsutum\_v2.1

MEVTIKEEVRAEIKIWNYVLGYVKIAVVKCAIELGIADVIENYGSPMPLSELATALRCEPSRLHRIMRFMVHDRIFKQEPINQHTVGFSSTPLSRLLMKGGQKSMAALILLMSSPTCLAPWHSLSARVLETGNNISPFEVANGKDLWSYAEANPDFRELFNNAMGCDARLTVQATIEGCPEVFDGVESLVDVGGGNGTALSLLVKAFPWIRGINFDLPHVVAVAAKSDSIENVGGDMFMSIPNADAAFLVWVLHDWDDEECIKILKKCREAIPEDKGKVIIVEAVLEEDKEGDELGGVGC\*

>Gohir.D04G168900|Gohir.D04G168900.1|Ghirsutum\_v2.1

MGDMEVTVKEEARAEIKIWNYVLGYAKIAVVKCAIELGIADTIENYGSPMPLSELATALRCEPSRLHRIMSFMVHDRIFKQEPINQHTVGFSSTPLSRLLIKRGEKSMAAFILLMSSPTCLAPWHSLSARVLETGNNISPFEVANGKDIWSYAEANPDFRELFSNAMGCDARLTVQATIEGCPEVFDGVESLVDVGGGNGTALSLLVKAFPWIRGINFDLPHVVAVAAKSDSIENVGGDMFMSIPNADAVFLMWVLHDWDDEECIKILKKCREAIPEDKGKVIIVEAVLEEDKEGDELGGVGLMLDTALMAITNKGKERTLKEWSYVLRQSGFTRFNVKPTRAVQFVIEAYP\*

>Gohir.D12G037100|Gohir.D12G037100.1|Ghirsutum\_v2.1

MGDIKVRGKKEDEDEKAEVEIWNYVFGHVKIAVVKCAIELGIADAIDKHGSPMTLSQLTTTLKCEPPRLYRILRFLVHYQILKEEPVTQDSIGFALTPLSRRLIRHGERSMAALILLESSPVMLAPWHSLSARVLDSGNSPFETAHGKDVWSYAEENPGHSKLIDEAMACDARVAVRALIEGCPRVFDGIKSLVDVGGGNGTALSMLVKAFPWMHGINFDLPHVVAVAPKVDGIEYVGGDMFECVPKADAAFFMWVLHDWDDEECIQILKKCREAIPQDKGKVIIVESVLEEDENDKLEFVGLMLDMVMMAHTNKGKERTLKEWKYVLGEAGFTRINVKPIHAVQSIIEAYI\*

>Gohir.D12G036900|Gohir.D12G036900.1|Ghirsutum\_v2.1

MGDIKVRGKKEDEDEKAEVEIWNYVFGHVKIAVVKCAIELGIADAIDKHGSPMTLSQLTTTLKCQPSRLYRIMRFLVHYQIFKEEPITKDSIGFALTPLSRRLSRHGERSMAAMILLQSSPVTLAPWHSLSARVLDSGNSPFETAHGKDVWSYAEENSGHSKLIDEAMACDARVAVRAIIEGCPQVFDGIKSLVDVGGGNGTALSMLVKAFPWIHGIDFDLPRVVAVAPKVDGIEYVGGDMFECVPKADAAFFMWVLHDWGDEECIQILKKCREAIPQDKGKVIIVESVLEEDENDKLEFVGLMLDMVMMTHTNKGKERTLKEWTYVLGQAGFTRIDVKPIHAVQSVIEAYI\*

>Gohir.D02G181200|Gohir.D02G181200.1|Ghirsutum\_v2.1

MERIELDEAMLQGQAEIWRYLYSFADFMALTSAVELRIADIIHSNGGAATLSQIASCISDGLTSPDITALARIMRLLVRRKIFTIHPPLDGGDPLYNLTHSSRWLLHDSEQTLAPMVLMENHPWQMAPWHYFSQCVKEGGTAFKKAHGCEIWDLTSRDPNFNKLFNDGLACTSKFITSAILSGYKQGFNSIGSLVDVGGGTGGLISEIVKVYPHIKGVNFDLPHVVSTAPAYNGVSHIGGDMFNAIPNTDAIIIKWVLHNWNDEECIKILRNCKKAIPRENGKVIIVEIILKEDGSGVFDDIGFVMDLVMFAHNSGKERTEAEWKKILEGGGFSHYKIINIPAMVSIIEAYPDAQ\*

>Gohir.D02G181400|Gohir.D02G181400.1|Ghirsutum\_v2.1

MSSQESGREKETIELDEARLQGQAEIWRYMFSFADSMALKSAVELRIADIIHSHGVAITLSKIASCINGSLTSPDTTTLARIMRLLVRRKIFTVHHPSDGGDPLYDLTHSSRWLLHDSEQTLAPMVLMENHPWLIAPWHCFSQCVKERGIAFKKAHGREIWDLASGNPEFNKLFNDGLACTSKVVTSAILSGYKQGLSSIESLVDVGGGIGGLISEIVKAYPHIKGVNFDLPHVVLAAPAYNGIFHVGGDMFHAIPNANAVIMKWVLHDWGDEDCIKILRNCRKAIPRENGKVIIVEVVVKAEGSGVFDDMGFIFDLLMIAHSSGGKERTEVEWKKILEEGGFSRYKIIDIPALPSIIEAYPDDQ\*

>Gohir.D02G181300|Gohir.D02G181300.1|Ghirsutum\_v2.1

MERIELDEAMLQGQAEIWRYLYSFADSMALKSAVELRIADIIHSNGGAATLSQIASCINDSLTSPNITTLARIMRLLVRRKIFTIHPPSDGGDPLYDLTHSSRWLLYDSEQTLVPMVLMENHPWQMAPWHYFSQCVKEGGVAFKKAHGCETWDLASRNPDFNKLFNDGLACTSKFITSAILSGYKQGFNSIGSLVDVGGGTGGLISEIVKVYPHIKGVNFDLPHVVSTAPAYNGVSHIGGDMFHAIPNTDAIIMKWILHDWTDEECIKILRNCKKAIPRENGKVIIVEIILKEDGSGVFDDIGFVMDLVMFAHTNGKERTEAEWKKILEGGGFSHYKIINIPALVSIIEAYPDAQ\*

>Gohir.D10G206300|Gohir.D10G206300.1|Ghirsutum\_v2.1

MDMVNANGEHVNELLQAQAHVWNHIFNFINSMSLKCAIDLGIPDIIQNHGKPMTITELVAALPMLNPTKACNIYRLMRILVHSGFFAQRNLCNDAQEDGYVLTNASRLLLKDNPLSVTPFLKAMLDPILTEPWHCLGTWFKNNDHTPFDTTHGKTFWDYAGHDQKLNSLFNEGMASDARLVNSILIDKCKKVFEGLNSLVDVGGGTGTLSKAIVDAFPHLECIVLDLPHVVANLQDSGNLKYVAGDMFKEIPASDAILLKWILHDWNDDECLKILKRCKEAISRQNKKGGKVMIIDMVLMKNEKMNGEAFNSTETQLFFDMLMMVLVTGKERQEEEWAKLFFAAGFSNYKITPILGLRSLIQVFP\*

>HORVU2Hr1G004710|HORVU2Hr1G004710.1|Hvulgare\_r1

MTLKLLAEVSPQELLEALAGLQNHLLGYIKSMSLRCVVDLGIPDAIHCRGGTATLADIVTDTKVHPGKVADLQRVMKLLTTSGIFTATPNAGDDDDTMVYGLTTACRILVGWCNLSPIVPFLVNPLVVSSFFSMPAWFRTEPEAAGAGSLFELAHGCSQWEMVSKDAGFKNVLNNSMAADSQVFLEVIIVDKGRIFRGLRSLVDVGGGNGAGTQVIAKAFPRIKCTVMDLPHVVVSGQAAAGDDILSFVAGDMFQSIPSADAVLLKNILHDWGHDDCVKILKHCKEAIPARNAGGKVIIIDMVRGSANGDRKINEMEAIQNLFMMYITGVERNEIEWKMIFSDAGFSDDYKILPILGPYSVIEIYP\*

>HORVU2Hr1G007720|HORVU2Hr1G007720.1|Hvulgare\_r1

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>HORVU3Hr1G007570|HORVU3Hr1G007570.4|Hvulgare\_r1

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>HORVU3Hr1G029150|HORVU3Hr1G029150.1|Hvulgare\_r1

MATQAQQLAVPTEAELLQGQADLWRHSLYYMTSMAFQCAVKLGIPTTIHSLGGAASLPDLVAALSLPPAKLPYLRRIMRLLATSGVFAADSAAADVVATYRLTPLSWLLLDGVAVDGHPSQTSLVLAATSRHCLEAAMGLSDWFKKDVAASPFQDLHGVTLFDGTMAEQDPEVDAVFNDALASHDNSGFLAVLRECGGTLFQGLESLTDCCGGDGTTARAIVEAFPQIKCTVLDLPRVIDNVPADGVVNYVAGDMFNSVPFAQAVLIKLVLHHWSDEDCVRILAQCKKAIPPREEGGKVIVIDIVVDSSSGPTHEAELLMDVAMMVMTNGRQRDETDWSEIFIKAGFSDYKVVKKLGARGVFEVYP\*

>HORVU3Hr1G026150|HORVU3Hr1G026150.1|Hvulgare\_r1

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>HORVU3Hr1G110170|HORVU3Hr1G110170.3|Hvulgare\_r1

QNIMAENHQAVKMPTSSNKELLQAHAELWNLTFSYLKSMALECAIKLGIPTAIHRCGGTASLTDLLAALSIPESKKSYLPRLMRFLAASGIFTIDFLATGECANAGATVTYRLTPLSHLLVDGDDTYAHQCTSLSPFVLAQTNKYHVTAAMHFSDWFTSDEGSASAEMPYKMAHGTDHWEIMARDPKLNQVFNAGMAADTQFAMNFIINNCGEVFEGITSIVDVAGGTGTAAREIAKAFPHIKCSVLDLPNVINSISSDGLVNYIVGDMMSSIPTADAVFLKDVLHDWNDEDCVKILTQCKKAITKPGGKVIIVDMVVGSPSTSMFEGQVLFDMLMMVMTPGKEREEHEWGKIFMDAGFNHYKTRPIMGCMAITELYP\*

>HORVU5Hr1G066150|HORVU5Hr1G066150.2|Hvulgare\_r1

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>HORVU1Hr1G001570|HORVU1Hr1G001570.1|Hvulgare\_r1

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>HORVU1Hr1G089520|HORVU1Hr1G089520.1|Hvulgare\_r1

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>HORVU1Hr1G076660|HORVU1Hr1G076660.1|Hvulgare\_r1

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>HORVU1Hr1G076670|HORVU1Hr1G076670.2|Hvulgare\_r1

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>HORVU6Hr1G090510|HORVU6Hr1G090510.2|Hvulgare\_r1

MAGQAAEKVFVPTDAELLQAQSDLWRHSLCYLTPMSLRCAVDLGVPTAIHRLGGAASPSELVAALSLPASKLPFLARLLRQLATAGVFTSTDAGTYRLNPLSYLLVDGVRIDGDASQTAIVRAAASRYYVEAAMGLADWFRKDFDGAVPSPFEDVHGAAIFEESMALLDPEMDQLIHDAVAAHDHMGIGPVLRQCRELFEGLESLTDCGGGDGTTARSIVEAYPHINCTVLDLPKVMDKALPPAQQGVVKYVSGDLFHVVPPAQAVLLKLVLHFWSDEDCIKILAQCKKAVPPRDAGGKVIVIDIVLGSVSGPMLETQHLMDMLMLVMTRGRQREEKDWSEIFTKAGFSGYKIVKKLGARAVIEVYP\*

>HORVU6Hr1G003160|HORVU6Hr1G003160.2|Hvulgare\_r1

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>HORVU7Hr1G018870|HORVU7Hr1G018870.2|Hvulgare\_r1

SFEMENFTAGLCRCVAYLSTDAITYRNHTLITDRNGERRGRAMAAQADTIEVPTDAELLQAQADLWRHSLYYLSSMGLRCAVQLQIPTTIHRLGGVALLADLMAALSLPSVKMPFLHRLMRVLVTSGVFAADKDSESGGELYRLTPLSRILVDGVTDEHHSQKYFVLAVTAPHCAEAALGLADWFKKDLEPPVPSPFEDMHGAPVFDERTPLMDEEFDAVANEGLAAHDNLGIATILRECGDIFKGLESLTDCCGGDGTTARALVKAYPHIKCTVLDLPKVIDKAPKDGVVNYVAGDLFHTVPSSQAVMLKLVLHFWSDEDCVKILTQCKKAIPPHDEGGKIIIIDIVIGPSLGPIMFEAQLLMDMLMMVTTRGVQRSENDWRKLFMEAGFKDYKIVKKLGARCVIEVYP\*

>HORVU7Hr1G008260|HORVU7Hr1G008260.2|Hvulgare\_r1

MAVPSDAELLQAQADLWRHTLCYLTPMALRCAVELGIPTAIHRLGGAASPSDLIAALSLPPSKLSFLGRLLSQLATAGVFDSTDDMGTATYRLKPISYLLVDGVHIEGDACQTAIVRAASSRYYVEAALGLSEWFKKDFEGPVPSPFEDLHGATIFDDSMALLDPEMDKLVHEAKASHNHMGIGLVLRQCRELFQELESLTDLCGGDGTTARAIVRAYPHIKCTVMDLPKVIDKAPAEGVIKYVAGDIFHAVPPAQAVLLKSVLHLWSDEDCIKILAQCKKAIPPRGAGGKVIVIDIVLSSASGLMLETHHLVDMLKLVMTRGRQRDEKDWSDIFMKAGFSEYKVFKKVGARTVIEVYP\*

>HORVU7Hr1G117710|HORVU7Hr1G117710.10|Hvulgare\_r1

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>HORVU7Hr1G117850|HORVU7Hr1G117850.1|Hvulgare\_r1

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>HORVU7Hr1G018880|HORVU7Hr1G018880.1|Hvulgare\_r1

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>HORVU7Hr1G011340|HORVU7Hr1G011340.2|Hvulgare\_r1

MVLTREQRTDQGLLDAQLELWHISFGYVKSMALKSCLDLGIADAIHHHGGAATLSQIGAVATLHPSKICCLRRLMRVLTVSGVFSVQQPSPRDDVQVELVYTLTAVSHLLVSSASVNIVPVINLQLQPNIVSSFSELGAWFQHKLPEPDLFKLKHGKTFWEIAHHNAAFNTIVNDAMASDSRFLMDIAIRECGSVFEGIGSLVDVAGGHGGAAQAISKSFPHIKCSVMDLGHVIAGAPSGTDVQYIAGDMFESIPQADVVFLKWIMHDWSDDDCIKILKNCNKAIAPKDAGGKVIIVDMVVGGGPQDLKHKETQVLFDLYIMLLNGIERDEQEWKKIIMAAGFSDFKITPILGVRSIIELYP\*

>HORVU7Hr1G117890|HORVU7Hr1G117890.1|Hvulgare\_r1

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>HORVU4Hr1G076000|HORVU4Hr1G076000.2|Hvulgare\_r1

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>HORVU4Hr1G076050|HORVU4Hr1G076050.1|Hvulgare\_r1

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>HORVU4Hr1G012540|HORVU4Hr1G012540.1|Hvulgare\_r1

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>HORVU4Hr1G085680|HORVU4Hr1G085680.2|Hvulgare\_r1

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>cds.Jr16\_05020\_p1

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>cds.Jr13\_24380\_p1

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>cds.Jr13\_26200\_p1

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>cds.Jr07\_09880\_p1

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>cds.Jr07\_09890\_p1

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>cds.Jr07\_09710\_p1

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>cds.Jr07\_09860\_p1

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>cds.Jr10\_14980\_p1

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>cds.Jr12\_07430\_p1

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>cds.Jr04\_16510\_p1

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>cds.Jr01\_20680\_p1

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>cds.Jr07\_09790\_p1

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>cds.Jr16\_03670\_p1

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>cds.Jr10\_15890\_p1

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>cds.Jr16\_08680\_p1

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>cds.Jr04\_07880\_p1

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>cds.Jr03\_07860\_p1

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>cds.Jr03\_07840\_p1

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>cds.Jr04\_07960\_p1

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>cds.Jr04\_07870\_p1

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>cds.Jr04\_07730\_p1

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>cds.Jr\_Scaffold\_205\_00020\_p1

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>cds.Jr09\_08980\_p1

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>cds.Jr03\_07850\_p1

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>cds.Jr01\_20610\_p1

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>cds.Jr\_Scaffold\_58\_00010\_p1

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>cds.Jr04\_07760\_p1

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>cds.Jr04\_12690\_p1

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>cds.Jr01\_20620\_p1

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>cds.Jr09\_09000\_p1

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>cds.Jr09\_08970\_p1

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>cds.Jr13\_09690\_p1

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>cds.Jr10\_15840\_p1

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>cds.Jr\_Scaffold\_205\_00010\_p1

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>cds.Jr04\_07740\_p1

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>cds.Jr06\_10640\_p1

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>cds.Jr07\_09870\_p1

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>cds.Jr04\_07890\_p1

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>cds.Jr06\_10690\_p1

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>cds.Jr04\_07970\_p1

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>cds.Jr\_Scaffold\_661\_00050\_p1

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>cds.Jr04\_07950\_p1

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>cds.Jr09\_08990\_p1

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>PSS19510 pep chromosome:Red5\_PS1\_1.69.0:LG10:13610913:13614144:1 gene:CEY00\_Acc11603 transcript:PSS19510 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:Caffeic acid 3-O-methyltransferase

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>PSS14478 pep chromosome:Red5\_PS1\_1.69.0:LG13:15860726:15862145:1 gene:CEY00\_Acc15046 transcript:PSS14478 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:Trans-resveratrol di-O-methyltransferase

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>PSS12132 pep chromosome:Red5\_PS1\_1.69.0:LG14:17477518:17478984:-1 gene:CEY00\_Acc16343 transcript:PSS12132 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:(R,S)-reticuline 7-O-methyltransferase

MEGETNREEEEIQAQVDIWKYVFGFVDMAVVKCAIELGIAEVVESHEGPVTISELSSALGCSQSSLYRIMRFLVHRKFFKEDHNTNQGAIGYVQTPMSRLLLRNGEKSMAAFVLLESSPVMLAPWHGLSARVLAKGDLAFESTHGKDIWSYAATNPAHSKLINDAMACDARVAVAAIIDGCPDLFNGMDSVVDVGGGDGTTLRLLVKACPWIRGINFDLPHVVSEAPACDGIEHIGGDMFVSVPKADATLLMWVLHDWGDDECINVLRKCKEAIPKDKGKVIIIEGVVEEEEEDKLKYVRLMLDMVMMAHTNTGKERTSKEWVHLLIGAGFSRYTIKRIKAVQSIIEAYP

>PSS11908 pep chromosome:Red5\_PS1\_1.69.0:LG14:13951197:13953369:-1 gene:CEY00\_Acc01300 transcript:PSS11908 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:Caffeic acid 3-O-methyltransferase

MTTFEYHGTNPRSNKLFNQGMSNLSTITMKKVLDSYQGFEGLTTIVDVGGGTGASLNMILSKYPTIKGINFDLPRDFCICGVSNSGIGFGAGIPGPRSGRGSGLQQNPRRGSGRGSGLKKISGIGDGDTNLRPRPAPLPSLVGGDMFVSVPNGDAIFMKWICHDWSNEHSSKFLKNCYNALPNNGKVIVAEYILPVALDTSLAMKSVVDMDIIMLAYSQGGKERTEKEFEALAKGAGFEGFRVMCCAFNTYVMEFLKKI

>PSS04505 pep chromosome:Red5\_PS1\_1.69.0:LG18:13044644:13047850:-1 gene:CEY00\_Acc20359 transcript:PSS04505 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:Caffeic acid 3-O-methyltransferase

MGSITTNQTVAIRSEEEEACLFALQLANASVLPMVLKSAIELDLLEIMAKAGPGAYVSPSELAAQLSTTNPDAPAMIDRILRLLTSYSVLKCDLRDLPDGGVERLYGLEPVCKFLTRNADGVSLAPLALMTQDKVLMQSWYHLKDAVVDGGIPFNKAYGMSAFEYHGTDPRFNKVFNQGMSNHSTFTMKKILETYHGIESLTTLVDVGGGIGATLNMIVSKYPSLKGINFDLPHVIEDAPTYPGVEHVGGDMFISVPKGDAIFMKWICHNWSDEHCLKFLKNCYDSLPDDGKVIISECILPVSPNTELATKTVFHLDIIMLSHYPGGKERTEKEFEALAKGAGFEGFRVACYVFNTYIIEFLKKI

>PSS32943 pep chromosome:Red5\_PS1\_1.69.0:LG3:7186730:7187815:1 gene:CEY00\_Acc03239 transcript:PSS32943 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:Caffeic acid 3-O-methyltransferase

MFVSVPKGDAIFMKWICHDWSDEHCLKFLKNCYDSLPDDGKVIISECILPVAPDTGLATKTVFHIDIIMLAHNPGGKERTEKEFEALAKGAGFEGFRVACCAFGTYIMEFLKKI

>PSS32944 pep chromosome:Red5\_PS1\_1.69.0:LG3:7191631:7193152:1 gene:CEY00\_Acc03240 transcript:PSS32944 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:Flavone 3'-O-methyltransferase

MIRYHLKDAVVDGGIPFNKAYGMSAFEYHGTDPRFNKVFNQGMYHLKDAVVDGGIPFNKAYGMSAFEYHGTDPRFNKVFNQGMSNHSTFTMKKILETYHGFEGLTTLVDVGGGIGATLNMIVSKYPTVRGINFDLPHVIEDAPT

>PSS32279 pep chromosome:Red5\_PS1\_1.69.0:LG3:306049:309984:1 gene:CEY00\_Acc02578 transcript:PSS32279 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:Caffeic acid 3-O-methyltransferase

MGSTSEAQITPTDQEEAFLFAMQLASASVLPMVLKSAIELDLLEAIARAGPAAYVSPSDLAAQLSTTNPHAAVMLDRILRLLTSYSVLHCTLRTLPNGGVERLYGLAPVCKFLIKNEDGVSMAPLLLMNQDKVLMESWYHLKDAVLDGGIPFNKAYGMTAFEYHGTDTRFNKVFNQGMSNHSTITMKKIMDSYQGFEGLNTIVDVGGGTGATLNMILSKYPAIKGINFDLPHVIEDAPSYPGVEHVGGDMFVSVPNGDAIFMKWICHDWSDEHCSKFLKNCYDALPNNGKVIVAECILPIAPDTSLATKNVVHIDVIMLAHNPGGKERTEKEFEALAKGAGFEGFRVMCCAFNTHVMEFLKKI

>PSS31563 pep chromosome:Red5\_PS1\_1.69.0:LG4:5292021:5295031:-1 gene:CEY00\_Acc07226 transcript:PSS31563 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:(RS)-norcoclaurine 6-O-methyltransferase

MASFLLLQSSPALLATWHGLSARVLTNGPSAFETTHGKDIWSYVETNPALSKLFNESMACDARRVVPEIINGCPGLLDGLDSLVDVGGGNGTTMRLLVKACDWIRDINFDLPHVVSDAPACVRVEHVGGDMFDSVPNADAAFLMWVLHDWGDDECIRILKNCREAISKDKRKVIIVEAVVEEKEDKLGHVRLMLDMVMMAFTNNGKQRTSKEWAHLLREAGFSRYTVTQIKSVKSVIEAYP

>AT1G21100.1 (AtASMT1)

MGYLFQETLSSNPKTPIVVDDDNELGLMAVRLANAAAFPMVLKAALELGVFDTLYAAASRTDSFLSPYEIASKLPTTPRNPEAPVLLDRMLRLLASYSMVKCGKALSGKGERVYRAEPICRFFLKDNIQDIGSLASQVIVNFDSVFLNTWAQLKDVVLEGGDAFGRAHGGMKLFDYMGTDERFSKLFNQTGFTIAVVKKALEVYEGFKGVKVLVDVGGGVGNTLGVVTSKYPNIKGINFDLTCALAQAPSYPGVEHVAGDMFVDVPTGDAMILKRILHDWTDEDCVKILKNCWKSLPENGKVVVIELVTPDEAENGDINANIAFDMDMLMFTQCSGGKERSRAEFEALAAASGFTHCKFVCQAYHCWIIEFCK

>AT1G21110.1 (AtASMT2)

MGYLFEETLSSNPKTPIVVDDDNELGLMAVRLANAAAFPMVLKASLELGVFDTLYAEASRTDSFLSPSEIASKLPTTPRNPGAPVLLDRMLRLLASYSMVKCEKVSVGKEQRVYRAEPICRFFLKNNIQDIGSLASQVIVNFDSVFLNTWAQLKDVVLEGGDAFGRAHGGMKLFDYMGTDERFSKLFNQTGFTIAVVKKALEVYQGFKGVNVLVDVGGGVGNTLGVVTSKYPNIKGINFDLTCALAQAPTYPGVEHVAGDMFVDVPTGNAMILKRILHDWTDEDCVKILKNCWKSLPQNGKVVVIELVTPDEAENGDINANIAFDMDMLMFTQCSGGKERSRAEFEALAAASGFSHCQFVCQAYHCWIIEFCK

>AT1G21120.1 (AtASMT3)

MGYLFEETLSSNPKTPIVVDDDNELGLMAVRLANAAAFPMVLKASLELGVFDTLYAEASRTDSFLSPSEIASKLPTTPRNPGAPVLLDRMLRLLASYSMVKCEKVSVGKGERVYRAEPICRFFLKNNIQDIGSLASQVIVNFDSVFLNTWAQLKDVVLEGGDAFGRAHGGMKLFDYMGTDERFSKLFNQTGFTIAVVKKALEVYQGFKGVNVLVDVGGGVGNTLGVVTSKYPNIKGINFDLTCALAQAPSYPGVEHVAGDMFVDVPTGDAMILKRILHDWTDEDCVKILKNCWKSLPENGKVVVIELVTPDEAENGDINANIAFDMDMLMFTQCSGGKERSRAEFEALAAASCFTHCKFVCQAYHCWIIEFCK

>AT1G21130.1 (AtASMT4)

MGYLLEETLSSNSKTPIVIDDDNELGLMAVRLANAAAFPMVLKAALELGVFDTLYAEASRSDSFLSPSEIASKLPTTPRNPEAPVLLDRMLRLLASYSVVKCGKVSEGKGERVYRAEPICRFFLKDNIQDIGSLASQVIVNFDSVFLNTWAQLKDVVLEGGDAFGRAHGGMKLFDYMGTDERFSKLFNQTGFTIAVVKKALEVYQGFKGVNVLVDVGGGVGNTLGVVASKYPNIKGINFDLTCALAQAPSYPGVEHVAGDMFVDVPTGDAMILKRILHDWTDEDCVKILKNCWKSLPESGKVVVIELVTPDEAENGDINANIAFDMDMLMFTQCSGGKERSRAEFEALAAASGFTHCKFVCQAYHCWIIEFCK

>AT1G33030.1 (AtASMT5)

MEEQNLSSYAMILSSSSVLPMVLKTAIDLGLFDILAESGPSSASQIFSLLSNETKKHHDSSLVNRILRFLASYSILTCSVSTEHGEPFAIYGLAPVAKYFTKNQNGGGSLAPMVNLFQDKVVTDMWYNLKDSVLEGGLPFNNTHGSSAVELVGSDSRFREVFQSSMKGFNEVFIEEFLKNYNGFDGVKSLVDVGGGDGSLLSRIISKHTHIIKAINFDLPTVINTSLPSPGIEHVAGDMFTNTPKGEAIFMKWMLHSWDDDHCVKILSNCYQSLPSNGKVIVVDMVIPEFPGDTLLDRSLFQFELFMMNMNPSGKERTKKEFEILARLAGFSNVQVPFTSLCFSVLEFHKNK

>AT1G51990.1 (AtASMT6.1)

MISLQTSGGSSEEEDMLLAIQLGGLNFVPYIVKTARELDLFEIMAKARPLGSYLSPVDLASMAAPKNPHAPMMIDRLLRFLVAYSVCTCKLVKDEEGRESRAYGLGKVGKKLIKDEDGFSIAPYVLAGCTKAKGGVWSYLTEAIQEGGASAWERANEALIFEYMKKNENLKKIFNESMTNHTSIVMKKILENYIGFEGVSDFVDVGGSLGSNLAQILSKYPHIKGINFDLPHIVKEAPQIHGVEHIGGDMFDEIPRGEVILMKWILHDWNDEKCVEILKNCKKALPETGRIIVIEMIVPREVSETDLATKNSLSADLTMMSLTSGGKERTKKEFEDLAKEAGFKLPKIIYGAYSYWIIELYPN

>AT1G51990.2 (AtASMT6.2)

MISLQTSGGSSEEEDMLLAIQLGGLNFVPYIVKTARELDLFEIMAKARPLGSYLSPVDLASMAAPKNPHAPMMIDRLLRFLVAYSVCTCKLVKDEEGRESRAYGLGKVGKKLIKDEDGFSIAPYVLAGCTKAKGGVWYNVQHAIQEGGASAWERANEALIFEYMKKNENLKKIFNESMTNHTSIVMKKILENYIGFEGVSDFVDVGGSLGSNLAQILSKYPHIKGINFDLPHIVKEAPQIHGVEHIGGDMFDEIPRGEVILMKWILHDWNDEKCVEILKNCKKALPETGRIIVIEMIVPREVSETDLATKNSLSADLTMMSLTSGGKERTKKEFEDLAKEAGFKLPKIIYGAYSYWIIELYPN

>AT1G62900.1 (AtASMT7)

MRVFELIGSNEQFAEMFNRTMSEASTLIMKKVLEVYKGFEDVNTLVDVGGGIGTIIGQVTSKYPHIKGINFDLASVLAHAPFNKGVEHVSGDMFKEIPKGDAIFMKWILHDWTDEDCVKILKNYWKSLPEKGKVIIVEVVTPEEPKINDISSNIVFGMDMLMLAVSSGGKERSLSQFETLASDSGFLRCEIICHAFSYSVIELHK

>AT1G63140.1 (AtASMT8.1)

MENHLQHSLTIIPKPDLIKEEQRYHEDTVSLQAERILHAMTFPMVLKTALELGVIDMITSVDDGVWLSPSEIALGLPTKPTNPEAPVLLDRMLVLLASHSILKYRTVETGDNIGSRKTERVYAAEPVCTFFLNRGDGLGSLATLFMVLQGEVCMKPWEHLKDMILEGKDAFTSAHGMRFFELIGSNEQFAEMFNRAMSEASTLIMKKVLEVYKGFEDVNTLVDVGGGIGTIIGQVTSKYPHIKGINFDLASVLAHAPFNKGVEHVSGDMFKEIPKGDAIFMKVSRK

>AT1G63140.2 (AtASMT8.2)

MENHLQHSLTIIPKPDLIKEEQRYHEDTVSLQAERILHAMTFPMVLKTALELGVIDMITSVDDGVWLSPSEIALGLPTKPTNPEAPVLLDRMLVLLASHSILKYRTVETGDNIGSRKTERVYAAEPVCTFFLNRGDGLGSLATLFMVLQGEVCMKPWEHLKDMILEGKDAFTSAHGMRFFELIGSNEQFAEMFNRAMSEASTLIMKKVLEVYKGFEDVNTLVDVGGGIGTIIGQVTSKYPHIKGINFDLASVLAHAPFNKGVEHVSGDMFKEIPKGDAIFMKWILHDWTDEDCVKILKNYWKSLPEKGKVIIVEVVTPEEPKINDISSNIVFGMDMLMLAVSSGGKERSLSQFETLASDSGFLRCEIICHAFSYSVIELHK

>AT1G76790.1 (AtASMT9)

MGHLIPQTGDEETELGLAAVRLANCAAFPMVFKAAIELGVIDTLYLAARDDVTGSSSFLTPSEIAIRLPTKPSNPEAPALLDRILRLLASYSMVKCQIIDGNRVYKAEPICRYFLKDNVDEELGTLASQLIVTLDTVFLNTWGELKNVVLEGGVAFGRANGGLKLFDYISKDERLSKLFNRTGFSVAVLKKILQVYSGFEGVNVLVDVGGGVGDTLGFVTSKYPNIKGINFDLTCALTQAPSYPNVEHVAGDMFVDVPKGDAILLKRILHDWTDEDCEKILKNCWKALPENGKVIVMEVVTPDEADNRDVISNIAFDMDLLMLTQLSGGKERSRAEYVAMAANSGFPRCNFVCSAYHLWVIELTKQA

>AT1G77520.1 (AtASMT10)

MTNHLQDPLPTYPKPVLTKEEQEVDEKMVSLQAESIVNTVAFPMVLKAAFELGVIDTIAAAGNDTWLSPCEIACSLPTKPTNPEAPVLLDRMLSLLVSHSILKCRMIETGENGRTGKIERVYAAEPVCKYFLRDSDGTGSLVPLFMLLHTQVFFKTWTNLKDVILEGRDAFNSAHGMKIFEYINSDQPFAELFNRAMSEPSTMIMKKVLDVYRGFEDVNTLVDVGGGNGTVLGLVTSKYPHIKGVNFDLAQVLTQAPFYPGVEHVSGDMFVEVPKGDAVFMKWILHDWGDEDCIKILKNCWKSLPEKGKIIIVEFVTPKEPKGGDLSSNTVFAMDLLMLTQCSGGKERSLSQFENLAFASGFLRCEIICLAYSYSVIEFHK

>AT1G77530.1 (AtASMT11)

MSNHLQDPLTTYPKPGLTKEEQEIDEKMVSLQAESIVNAVAFPMVLKAALELGVIDTIAAASNGTWLSPSEIAVSLPNKPTNPEAPVLLDRMLRLLVSHSILKCCMVESRENGQTGKIERVYAAEPICKYFLKDSDGSGSLSSLLLLLHSQVILKTWTNLKDVILEGKDAFSSAHDMRLFEYISSDDQFSKLFHRAMSESSTMVMKKVLEEYRGFEDVNTLVDVGGGIGTILGLITSKYPHIKGVNFDLAQVLTQAPFYPGVKHVSGDMFIEVPKGDAIFMKWILHDWGDEDCIKILKNCWKSLPEKGKVIIVEMITPMEPKPNDFSCNTVLGMDLLMLTQCSGGKERSLSQFENLAFASGFLLCEIICLSYSYSVIEFHK

>AT3G53140.1 (AtASMT12)

MENESSESRNRARLAIMELANMISVPMSLNAAVRLGIADAIWNGGANSPLSAAEILPRLHLPSHTTIGGDPENLQRILRMLTSYGVFSEHLVGSIERKYSLTDVGKTLVTDSGGLSYAAYVLQHHQEALMRAWPLVHTAVVEPETEPYVKANGEAAYAQYGKSEEMNGLMQKAMSGVSVPFMKAILDGYDGFKSVDILVDVGGSAGDCLRMILQQFPNVREGINFDLPEVVAKAPNIPGVTHVGGDMFQSVPSADAIFMKWVLTTWTDEECKQIMKNCYNALPVGGKLIACEPVLPKETDESHRTRALLEGDIFVMTIYRTKGKHRTEEEFIELGLSAGFPTFRPFYIDYFYTILEFQK

>AT4G35150.1 (AtASMT13)

MEESKRNLLDEEAKASLDIWRYVFGFADIAAAKCAIDLKIPEAIENHPSSQPVTLSELSSAVSASPSHLRRIMRFLVHQGLFKEVPTKDGLATGYTNTPLSRRMMITKLHGKDLWAFAQDNLCHSQLINEAMACDARRVVPRVAGACQGLFDGVATVVDVGGGTGETMGILVKEFPWIKGFNFDLPHVIEVAQVLDGVENVEGDMFDSIPASDAVIIKWVLHDWGDKDCIKILKNCKEAVLPNIGKVLIVECVIGEKKNTMIAEERDDKLEHVRLQLDMVMMVHTSTGKERTLKEWDFVLTEAGFARYEVRDFDDVQSLIIAYRS

>AT4G35160.1 (AtASMT14)

MSSDQLSKFLDRNKMEDNKRKVLDEEAKASLDIWKYVFGFADIAAAKCAIDLKIPEAIENHPSSQPVTLAELSSAVSASPSHLRRIMRFLVHQGIFKEIPTKDGLATGYVNTPLSRRLMITRRDGKSLAPFVLFETTPEMLAPWLRLSSVVSSPVNGSTPPPFDAVHGKDVWSFAQDNPFLSDMINEAMACDARRVVPRVAGACHGLFDGVTTMVDVGGGTGETMGMLVKEFPWIKGFNFDLPHVIEVAEVLDGVENVEGDMFDSIPACDAIFIKWVLHDWGDKDCIKILKNCKEAVPPNIGKVLIVESVIGENKKTMIVDERDEKLEHVRLMLDMVMMAHTSTGKERTLKEWDFVLKEAGFARYEVRDIDDVQSLIIAYRS

>AT5G37170.1 (AtASMT15)

MTNHHQESLTTYPKPGPTREQEQVDEEMMSMQMQALRITNSLAFPMGVWLSPSEIAFGLPTKPTNPEAPMLIDRMLRLLVSHSILKCRLVETGENNRTESTQRVYAAEPDTSEGCDTRRKRCIQFCPWHGTLRIRCTDEQFAAIFNQAMSDSSTMIMTKILEVYKGLKDVNTLVDIGGGLGTILNLVISSKYPQIKGINFDLAAVLATAPSYPGVEHVPGDMFIDVPKGDAIFMRRILRDWNDKDCVKILTNCWKSLPEKGKVIIVDMVAPSEPKSDDIFSKVVFGTDMLMLTQCSCGKVRSFAQFEALASASGFHKCEVSGLAYTYSVIEFHK

>AT5G53810.1 (AtASMT16)

MANHLQVPLTKPDRVKEEQEVEEEARLLARRLANAAASPMVLKAALELGVIDTITTVGGGDLWLSPSEIALRLPTKPCNLEAPALLDRMLRFLVSHSVLKCRTVIEENGQTGKVERVYAAEPVCKYLLNKSDDVSGSFASLFMLDLSDVFIKTWTHLEDVILEGRDAFSSAHGMKLFEYIQADERFGKVFNRAMLESSTMVTEKVLKFYEGFKDVKTLVDVGGGLGNTLGLITSKYPHLIGINFDLAPVLANAHSYPGVNHVAGDMFIKIPKGDAIFMKWILHDWTDEQCVAILKNCWKSLEENGKLIIVEMVTPVEAKSGDICSNIVFGMDMTMLTQCSGGKERDLYEFENLAYASGFSRCAIVCAVYPFSVIEIYK

>AT5G54160.1 (AtASMT17)

MGSTAETQLTPVQVTDDEAALFAMQLASASVLPMALKSALELDLLEIMAKNGSPMSPTEIASKLPTKNPEAPVMLDRILRLLTSYSVLTCSNRKLSGDGVERIYGLGPVCKYLTKNEDGVSIAALCLMNQDKVLMESWYHLKDAILDGGIPFNKAYGMSAFEYHGTDPRFNKVFNNGMSNHSTITMKKILETYKGFEGLTSLVDVGGGIGATLKMIVSKYPNLKGINFDLPHVIEDAPSHPGIEHVGGDMFVSVPKGDAIFMKWICHDWSDEHCVKFLKNCYESLPEDGKVILAECILPETPDSSLSTKQVVHVDCIMLAHNPGGKERTEKEFEALAKASGFKGIKVVCDAFGVNLIELLKKL

>Caril.10G053100

MDLVNGQGASDEQSRLQSHLYKNMLGFTDSMSLYCAIQLGIPDIIHNHGQPITLKQLASKLRIHPQKTSCMHRLMRLLVYSGFITKTAAVVHEDQEEEEAYALTASSRVVLKDKVTGLSPLVQAILDPAVVNSWYSLGDWFRGTELTPFVKAHGMGFFDYCNQNQEYGITFDEGMASDSRLMSKVIKDYKTIFEGLDSLVDVGGGSGTVSRIISEAFPHIKCTVFDLPQVVANLPDDKNLKYVGGDMFQSIPAADAILMKWILHDWSDEECINILKRCKEAIRSKGKDGKIIIIDVVINEEEEEHDITKAKLFLDALMMILLTGKERTKKEWEKLFLDAGFSHYKIVASYGLKSLIEVYPN\*

>Caril.05G088800

MESKREKEMGSTQRSEWDEEEEQAEVDIWKYMFGFTEMAVVKCAVELGIADTIESHGGGPMTLSELSSTLGCDPSPLYRVMRFLTHRGIFKEMPTTQGSPGYGQTRLSSRLLRNGEHSMAALILLHNSPVMLAPWHSLSAHVLAYETAPFDVVHGEDIWRYAAENPGHSRLFNEAMACDARLVVPAMLQGCPEVFDGLSSLVDVGGGNGTTLQLLVKSCQWIRGINFDLPHVVSDAAEFPGIEHVGGDMFATVPKADAAFVKWVLHIWGDKECIQILKKCRESIPEGKGKVIIVEAVLDQEAKISDKLTEARLALDMIVMAHTTTGKERTLEEWGLVLEKAGFSKYTVKPIRAVQSVIEAFP\*

>Caril.05G088700

MENTKRTEWDEEEEQAEVSIWKYIFRFTEMAVVKCAIELGIADTIESHGGGPMTLSELSSTLGCDPSPLSRVLRFLTHRGIFKEMPTTKGSPRYAQTRLSSRLLRKGEHSMAALILFESRPVMLAPWHRLSARVLAYETAPFEVVHGEDIWRYAAENPGHSRLINEAMACDARLVVPAMLQGCPEVFDGLSSLVDVGGGNGTTLQLLVKSCQWIRGINFDLPHVVSDAAEFPGIERVGGDMFASVPKADAAFLKNVLHDWGDNECIQILKKCRESIPEGKGKVIIVEAVIDQEAKISDKLTDVRLALDMIMMAHTTTGKERTLEEWGLVLGKAGFSKYTVKPIRAVQSVIEAFP\*

>Caril.05G088600

MENTQRTEWDEEEEQAEVGIWKYIFGFTEMAVVKCAIELGIADTIESHGGGPMTLSELSSTLGCDPSPLSRVMRFLTHRGIFKEMPTTKGSPGYAQTRLSSRLLRNGEHSMAALILLESSPVMLAPWHSLSAHVLAYETAPFDVVHGEDIWRYAAENPGHSRLINEAMACNARLVVPAILQVCPEVFDGLSSLVDVGGGNGTTLQLLVKSCQWIRGINFDLPHVVSDAAEFPGIEHVGGDMFASVPKADAAFLKQWVLHDWGDNECIQILKKCRESIPEGKGKVIIVEAVIDQEAKISDKLTAVRLALDMMMMAHTTTGKERTLEEWGLVLGKAGFSKYTVKPIRAVQSVIEAFP\*

>Caril.05G088500

MENTHRTEWDEEEEQAEVGIWKYIFGFTEMAVVKCAIELGIADTIESHGGGPMTLSELSSTLGCDPSPLSRVMRFLTHRGIFKEMPTTKGSPGYAQTRLSSRLLRNGEHSMAALILLESSPVMLAPWHSLSARVLAYETAPFDVVHGEDIWRYAAENPGHSRLINEAMACNARLVVPAILQGCPEVFDGLSSLVDVGGGNGTTLQLLVTSCQWIRGINFDLPHVVSDAAEFPGIDYVGGDMFASVPKADAAFINNVLHDWGDNECIQILKKCRESIPEGKGKVIIVEAVIDQEAKISDKLTDVRLALDMIMMAHTTTGKERTLEEWGLVLGKAGFSKYTVKPIRAVQSVIEAFP\*

>Caril.09G064200

MDLIHAQGEGEREQFQAQSHLYKHVFNYIGSMSLKCAVQLGIPDIIYNHGQPITLPELVSKLQIHPSKAGFVPRLMRLLVHSGLFAATVRVKNQEEEEAYDLTPSSRVLIKDQVSNLSPFVLAMINPALVTPCHDLGNWLQGEKVTPFESVHGMSFWDYNDQNPEFNSLFNEAMASDSGMMNFIIKDCKAVFEGLDTLVDVGGGTGTCARIISEEFPHLKCTVFDLPHVVANLAADSLKLNYVAGDMFESIPSADALLLKLVLHGWSDEHCVKILKKCREAISKNGKGEGKVIIIDVVINEKKEEHEMTEAKLLFDMLMMVVTSGKERDEKDFKKLFLEAGFNRYKITPIYGLRYLNLPHTTVMGFENNDKVAWVERIMQIDRRDIGTALSVISSNISAATFLASISLTLCSLIGAWMANSSNYFMQGLVYGDTRPSTMSIKYISLLICFLLAFSCFVQSARNFVHANYLLSTPDSNIPVRNVELVILRGGDFWSLGLRALYFALDILLWFFGPIPMFVSSIVMVIIFHYLDTNTTLLHKHGSPQKQMVETVAV\*

>Caril.09G064300

MDLVNCGQEASELFRVQSHLYKHLFSFIDSMSLGCAIQLGIPDIIHSHGQPMTLPQLVSKLHIDPKKTICVHRLMRLLSHSGFFTKTTTVHEDREEEEAYALTPSSRLVLKDDRTSLSPFVVAMLDPALVNPWYSLGDWFRGTELTPFAKAHGMGLWDYCNENPEYGDTFNEAMASDSQFMRLVVKDYKPIFEGLGSLVDVGGGTGTMARIISEAFPHIKCTVYDLPHVVANLPESSNFNYVGGDMFQSIPPADAIMFKWIMHDWNDEDCVNILKRCKEAITSKGYKEGNKVIIIDVVINEEKDDEDITKAKLLFDTLMMVLLPGKERTKKEWEKLFLEAGFSRYKIAASYGMKSLIEVYP\*

>Caril.04G128700

MSGLRQPSFELVPEEHLAKLLNAQALIWNRIFNFINSMSLKCAIQLGIPDIIHNHGKPMTLSELLVALPIHPTKACNVSRLMRILIHSGFFVAEKIIGNDQEERYALTDASRLLLKDNPLSVTPFLIAMLDPVLTKPWHFLTAWFQNEDLTPFDTAHGKKFWDYGGHDPKLNHLFNDAMASDARLVMSVVIDKCSAVFSGLESLVDVGGGTGTVAKAIADAVPSMECTVLDLPHVVAGLEGSKKLKYIGGDMFEAVPPADAILLKWILHDWNDEECIKILGRCKEAITSNDKKGKVIIIDMIVQNQKEDDEESIETQLFFDMLMMVMATGKERNEKEWAKLFFDAGFSDYKITHILGLRSLIEVYP\*

>Caril.04G128600

MSSFRMNSFKLIPGEHATELLNAQAHIWNHIFNFINSMSLKCAIQLGIPDIIHSHGKPMTLSELLVALPIHPTKACNVPRLMRILIHSGFFVAEKMFENDQEERYALTDASRLLLKDNPLSVTPFLVAMLDPVLTKPWHFLTAWFQNEDLTPFDTAHGKKFWDYGEHEAKLNHFFSDAMASDARFVVSVLIDKCSAVFDGLESLVDVGGVTGTVAKAIADAFPSMECTVLDLPHVVAGLEGSERLKYIGGDMFEAVPPADAILLKWILHDWNDEECIKILGRCKEAITSTDKKGKVIIIDMIVQNQKEDDEDRESIETQLFFDMLMMVLVTGKERNEKEWAKLFFDAGFSDYKTTHKLGLRSLIEVYP\*

>Caril.04G128300

MSSFRQHSFKLVPGEHATELLNAQAHIWNHIFNFINSMSLKCAIQLSIPDIIHNHAKPMTLSELLVALPIHPTKARHIPRIMRILIHSGFFVAEETIGNDEEERYALTDASRLLLKENPLSVTPFLLAVLDPVLTKPWQFLTAWFQNEDLTPFDTAHGQMFWDYGCHEPRLNNFFNDAMASDARLVMSVVIDKCSAVFGRLESLVDVGGGTGTVAKAIADAFPSMECTVLDLPHVVACSEGSKNLKYIGGDMFEAVPPADAILLKWILHDWNDEECVKILRRCKEAIMSNGKKGKVIIIEMIVQNQKEDDKESIETQLFFDMLMMVLVTGKERNEKEWAKVFFDAGFSEYKITHILGLRSLIEVYP\*

>Caril.03G167400

MERKEEVALLKGQAEIWQHLFAFADSMALKCAVELRIADIMHSHSVPITLSQIASAIDSPSPDIPYLSRIMRSLVYKKIFTEHHPSDGGEKLYGPTHTSRWLLHDAELTLAPMVLMENSQRQLAPWHFLSQCVKEGGIAFKKAYGVEMWDFAARNPEYNKIFNDAMACTTKIMMGVLLAEYKDGFGSIGSLVDVGGGTGEMIAEIIKQHPNINGFNFDLPHVVATAPVHEGVSHVGGNIFEAIPNANAILLKCVLHDWSDEHCIKILRNCKKTVPQKTGKVIIVDIVIEKDNDDLFQETRMVYDLLMMAHTTGGKERSELEWKQLLEEGGFPRYKIIKLPAITSIIEAYPE\*

>Caril.03G167000

MELTTMEAMIQGEAKLWGNIFAFTDSMALRCVLELGIVDIIHSHGGPITLSQIAAGIDSPSLNIDNLARLMRLLVRKDIFTTHHQPSDCGEITLYGLTPHTSRWLMRGSEFSLVPFILMQSHPELMTSWLCLSQCVKEGGTAFSKVHGCEVRDFAHKSPKFNKMFNDAMACTAKLVAERILWGYRDGFSSINGSLVDVGGGTGEMVAKIVKAHPHIKAINFDLPHVITTAPMQLGVSHIEGNMFEAIPNADAILLKRVLHGFSDEDCIKILKNCAKAIPKKTGKIIIVEHVLEPNGNGPFDETGLVFDLIMMLLAPSGKERTELDWKKLLKEGGFPHHKIIKIPAFPSIIEAHPA\*

>Caril.03G185200

MERKEEVALLKGQAEIWQLLFAFADAMALKCAVELRIADIIHSHSVPITLSQIASAIDSPSPDIPYLSRIMRSLVYKKIFTEHHPSDGGEKLYGPTHTSRWLLHDAELTLAPMVLMENSQRQLAPWHFLSQCVKEGGIAFKKAHGVEMWDFAARNPKFNKIFNDAMACTTKIMMGVLLAEYKDGFSSIGSLVDVGGGTGEMIAEIIKLHPHIKGFNFDFPHVVATAPVHEGVSHVGGNMFESIPNANAILLKCVLHDWSDEQCIKILRNCKKTVPQQTGKVIIVDIVIEKDNDDLFRETRMVYDLLMMAHTTGGKERSELEWQQLLEEGGFPRYKIIKLPAITSIIEAYPE\*

>Cre03.g148800

MQPDVKPVLDLLNGFRASQTLLTAVQLGLFECLEHTNELSVDGLASALAHRLPGSPAPSLDGLDRLCRACVALGLLSSPANGQFALTDAARAYLLASAPQSLAGYCVHSSQVVWPLFGGLPAAVTTGSNVWQQQFGAPGSDVFARVYDTPGAVRRFMSGMHSFATLSAPAVVRAFDLSFATRLLDLGGATGALAAAACAAYPSLEEAVVVDLPHVLELAQRHFAPTAAPREPAAPAEVQGAGGGGGGGFGGGGDGGGSGGGGSGDCGCNGRLRWLAADFFTETDKLPQQVDLVVLSRILHDWDGPRCAQLLARVHGLLRPGGAVLVAEMLLQPDRLGPPAALLQDLNMLCQTHGRERSLAEYEQLLQAAGFVDVRGHVTGTYLDAVLARKPEQHL\*

>Cre05.g240400

MMTWGGILCLNADRSFPMFTHLPHVLRHGELPPESKQSIPDILTTFGSDVAAAEFFAEGMTGASLGNFNLLARSFPFARYTSLGDLGGSSGCLACCVAAAHPHLTATTYDLAPVHAAAERHVRAQGLEGRVQVVDYDFFSPAAVPGRHDVIALGMVLHDWGLPRKMQLLRKAYAALPPGGALIAIDHLVDCRRAGSPLQLGMSLTMLLEFGAAESAFDYSYEEFCGWVREVGFSSTQLIDLVGTAKAAVAYK\*

>Cre08.g365800

MEPPQQQPQQQQLARAPSRSPPSSAQDGNAAADSVSRAGSSSSSCGACCGLQTALSSPVLKAVRTVPADKAAALENLIRGSWAPNAIYCLCRLGVPDALGAAPAAALSPAELASRLHCSAPCLRRLLRLCAAYGLLVECASRGEGGGGWGGGEGGGGSGEGGKGGEGGEGGKQTRGDVGGVGGGGLTDGSQAEAGDVRAGAGKGEREEGEGRGVEEEGEQVERTASGGSGTSSSCTGASSSGGSSSSAGTAAATAATRSSSGSSADCGSSTATAAATAAATAIAAGASPAAATAGAAATCLEARTFFYLTDIGTMLQSSHPSCMHWLALMLGLPGHYVSRGHLYDNVKQGRMGFETAFGCDWYTYVSHHSFERRAFDAAMTATSTAAAQAVAAGYDFSRHGTVMDVGGGQGLLMAAILHTHSGVRAGYVMEVPGVVAAARRLGQRGMERLRYVEGDFFQPFPRPADGSPLECVVMRLVLHDWPDAEAAQILRHARKALLAPPTHHAAAAASEEEAAAADEVEAEEEEEPASGAAPTTAATAAAPTAAAAATAAEALLLLRRLLVVEAVLPELVTPPAVAADPAAPAAAVAAADGGCSIIGDGGDGGAAATADLVQRLEFDMGMMLMTQGRERSLSEWRQLLRAGGFELQQVVMTGGDGSSNGSGRSSSSGGSSGSSTAGSSGGSGGGSGGSGSGSSSGGECGSSSAARMPRLPVLVARPLLGRELGEEGE\*

>Cz13g11100

METVAVPYALFVVGVAYIAITAVIFTAAFWFISPMFTINRRRSQYFDDWNVALHVPWVFWHIGAWWFRIQELLGNYVLPAPQRVMDLATQYMKSQVIIVIAELGIPDLLRKRPMNGSELAVALDLHQGYMERVLRVAERLQLLKITEIPNKSDPLGAPTRVYELTQLSAVLCEDHPNSVKYMVQLMGDHFQPAGCLGEGVRTGKTPYMLWAHGQTHWQHMTAEPELYERFNRAMTNMNNLSPIQAIFMEYSFKQFDRCIDVGGGLGSFVAGCMRMYPHMQGGVFDLPHVIEHSKKVWESQHKQLSNRITFYPGSFFEPNSIPMSQAGKQTVYMLREILHDWDDNDSIKILRSVRNAIGSNVSNCKLLIVEACIANSMKATHTPRMTGDVHMMMQYGDAKERDEREFKEVLDVSGFRLTRVIPTKGLFFILEAVPV\*

>Cz04g10170

MWFRLQETLGNYVIPAPQRVLEWATRYMTSQVVIVLAELGIPDLLKNAPMTGQELASGIKAHQEYLESLLRLAVRMGLVNVTETSPSSKLDSMLDSATAPQKTYHLTDISAALCEDHPNSVKYMVQMTGDNFGAGAYLAQGIKQGKAPYTLYSGGVTYWQHMTKVPELHARFNRRSTWWCGCVAGSDADNAAAAAADTTLLLLLLILLCHHLFLFLSSSFLFILLLLQLETDMNNMSPVEAVFQAYSFKGVACCVDVGGGLGSFLAACMTQYPRMLGCVFDLPHVIEHSKQVRDTTHADLLDRVTFQSGSFFASDNVPCAAAGSTTIDLLRELLHNWSSSECVKILQTLRRSMTSAPRSKLLILEPCIADSMQSMHTPRLVHDLTMLVQFGDAKERDEREFEQLLGAAGFRLERVIPTKGLFFIVEAVPGGSR\*

>Cz06g29090

MFAVTNLEVPERLVSGPKTSAQLACECGVNPEWMDRVCKAAAAMGLLGTEEATAIAGIDGQQDTKVVKPGTAEHPSIGTDSSVDAECTRDQMHKNHNITADIIAGTGQTLHSQKHPAASTAEQLRVQPSTTRLYKNTATSSVLCKGHPSSVKAFVKFFEHQFGAFGHLSQGLKQGVTPYELYSGGVTFWEHCCTDEALGTVFDEAMQAQKWLGSVAVVTDYHWGQYRAVIDIAGGIGGFLSELLQQYPQLQGVLLDLEQPVQRGKQWWSTQHPDKLNRIRFHAGDMFEPSSIPSPPSPSDNLQLDEGQTRQDTVYTLRNILHDWPDADCVKILRAIRSRITDQQVQSGAVRLAVVEMTSMEDVMPALLRFRTQFDMNMLMSFGHGKERDRAGFNALFEASGFKLLRVVPTRSVYLVLEAAPV\*

>CDP20220 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_1012:2402:3567:1 gene:GSCOC\_T00005623001 transcript:CDP20220 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDLARNIGDHTGELFQAQAHIWSHIFNFINSMSLKCAIQLGIPDVIHKHGQPMTLDQLIDALPIKNAKATFIYRLMQNLIHSGFFIEAKIPGNENDNQKGYLLTPASELLLKSNPFSVTPFLLAMLDPTLTDPWHHLSQWFQNSDETPFYTCHGRSLYDFASHEPRINQFFNKAMASDARLVSSVVTKDCKHVFEGLNSLVDVGGGTGTLAKAIADAFPSLKCTVLDLPHVVDGLESSKNLAYVGGNMFEAIPPANAVLMKWILIDWSDD

>CDP22155 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_11254:2:510:1 gene:GSCOC\_T00006900001 transcript:CDP22155 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

AIPPADDVTMKLILHDWNDEECVQMLRKCKEAIPSKENGRKVIIIDMVLNDQQKGADDHEAIESQLFFDMLLMVLVTGKQRNEREWAKLFSEAGFNDYKTTLVLGRIH

>CDP20595 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_1411:19161:19642:-1 gene:GSCOC\_T00013329001 transcript:CDP20595 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MKWILHDWNDEECVQMLRKCKEAIPSKENGRKVIIIDMVLNDQQKGADDHEAIESQLFFDMLMMVLVTGKQRNEREWAKLFSEAGFNDYKTTLVLGRIH

>CDP20594 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_1411:1343:2459:-1 gene:GSCOC\_T00013328001 transcript:CDP20594 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MEKAENLVELIEAQTHVWNAMFHFKKSACLGIPDVISNHGKPITLSDLISVIIIDSVMGSQIQDETSFETEFSLDMQMLVMLGPAKERTGKEWSKLFSDAGFSSYKVYPVLGMRCLIEVYP

>CDP20700 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_1587:23117:26022:1 gene:GSCOC\_T00008849001 transcript:CDP20700 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDSLAETTKNHGVALKEEEEEEEHFSYAMQLVTSAAQPMVLLAAIRLDVFEIIARAGPGAQLSPSEIAANVSSENPNAAAMLDRMLRLLASYSVLTCSVATDVDGDHDIQTPTRVYGLAPVAKFFVQNKTKGGGSLGSVLGLLQDKVFIDSWYQLEDAVRKGGDPFHRAHGTHAFEFLGSDPRFNEVFNKAMIHHTAIVINRMLERYKGFEHLKTLVDVGGGLGMNLNIITTKYPSLKGINFDLPHVIQHAPAYPGVEHVGGDMFESVPQGDAIFMKWILHDWDDGHCLKLLKNCYKALPDNGKVIAVDAILPVVPDDSARDKATCQADLVVVTQYRGGIERYETEFLALATAAGFKGISVKCFVCNLWVMEFYK

>CDP18606 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_257:223381:227546:1 gene:GSCOC\_T00000316001 transcript:CDP18606 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MECTGKITMQAILSVFKGTYWDGVETLVDVGGGTGATIAEIVKVYPHIKGINFDLPHVVATAPKYDGVSHVGGDMFDAIPSAQAVFMKWIMHDWCDEDCVKILKNCRRAIPEKTGKVFIVEVVLKPDGDGLFDSIGMILDLLMIAHSSGGKERTEPEWKKLLDKGGFPRYKITEIPACFSIIEAYPE

>CDP21212 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_2810:4514:7277:1 gene:GSCOC\_T00000226001 transcript:CDP21212 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDLARNIGDHTGELFQAQAHIWNHMFNFINSMSLKCAIQLGIPDVIHKHGQPMTLDQLIDALPIKNAKAPFVYLLMQILIHSGFFIEAKIPGNENDNQKGYLLTSAAELLLKSNPFSMTPLLLFTLDPTLTDPWHHLSQWFQNSDETPFYTCHGRSLYDLASHEPRLNQFFNEAMASDTRLVSSVVTKDCKHVFEGLNSLVDVGGNMFEAIPPADAVLMKWILIDWSDDECVQILKKCKEAIPSKEKRGKVIIVEMFCKSQQKGDDDHEAIETQLFFDMAVMVLVKGRQRNEKDWAKLFTEAGFSDYKITAVLGLRSIIEVYHN

>CDP21213 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_2810:13992:14553:1 gene:GSCOC\_T00000228001 transcript:CDP21213 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MACDSQLVGSILIRDCKDVFSGLNSLVDVGGGTGTLAKEIADAFLDLNCIVTDLPHVVDGLVANNKSLAFVGGDMFVAIPPADDVIMKWILHDWNDEECVQMLRKCKEAIPSKENGGKLNFSVIR

>CDP21231 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_2893:3934:4143:-1 gene:GSCOC\_T00001556001 transcript:CDP21231 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MFCKSLQKGDDDHEAIETQLLFHMLMMVLFKGRQRNEKDWAKLFTETGFSDYKITAVLGLRSIIEVYYN

>CDP21551 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_4795:1107:3100:1 gene:GSCOC\_T00011418001 transcript:CDP21551 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MSLKCAIQLGIPDIIHMHGQPMALAQLIDALPINNAKAPFVYRLMRILIHSGFFIKAKIPDNEGQEGYALTPASKLLLANDPFSLTHTMVIKNCKDVFMGLNSLIDVGGGTGTVAKAIADAFPHLECSVLDLPHVVDGWESSKNLAYVGGDMFEAIPPADAVLLKWILHDWSDEECVQILRKCKEAIPSKEKGGKVIIIDMLLKSQQNGDDDAEAIETQLFFDILMMVHAKGRERNEKDWEKLFLEAGFNGYKITPVLGLRSIIEVYYY

>CDP21582 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_5086:336:1778:-1 gene:GSCOC\_T00010868001 transcript:CDP21582 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MPTCYSQEGKQNRQLIKKMDLSRNGDANELLQAQAHIWNRIFNFINSMSLKCAIQLGIPDIIHKHCKPMTLDELTNALPIGNAKAPFVYRLMRILIHSGFFIEAKISQHDEEEGYMLTSSSKLLLKDEPLSLTAFLLSMLDPTLMDPWYHLSQWFQNYSDVNPFKTCHGKVAWELAGQDQKLNNFFNEGMASDSRLVGSILIRDCKDVFSGLNSLVDVGANNKNLAFVGGDMFVAIPPADAVIMKWILHDWNDEECIQILKKCKEVIPSKQNGGRAIIIDMVLNDQQKGADDDEAIETQLFFNMLMMVLVTGKQRNEKERAKLFSEVGFNDYKITSVLGLRSLIKVYY

>CDP21583 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_5086:2236:3679:-1 gene:GSCOC\_T00010869001 transcript:CDP21583 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDLARNLGDHGGEFFQAQAHIWNHIFNFINSMSLKCAIQLGIPDIIHKHGQPMTLDQLIDALPIKNAKAPFIYRLMRILIHSGFFNSDESPFYTCHGRPLWELAGHEPRLNQFFNEAMASDARLVSSLVIKDYKHVFEGLNSLVDVGGGTGTFAEAIADAFPRLKCTVLDLPHVVNGLESKNLAYVGGDMFEAIPPADTVLLKWILHDWSDEECVQILRKCKEAIPSKEKGGKVIIIDILLKSQQKGDDDHEAIETQLLFDMLMMVLLKGRERNEKDWAKLFFGAGFNDYKITAALGLRSIIEVYYY

>CDP21661 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_5489:1323:2770:-1 gene:GSCOC\_T00006934001 transcript:CDP21661 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDLARNIGDHTDELFQAQAHIWNHIFNFINSMSLKCAIQLDIPDVIHKHGRPMTLDQLIDALPIKNEKAPFVYRLMQILIHSGFFIEAKIPGNENDNQKGYLLTSASELLLKSNPFSVTPFLLAMLDPALTDPWHHLSQWFQNSYESPFYTCHGRSLYDFASHESQLNQFFNEAMASDARMVSSVVTKDCKHVFESLNSLVDVGGGTGTFAKAIADAFPRLKCTVLDLPHVVDGLESTKNLGYVGGNMFEAIPPADAVLMKWILIDWSDDECVQILKKCKEAIPSKEKGGKVIIVDTFCKSLQKGDDDHEAIETQLFYDMGAMVLVKGRQRNEKDWAKLFSEAGFCDYKITAVLGLRSIIEVYY

>CDP19711 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_627:37926:39322:-1 gene:GSCOC\_T00003634001 transcript:CDP19711 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MEKVENLGELIEAQTHVWNAMFHFKKSACLKCAVELGIPDVIRNHGKPITLSDLISVLPIHPSKSAHIFRLMRFLANSGFFVENPQGYALTSAGRLLLKDEPFNVRAHIFLSCDPAMLKPWNFLTKWFQNDDPSPFDTAYGNNFWHYNAQEVRFGKMFNEAMASDNQLSVEVLMTKCKFVFEGLTTLADVGGGTGKVDRAIAQNFPNIKCTVYDLPHVVANQEGAENLEFLAGDMFQSVPRANAILLKRILHDWSDEDCLKILKNCKKAIPEKDNGGKVIIIDGVMGSQIQDKTSFETEFSMDMQMLVMLGPAKERTEKEWSKLFSDAGFSSYKVYPVLGMRCLIEVYP

>CDP19709 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_627:22812:24128:1 gene:GSCOC\_T00003631001 transcript:CDP19709 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MERVENLTELLAAQNHVGNQMPNFRKSASLKCAIELGIPDAINQHGKPITLSELVSALPINPSKANHIYRLMRFLSNAGFFVLQDQGYALTAAGRLLLKEEPFNLRAFIFYTSDPVLVKPWNSLTEWFRNDDPSPFHTAHGKNFWAYAAEEPNFANLFNEAMANDSTLTVQVMMTQCKFVFDGLTSLVDVGGGTGAVARAIAQNFPNLECVVCDLPHVIAGQEGTENLDFVAGDMLEKVPAADAILLKWILHDWSDDDCVKILKNCKEAIPGRDKGGKVIIIDMILESHMKDDESVETQFVVDMQMLTCYGAKERTEKEWAKVFQDAGFSDYKVLPVLGVRCLIEVYP

>CDP19708 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_627:20269:21897:-1 gene:GSCOC\_T00003630001 transcript:CDP19708 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MFNEAMASDNQLSVEVLMTKCMSVFEGLTTLADVGGGTGKVARAIAQNFPNIKCTVYDLPHVVANQEGAENLEFLAGDMFQSVPRANAILLKVTKAILKSSITIFPANAWILHDWNDEECVQILRKCKEAIPSKENGGKVIIIDMVLSDQQKGADDHEAIETQLFSDMLMMVLLRGKQRNEREWAKLFSEAGFNDYKITPVLGLRSLVEVYY

>CDP19714 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_627:60045:62926:-1 gene:GSCOC\_T00003638001 transcript:CDP19714 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MEKVENLGELIEAQTHLWNAMFHFKKSACLKCAVELGIPDVIRNHGKPITLSDLISGIAQNFPNIKCTVYDLPHVVANQGAENLEFLAGDMFQSVPRANAVLLKRILHDWSDEDRDHYRQCNGEDYAFGSCAFRFHPETGNAFQHRPASCLWTANSLFQIKRQLPRKIIVHLSKTKMSKLADQN

>CDP19712 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_627:49877:50652:-1 gene:GSCOC\_T00003636001 transcript:CDP19712 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MEKADNLGDLLEAQAHVWNAMFHFKKSACVKCAVELGIPDLISNHGKPITLSDLISVLPIHPSKSAHIFRLMRFLANSGFFVENPQGYALTSAGRLLLKDEPFNVRAHIFLSCDPALLKPWNFLTDSIWKMFNENMASDNHLFVEVLMTKCKSVFEGLTTLADVGGGTGKVARAIAQNFPNIKCTVYDLPHVVANQGGAENLEFVAGDMFQSVPRANAILLKVTKAILSLNF

>CDP19713 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_627:53255:55089:1 gene:GSCOC\_T00003637001 transcript:CDP19713 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MERAENLTELLAAQNHVRNQMLNFRKSASLKCAIELGIPEAINQHGKPITLSELVSALPVNPSKASHIYRLMRFLSKAGFFVLQDQCYALTAAGRLLLKDDPFNLRALIFFMSDPVLVKPWNSLTEWFRNDDPAPFDTAHGKNFWAYAAEEPNFANRFNEAMANDSTFIVQVMMTRCKFVFDGLTSLVDVGGGTGTVARAIAQNFPNLECVVCDLPHVIACQEGTENLDFVAGDMLEKVPTADAILLKKPDSIHDWSDEDCVKILKNCKEAIPGRNKGGRVIIIDMILESQIKDDESVETQVGMDMQMLMCHAAKERTEKEWAKLFRDAGFSYYKILPVFGVRCLIEVYH

>CDP19754 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_661:39199:42033:1 gene:GSCOC\_T00012515001 transcript:CDP19754 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MLQLLASYSVLTCSVAEADASISSQRRVYGLAPVAKYFVQNKTYAAGGGGVSLGPLLALLQDKVFIDSWYQLEDAVREGGVPFDRVHGVHAFEYPARDPRFNEVFNKAMINPTTIAINRIVQRYKGFEHLKTLVDVGGGLGVTLGVITAKYPSLKGINFDLPHVIQHALVYPGVEHVGGDMFESVPQGDAIFLRSILHDWDDGRCLKLLKNCFKALPKDGKVIVVDAIVPVVPDTSACIKAICQSDLFMMAQNPGGKERSEAEFLDLATAAGFRGIRVECFVCNAWVMEFYK

>CDP19753 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_661:28856:31077:1 gene:GSCOC\_T00012514001 transcript:CDP19753 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDSLSKATNNVVVEAGLDEQEEQHFSYAMQLVTSVSLPMVLLAVIRLDVLEVIAEAGPGAQLSPWDIAAQVCPKNPDAAAMLDRMLRLLASFSVLTCSVAEADARISSQRRVYGLTPVAKYFVQNKTYGAGGGVSLGPLLALVQDKVFIDSWYQLEDAVREGGVPFDRVHGMHAFEYPARDPRFNEVFNKAMVNRTTIAINRMVERYKGFEHLKTLVDVGGGLGVTLSVITAKYPSLKGINFDLPHVIQHAPVYPGVEHVGGDMFDSVPQGDAIFLRLILHDWDDGRCLKLLMNCFKALPKDGKVIVVDAIVPVVPGTSACIKAICQSDLIMMAQNPGGKERSEAEFLDLATAAGFRGIRVEFFVCNAWVMEFYK

>CDP19755 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_661:43935:46614:1 gene:GSCOC\_T00012516001 transcript:CDP19755 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDSSSRATDNVVVEAGLDEQEEQHFSYAMQLVTSVSLPMVLLAAIRLDVLEVIAQAGPGAQLSPWDIAAQVGPKNPDAAAMLDRMLQLLASYSVLTCSVAEADASISSQRRVYGLAPVAKYFVQNKTYAAGGGGVSLGPLLALFQDKVFIDSWYQLEDAVREGGVPFDRAYGVRAFEYPGRDPRFNEVFNKAMINHATIAINRIVERYKGFEHLKTLVDVGGGLGVTLSVITTKYPSLKGINFDLPHVIQHAPVYPGVEHVGGDMFESVPQGDAIFMKWILHFWDDGRCLKLLKNCFKALPDHGKVIVVDPILPVVPDTSAGIKATCQSDLITMTQNPGGKERSEAEFLDLATAAGFRGIMVVCFVCNVWVMEFYK

>CDP21787 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_6650:661:2111:1 gene:GSCOC\_T00004245001 transcript:CDP21787 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDLARNLGDHTGELFQAQAHIWNHIFNFINSMSVKCATQLGIPDVIHKHGQPMTLDQLIDALPIKNAKAPFVYRLMQILIHSGFFIEAKIPGNENDNQKGYLLTSASELLLKSNPFSMTPFLLAMLDPTLTDPWQNLSQWFQNSDETPFYTCHGRSIYAFASHEPWLNQFFNEAMASDTRLVSSVVTKDCKHVFESLNSLVDVGGGTGTFAKAIADAFPRLKCTVLDLPHVVDGLESSKNLAYVGGNMFEAIPPADAVLMKWILIDWSDDECVQILKKCKEAFPSKEKGGKVIIVDMFCKSLQKGDDDHETIETQLFFDMEVMVLLKGRQRNEKDWAKLFTEAGFSDYKITAVLGLRSIIEVYYY

>CDP21836 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_7029:61:1617:-1 gene:GSCOC\_T00010736001 transcript:CDP21836 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDLARNIGDHTGELFQAQAHIWNHIFNFINSMSVKCAIQLGIPDVIHKHGQPITLDQLIDALPIKNAKAPFVYRLMQILIHSGFFIEAKIPGNENDNQKGYLLTSASELLLKSNPFSMTPFLLAMLDPTLTDPWHHLSQWFQNSDETPFYTCHGRSIYAFASHEPWLNQFFNEAMASDTRLVSSVVTKDCKHVFESLNSLVDVGGGTGTFAKAIADAFPRLKCTVLDLPHVVDGLESSKNLGYVGGNMFEAIPPADAVLMKWILIDWSDDECVQILKKCKEAIPSKEKGGKVIIVDMFCKSLQKGDDDHEAIETQLFFDMVVMVLLKRRQRNEKDWAKLFTEAGFSDYKITAVLGLRSIIEVYYY

>CDP19840 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_721:54453:56457:1 gene:GSCOC\_T00005422001 transcript:CDP19840 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDLARNIGDHTGELFQAQAHIWNHIFNFINSMSVKCAIQLGIPDVIHKHGQPMTLDQLIDALPIKNAKAPFVYRLMQILIHSGFFIEAKIPGNENDNQKGYLLTSASELLLKSNPFSVTPFLLAMLDPALTDPWHHLSQWFQNSDETPFYTCHGRSIYAFASHEPWLNQFFNEAMASDARMVSSVVTKDCKHVFEGLNSLVDIGGGTGTFAKAIADAFPRLKCTVLDLPHVVDGLESSKNLAYVGGNMFEAIPPADAVLMKWILIDWSDDECVQILKKCKEAIPSKEKGGKVIIVDTFCKSQQKGDDDHEAIETQLFYDMGAMVLVKGRQRNETDWAKLFSEAGFSDYKITAVLGLRSIIEVY

>CDP19839 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_721:16718:18545:1 gene:GSCOC\_T00005419001 transcript:CDP19839 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MSVKCAIQLGIPDVIHKHGQPMTLDQLIDALPIKNAKAPFVYRLMQILIHSGFFIEAKIPGNENDNQKGYLLTSASELLLKSNPFSMTPFLLAILDPTLTDPWHHLSQWFQNSDETPFYTCHGRSIYAFASHEPWLNQFFNEAMASDTRLVSRVVTKDCKHVFEGLNSLVDVGGGTGTFAKAIADAFPRLKCTVLDLPHVVDGLESSKNLAYVGGNMFEAIPPADAVLMKWILIDWSDDECVQILKKCKEAIPSKEKGGKVIIVEMFCKSQQKGDDDHEAIETQLCYDMEVMALGKGRQINEKDWAKLFSEAGFCDYKITAVLGLRSIIEVYYY

>CDP21928 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_7886:1776:2943:1 gene:GSCOC\_T00007655001 transcript:CDP21928 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDLGRNGHANELLQAQAHIWNHIFNFINSMSLKCAIQLGIPDIIHKQGKPMTLDELQCSSNWQCKSPTLSLNNFFNEGMASDSRLVGSILIRDWKDVFSRLNSLVDVGGGTGTLAKEIADAFLDLHCIVPDLPHVVDGLVANNKSLAFVGGNMFVAIPPADDVIMKWILHDWYDEECVQILRKCKEAIPSNGNGGKLNFSLIR

>CDP22007 pep supercontig:AUK\_PRJEB4211\_v1:scaffold\_8978:1360:2229:-1 gene:GSCOC\_T00004618001 transcript:CDP22007 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDTNDEGSKLHHGQAKIWKHLFGFVDSMALKSALELQIADIIHFHGRPLSLSEISSNITNSSSPNIPYLARIMRLLVRNKIFTSSEVRPGHGGDTPSTILYDLTPASNWLLNNNDPLSLAPFILMENHPWLLSPWHQLSACVREGGIAFQKSHGKEIWDFASQNPEFNKIFNDGMECTGMITVQAVLSGLKSANWDGVESLVDVGGGIGATIAEIVKAYPHIKGINFDLPHVVATAPKYDGVSHVGGDMFDAIPSAQAIFMKVLIFAKITAKSCCFLISPLYFLLWGDT

>CDP15753 pep chromosome:AUK\_PRJEB4211\_v1:1:15543419:15548682:1 gene:GSCOC\_T00015810001 transcript:CDP15753 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MESSVKTQLKSSSSSGENGKEGEKQNHFSYAMQLVSSASLTMVLYNAVKLNLFEIIAKAGPGAKLSPSEIASQLPVTNNPDAASMLDRMLRLLSSYSLFTCDVVEVAVDGGGGGETNVGYERVYGLSPVAEYFVPDEEGNSVAPLVELLQDKVLIDSWYELGNAVLEGGIPFNRVHGVHAFDFPSRDPKYNELFNKGMVGPTAIMMKELLQQYKGFEHLQTLVDVGGGLGITLHKIISKYPSIRGINFDLPHVIENAPSYPGVEHIDGDMFESVPGGDAIFMKMILHDWSDDHCLKLLKNCFKALPGHGKVIVVDLILPVKPDTSAFVKGIFQADALMMTQNPGGKERSESDVRALAIRAGFKDVKLQCLVGNVGVLELYK

>CDP15755 pep chromosome:AUK\_PRJEB4211\_v1:1:15650414:15653379:1 gene:GSCOC\_T00015815001 transcript:CDP15755 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MTKTLLDFHPMYELGNSLLEGGIPFNRVHGMHAFDYPSRDPRYNELFNKGMVGPTAITMKKLLQQYKGFEHLQTLVDVGGGLGITLHKIISKYPSIRGINFDLPHVIENAPSYLGVEHIGGDMFESVPGGDAIFMKMILHDWSDDHCLKLLKNCFKALPDHGKVIVVDLVLPVKPDTSAFVKGIFQTDALMMTQNPGGKERSESDVRALAIRAGFKDIKLECCVGSLGVLELYK

>CDO96828 pep chromosome:AUK\_PRJEB4211\_v1:2:13590430:13591236:1 gene:GSCOC\_T00013976001 transcript:CDO96828 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MEKVENLVELREAQDYAGTQIFNFRKCASLKCAIELGIPDVIAQHGKPIMLSGLISTLPINPSKSIHIHRLMRFLSNAGFFVQQNEGYSLSTAGRLLLKNEPFNMRAFIYYVSDPIALKPWNFLTEWFKNDDPSPFDTAHGKNFWSYAAAEPQFGKIFNEAMAGDSSLIVEVVVTQCKSVFEDLTSLVDVGGGTGEFAKAIVQNFPNLECLVCDLPHVVSNQQRTENLDFVAGNMLEMVPPGNAILLKVIRDIHPPCFNHLNFLRNKV

>CDP04982 pep chromosome:AUK\_PRJEB4211\_v1:2:569234:572303:1 gene:GSCOC\_T00019870001 transcript:CDP04982 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:Flavone 3'-O-methyltransferase 1 [Source:Projected from Arabidopsis thaliana (AT5G54160) UniProtKB/Swiss-Prot;Acc:Q9FK25]

MAEEEACLFAMSLASASVLPMVLKSAIELDLLELIAKAGPGAYVSPSELAAQLPTHNPEAPIMLDRILRLLATYSVLDCKLNNLADGGVERLYGLAPVCKFLTKNADGVSMAPLLLMNQDKVLMESWYHLKDAVLDGGIPFNKAYGMTAFEYHGTDPRFNKVFNQGMSNHSTITMKKILEVYRGFEGLKTVVDVGGGTGATLNMIISKYPTIKGINFELPHVVEDAPSHSGVEHVGGDMFVSVPKGDAIFMKWICHDWSDDHCRKLLKNCYQALPDNGKVILAECVLPEAPDTSLATQNVVHVDVVMLAHNPGGKERTEKEFEALAKGAGFKEFRKVCSAVNTWIMELCK

>CDO96819 pep chromosome:AUK\_PRJEB4211\_v1:2:13393220:13394026:-1 gene:GSCOC\_T00013964001 transcript:CDO96819 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MEKVENLVELREAQDYAGSQIFNFRKCASLKCAIELGIPDVIAQHGKPITLSGLISALPINPSKSIHIHRLMRFLSNAGFFVRQNEGYSLSTTGRLLLKNEPFNMRAFLYYVSDPIALKPWNFLTEWFKNDDPSPFDTAHGKNFWSYAAAEPQFGKIFNEAMAGDSSLIVEVVMTQCKSVFEDLTSLVDVGGGTGEFVKAIAQNFPNLECLVCDLPHVVSNQQRTENLDFVAGNMLEMVPPDNAILLKVIRDIHPPCFNHLNFLRNKV

>CDP18090 pep chromosome:AUK\_PRJEB4211\_v1:4:14231758:14239353:1 gene:GSCOC\_T00008263001 transcript:CDP18090 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MEKIKSILNFDHCYVVDDMNRYGGMALLWNEKTKVKDIKYSAFTIEVLIEDAEVKQEWWLVGIYASCDNQVRKNQWEVISRRKSLWGDNQIIMGDFNDVCSNEEKWGGRMREEWSFHDFRRFIQENQLIDVGFEGNPWTWSNQWQTGEIKQRLDRGLSSGGWHNLFEHTRCTHIESLGSDHSMLILDTMPGARTKRKKFFFDKRWIQREGIKEVVKKTWEEDVRGSRMFRVVNKIKRCRVALLKWRNGFIENSKKKRISDLKQRLMVEKRSGNEEMERKATILLLESSPVMLSPWLGLGRRVLANSPPPFDTYHGHDIWRYAQNNPAHSKLINDAMACDARVAVSAMIYRCPQVFEGISSLVDVGRGDGTALRTLLKACPWIHGINFDLPHVVSIAPRSDGVEHVGGDMFHSFPNADTAFIMSVLHDWGDDNCISILMNCKEAIPQDTGKVIIVEAVIDHEEGDDKLKDVGLTLDMVMMAHTTTGKERTSEEWAHILNQVGFSRHTMTHIQAVQSVIEAYL

>CDP18321 pep chromosome:AUK\_PRJEB4211\_v1:4:21609248:21611196:1 gene:GSCOC\_T00004357001 transcript:CDP18321 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MAGDSSLIDLTCLVMTQCMSVFEDLTSLVDVEGGTSEFTKAIAQNFPNLECLVCDLPHVVANQHRTENLDFVAGNMLEMVPPGDAILLKLIWQELALTKMAISILHDWSDDGCVKILKNCNNAIPERSKGGKVNMDMAMLVLHGAKETTEKEWAKLFQDAGFSNYKVFPVLGLRCLVEVYPD

>CDP15884 pep chromosome:AUK\_PRJEB4211\_v1:5:22549886:22551244:-1 gene:GSCOC\_T00016789001 transcript:CDP15884 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MERVENLTELLAAQHHVGNQMLNLRKSASLKCAIELGIPDAINQHGEPITLSELVSALPINPSKANHIYRLMRFLSNAGFFVLQDQGYALTAAGPMANDSTLIVQVMMTQCKFVFDGLTSLADVGGGTGAVARAIAQNFPNLKCVVCDLPHVIAGQEGTENLDFVAGDMLEKVPAADAILLKWILHDWSDEDCVKILKNCKEAIPGREKGGKVIIIDMILESQMKDDESVETQVGVNMQMLMGYGAKERSEKEWAKLFQDAGFSDYKALPLLGVCCLIEVYP

>CDP11862 pep chromosome:AUK\_PRJEB4211\_v1:5:20200513:20201617:-1 gene:GSCOC\_T00035133001 transcript:CDP11862 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MMMLLHLKLHFWGYAAGEPEFGKIFNEAMASDSNLTMEVLMTQSRLVFEGLESLVDVGGGTGKDGRAIVQNFPNIETYQIEDNEAIETQMSFDMQMLVLYGAKERTEKEWATLFSDADFSSYKIFPVLGIWCLIEVYP

>CDP16374 pep chromosome:AUK\_PRJEB4211\_v1:5:3036652:3039777:1 gene:GSCOC\_T00018212001 transcript:CDP16374 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDSLAETTKNHGVVLKEEDEEEEHFSYAMQLVTSAAQPMVLLAAIRLDVFEIIARAGPGAQLSPSEIAANVSSENPNAAAMLDRMLRLLASYSVLTCSVATDVDGDHDIQTPTRVYGLAPVAKFFVQNKTKGGGSLGSVLGLLQDKVFIDSWYELEDAVRKGGDPFHRAHGTHAFEFLGSDPRFNEVFNKAMVHHTAIVINRMLERYKGFEHLKTLVDVGGGLGMNLNIITTKYPSLKGNNFDLPHVIQHAPAYPGVEHVGGDMFESVPQGDAIFMKWILHDWDDGHCLKLLKNCYKALPDNGKVIAVDAILPVVPDDSARDKATCLADLVVVTQYRGGIERYETELLALATAAGYMIELGVIGYC

>CDP15888 pep chromosome:AUK\_PRJEB4211\_v1:5:22639859:22641778:-1 gene:GSCOC\_T00016793001 transcript:CDP15888 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDLARNGDHTGELFQAQAHIWNHIFNFINSMSLKCAIQLGIPDIIHKHGQPMALAQLIDALPINNAKAPFVYRLMRILIHSGFFIKAKIPDNEGQEGYALTSASKLLLANDPFSVTPFLLAMLDPILTDPWHHFSQWFQNSEETPFHTCHGTSLWELAGRQPQLNQFFNEGMASDARLVSTMVIENCKDVFMGLNSLIDVGGGTGTVAKAIADAFPHLQCSVLDLPHVVDGWESSKNLAYVGGDMFEAIPPADAVLLKWILHDWSDEECVQILRKCKEAIPSMEKGGKVIIIDMLLKSQQNGDDDAEAIETQLFFDMLMMVHVKGRERNEKDWEKLFLEAGFNGYKITPVLGLRSIIEVYYY

>CDP15886 pep chromosome:AUK\_PRJEB4211\_v1:5:22558654:22560311:1 gene:GSCOC\_T00016791001 transcript:CDP15886 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MERVENLTELLAAQNHVGNQMLNFRKSASLKCAIELGIPDAINQHGKPITLSELVSALPINPSKANHIYRLMRFLSNAGFFVLQDQGYALTAAGRLLLKEEPFNLRAFIFYMSDPVLVKPWNSLTEWFRNDDPSPFHTAHGKNFWAYAAEEPNFANLFNEAMANDSTLIVQVMMTQCKFVFDGLTSLADVGGGTGAVARAIAQNFPNLKCVVCDLPHVIAGQEGTENLDFVAGDMLEKVPAADAILLKWILHDWSDEDCVKILKNCKEAIPGRDKGGKVIIIDMILESQVKDDDSVETQVGVDMQMLMCYGAKERTEKEWAKLFQDAGFSDYKILPALGVCCLIAVYP

>CDP17644 pep chromosome:AUK\_PRJEB4211\_v1:6:31162623:31164330:1 gene:GSCOC\_T00001552001 transcript:CDP17644 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MDFARNGDHTGELFQAQAHIWNHLFNFINSMSLKCAIQLGIPDIIHKHGQPMALAQLIDALPINNAKAHFVYRLMRILIHSGFFIKAKMPDNEGHEGVTPFLLAMLDPILTDPWHHFSQWFQDNEETPFHSCHGTSMWELAGRQPRLNQFFNEGMASDARLVCTMVIKNCKDVFMGLNSLIDVGGGTGTVAKAIADAFPHLKCSVLDLPHVVDGSESSKNLAYVGGDMFEAIPPSDAVLLKWILHDWSDEECVQILRKCKEAIPSKEKGGKVIIIDMLLKSRQNGDDDDNAEAIETQLFFDMLMMVLVKGRERNEKDWAKLFFEAGFNGYKITPVLGLRSIIEVYYY

>CDP07899 pep chromosome:AUK\_PRJEB4211\_v1:8:20388651:20391118:1 gene:GSCOC\_T00025391001 transcript:CDP07899 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MECTGMITVQAVLSGLKSANWDGVESLVDVGGGIGATIAEIVKAYPHIKGINFDLPHVVATAPKYDGVSHVGGDMFDAIPSAQAIFMKWIMHDWDDDDCVKILKNCRRAIPEQTGKIFIVDVVLKPDGDGLFDSVRMKLDLVMIAHASGGKERTEPEWKILLQKGGFPRYNISAIPACLSVIEAYPE

>CDP18417 pep chromosome:AUK\_PRJEB4211\_v1:8:22333969:22337256:1 gene:GSCOC\_T00007228001 transcript:CDP18417 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MVLNAAVKLDVLEIIAKAGPGGKLSPSEIVSQMPTKNPDAPDFLDRMLRLLAGYSVLTCSVVDGGAGAHHERRYGLAPVAKYFIKHQYGATLRQLSVYLQNKLLMDSWYQLEGSVLEGGNAFKRTHGCELYTYMAKDPTYNEAFNKAMSCHTKVVLEKALECYKGFENLKTLVDVGGALGQAIHMITSKYPDIKGINFDLPHVIELAPPYPGIEHKGGDMFESVPEADAIFMKWILHNWDDEHCVKLLRNCYKALPNDGKVIVVDAIVPVNPENSDAAAKSNMQIDLFMMAVCSPGAKGRSELEFRALATEAGFRGIRVDCRLFDLWVLEFYK

>CDP00481 pep chromosome:AUK\_PRJEB4211\_v1:11:28813798:28817537:1 gene:GSCOC\_T00032433001 transcript:CDP00481 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MSSTNPSSPLPLLFTSMLLESLKLHKSTISSTMPADSSSSSSEKGHPMNSAIHLMWKSGSSLSSSYVKNKTFPGFPANTAAHCSKMVQPDSLLPCRTCRKPLPVKGFPFQAFSFCLRSVKGIFKHPWTSCRCRSACTLSPPRILAMTVRHVSRYDPRRRRGIRIRYLFIKFIIVLLHRHQFVGILRYALTPAGRLLLKDEPFNVRAYVFMAADPVVLKPWFFLTEWYQNDDLSPLYTAHGNNFWHYAAREVPFGQMFNNEVMANDSEFCIEVLMTKCKFVFEGLATLADVGGGTGKFARAIAKNFPSIKCTVYDLPHAVANEGGDKNVDFVAGDMFESVPYANAILLKLILHDWSDEDCTKILKNCRKAIAEKHDGGKVIIIDIVMGSRIQDKASLQTQINTDMQMLVALGPAKERTEKEWAKLFMEAGFTSYKVYPILGTVRSLIEVYP

>maker-chr01-exonerate\_est2genome-gene-33.22-mRNA-1:cds pep supercontig:Melonv4:contig2:3385694:3386853:1 gene:MELO3C018856.2 transcript:MELO3C018856.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MLESAFVEPSHFLSAWFRTDDQTPFETAHGMSFWEFVGNKQKDGDIFNAGMASDARLVMSVLIGKHKSVFEGVESLVDVGGGTGTMTKAIAKAFQQIECTVLDLPQVVAELKSDIPNFKYVEGDMFDAIPPADALLLKWILHDWSDEECVKILKKCKEAITSNGNKGKVMVIDLVLFNKKNDQDSIETQLFHDMLMMVVTGGKEREEKEWAKLIKEAGFSAYKIFPILGLRSLIEIYP

>maker-chr04-exonerate\_est2genome-gene-249.17-mRNA-1:cds pep supercontig:Melonv4:contig5:24916622:24918606:-1 gene:MELO3C026750.2 transcript:MELO3C026750.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MEENIELVEAQAHIWNHTFKYINSMSLKCVVELGIPDIIHNHGQPMSLSQLLESLHIHPSKAQCLSRLMRLLVHSGFFAQPQPDFFSLTPPSRLLLRENHKTAFDTTPFLLLILSPLMMSPWQTMSKWLCSQDDDQDQDHYSTAFELANGKPIWDYVKEEEESCGFGKLFHQTLECDSRLIGKVVSSECGEMFEGLRSLVDVGGGAGAMAKAIVEAFPHINCFVLDLPQVVANQKPKQHIQNLHFIEGDMFQKIPPANAVLLKSILHDWNDEESIKILKKCKESIPSRGEGGKVIIIEMVLEKELEQMKKSSVETQLC

>maker-chr01-exonerate\_est2genome-gene-34.55-mRNA-1:cds pep supercontig:Melonv4:contig2:3425986:3428094:-1 gene:MELO3C018859.2 transcript:MELO3C018859.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MYEWKKSRSQVLDTSPKCLDNYFSLVVLNMNMEAGGKKLAMGGDELLEAQSHIWNHIFNFINSMSLKCAIQLGIPDAIHSHGPNPMPLSLLVSSLQLHPNKTQFIYRLMRLLTHSGFFVQQEEGYILTNSSRLLLKDNHFAVSPFLLSMLQPALTDPWQFLSIWLQTDDRTPFETAHGMPFWEYMGNKAKDGEVFNEGMASDARLVMSVILEKHKSVFEGVESLVDVGGGTGTMAKAISQAFPQMECTVFDLPQVVAHLKEDQPNFKYVEGDMFKLIPPADVLLLKWILHDWSDEECVEILKNCKAAITSNGDRGKVMVIDIVLFGNKKDSMETQLLFDMLMMTLAGGKEREEEKWAELIKEAGFRSYKIFPIMGVRSLIEIYP

>maker-chr01-exonerate\_est2genome-gene-153.9-mRNA-1:cds pep supercontig:Melonv4:contig2:15329520:15330614:1 gene:MELO3C027370.2 transcript:MELO3C027370.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MKGINFDLPNVVSTSEKYDGVEHVGGNMLDFVPKADAAFFMWILHAWDDEDCIKILRNCKEAIGENKAGGKVIIIDSVIDENEENKMVTDIRLTLDIMMMTRSRKGRERSADEWTQLLINKAGFSRCTITPIPAAVPSIIQAFIS

>maker-chr04-exonerate\_est2genome-gene-249.25-mRNA-1:cds pep supercontig:Melonv4:contig5:24930131:24930448:-1 gene:MELO3C000525.2 transcript:MELO3C000525.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MNNSSGEGRGKVIIIEAVLEKENQMEDKESIETQLCGDVLMMATFNTAKRNEKEWKTLFLAAGFSHYSITSFLGLRSLIELYP

>maker-chr01-exonerate\_est2genome-gene-34.5-mRNA-1:cds pep supercontig:Melonv4:contig2:3400267:3400546:1 gene:MELO3C028075.2 transcript:MELO3C028075.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MGSNKSSEGAAVFDASLASDAKFVVSVLMEKCKGVFDGVGSLVDVGGGTGNVTKCIAQAFPQMECTVFDLPQVVADLKAEGNLKFVGGDMFQS

>maker-chr01-exonerate\_est2genome-gene-152.35-mRNA-1:cds pep supercontig:Melonv4:contig2:15280987:15283334:1 gene:MELO3C013313.2 transcript:MELO3C013313.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MNFAPQVSISKKEEEEARVQIWKYIFGFVEMAIVKCAIELRIGDTIESHGSPMTLSQLSTALNCSSSLLYRILRFLVRRGIFKQEITEENVISYDHTPLSRLLASSNNNSMAPLLLLESSPVMLAPWHRLSARIKGNGETPFEAAHGKDVWSFAAADPIHNIVINDAMSCTARVHTVPAILEDCPQIFEGIGSLVDVGGGNGTCLSMIVKAFPWIKGINFDLPHVISSSQQYIGVEHVGGNMLDSIPKADAAFIMWVLHDWDDETCIKILKNCKEAISEKRGKVIIVEAIIEERSEEENNNNNLGDVGLMLDMVMMAHTENGKERTIKEWGNVLRQAGFTRYTITPIRAVHSVIQGFL

>maker-chr11-exonerate\_est2genome-gene-114.8-mRNA-1:cds pep supercontig:Melonv4:contig12:11484721:11487090:1 gene:MELO3C019324.2 transcript:MELO3C019324.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MGENLNELLQSQAHVWNHALKFINSMSLKCVLELEIPDIIHNHGQPMSLSSLVAALHIEPTKAECLSRLMNLLVHSGFFTTAQTQAHDRAEDVKYSLTPSSKLLLHNKQATPFLFLALDKSTIASFQSLSSWFCSSNNNGQNYSNAFEMANGKLLWEYAAQEQTFANLFQQTMVCDSEMIGKIVKECSEVFEGLKSLVDVGGGTGVMGKAIVEAFPHITCTVFDLPQVISNQPLQNAKNLRFVEGDMFEEIIPLANAVLLKWLLTNFQKLMRDQSHQSRKKWILHDWNDEQSIKILKKCKDAIPSREKGGKLIIIDIVMEDKKEEKESTETQLLFDVLMMVNLGGKERNENEWKNLFMEAGFSGYKIISKLGLRSVIEVYPA

>maker-chr04-exonerate\_est2genome-gene-312.0-mRNA-1:cds pep supercontig:Melonv4:contig5:31193767:31196529:1 gene:MELO3C009403.2 transcript:MELO3C009403.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MVVGKETAPMEQHNASTTADSEIQNKARLAILELANMISVPMSLNAIVRLNVADAIWQNGSNSPLSASEILARVVPSGGGDAHNLERILRMLTSYGVFEEHLSPNSSNHRYSLTDVGKTLVTDTDGLSYAPYVLQHHQDALMRAWPRVHEAAIDSTTEPFVRANGEPAYSYYGKKTEMNELMQRAMAGVSVPFMKAVLDGYDGFKGVEKLVDVGGSAGDCLRMILQKYPSIKEGINFDLPEVVARAPPIPGVSHVGGDMFKSIPTADAMFMKWVLSTWTDDECKIILENCCKSLPVGGKLIACEPTLPEKTDESHRTRALLASDVFIMTIYKAKSKQRTEEQFRQLGLSAGFSALRPFHIDYFYCLLEFTK

>maker-chr01-exonerate\_est2genome-gene-152.41-mRNA-1:cds pep supercontig:Melonv4:contig2:15231414:15233627:-1 gene:MELO3C013310.2 transcript:MELO3C013310.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MEVKHKESSSEKEEDGQAIIQMWRYIFRFTEMAAIKCAIDLKIADIIESYGSPVTLSQLSSTLNCSSSLLYRILRFLIHRGIFKRETIDENQIGYSQTPMSRLLAINVENSMAPLLLLETSPVMLAPWQHLSAHLKNSDTSPFEIAHGKDLWNYAEANHEHNLLFNEAMACSAKVIVSAIIEGCGDVFDGVGCLVDVGGGNGSTLNILVKVCPWMKGINFDLPHVVCASPQYENVEHVAGNMFDFVPHADVAFLKWILHDWEDEECIKILKKCKEAIPKSGGKVIIIEAIIIEAEKGEKMKKKLSDVGLMFDLVMMAHTNKGRERTAEEWAFLIHQAGFTRHTITPLQAIQSLIQCFP

>maker-chr11-exonerate\_est2genome-gene-114.7-mRNA-1:cds pep supercontig:Melonv4:contig12:11475396:11476646:1 gene:MELO3C019323.2 transcript:MELO3C019323.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MFGIMLLKFINSMSLKCVLELGIPDIIHNHGQPMSLSSLVAALHIEPTKAECLSRLMNLLVHSGFFATAQEQDHDKAEDVKYSLTPSYKLLLHHSQATPFLFVSLDKAIIASFQSLSSWFRSSNNNGQNYSNAFEMANGKLLWEYAPQEQTFASLFQQTMVCDSEMIGKIVKQECSEVFEGLKSLVDVGGGTGVMGKAIVEAFPHITCTVFDLPQVISNQPLQNAKNLRFVEGDMFEEIIPPANAILLKWILHDWNDEQNIRILKKCKDAIRSREKCGKLIIIDIVMEDKKEEKESTETQLLFDVLMMVNLGGKEMNENEWKNLFMEAGFSGYKIISKLGLRSVIEVYPA

>maker-chr11-exonerate\_est2genome-gene-178.7-mRNA-1:cds pep supercontig:Melonv4:contig12:17829136:17830624:1 gene:MELO3C013600.2 transcript:MELO3C013600.2.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding

MEAKETNEAEALLQGQAEIWKYMLCFADSMALKCAVELHLADIINSHGSPISLSQISSSIAASNPSSSPQISYLNRIMRLLVRRNIFAAHHPSDGGDTLYGLTHSSKWLLRDSPLTLAPMAFSELHQWMVSPWLCFTEAVKEGGSPFKIAHGLDIWDFASKNPQFNHFFNDAMASTSKVVMNAILSVYQDGFNSLDSLADVGGGIGGSISEIVKAFPHIKGINYDLPHVISTAPVYEGVTHIGGDMFEDIPKVDAIFMKWILHDWNDKECVKILENCKKAIPEKRGKVIIVEVVLNEEGKGAFDDTKFYFDLLMLAHTNGKERTEKEWKTILEEAGFSRYNLIPLPALVSIIEAYPS

>AFZ23489

MVASEDRPTSLPVKLASLDMLNLITSYRVTQTIHVAAKLGIADLLKDGPKRSQELADDTATDASALYRLLRALASIGVFQEVEHDLFELTALGESLRSDVPGSMRAWAIMVGGEHHWQPWGHLLHSVQTGKPAFDHVFGMGPFEYYKQKPAAGQIFQEALGGLTQIVNSQILASYDFSSIQKLVDIGGGHGSLLSGILQANPEMLGVLFDQKSVIDQAAALLEDKGVYSRCELVAGDFFASVSKGGDAYILKHIIHDWDDERSVKILKNCYEAMSGDSKLLVVEMVIPSGNTPFYGKFLDIEMLVGYSGKERTADEYQNLFAQAGFKLTQIFGTQALVSVIEGVRA

>KAB1200567.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MDPVQAQAGASHELLEAQTHLYQHVFNYISSMSIKCVVQLGIPDIIHNHGKPITLPELASALEIHDPTKAGAIHRLMRLLVHNGFFAQTEVHGNQQEEEELYDLTPSSRILLKDNVMSLSKSVLASLHPAIMDPWHVLESWVRGDKVTPFENAHGMDFWNYAVQNPAFGTLYDEALASDSGMVNLVLRDCKSVFEGLDTLIDVGGDSSNLKFVGGDMFELIPSADAILLKLVLNNWGDEDCLKVLKKCREAISNNGNRGKVVIIDIVLNEKKDKHELTEAKLYFDLLMMIVVSGRQRYEKEWEKLFLEAGFSHYKIIPLFGLRSLVEVYP

>KAB1202878.1 Caffeic acid 3-O-methyltransferase 1 [Morella rubra]

MTAFEYQGKDLRLNNIFNKGMSDHSTFTMKKILETYKGFEGLTSVVDVGGGTGVVLNMTVSKYPSIKGINFDLPHVIADAPSYPGVVAAGVDHVGGDMFASVPRGDAIFMKWICHDWSDEHCMKLLKNCYDALPDNGKVIVVECILPVAPDTSLASKGICHVDIFMLVQTPGGRERTEEEFEAFAKGAGFQVFRVMGCAFNTSIMEFIKKSSA

>KAB1202983.1 Caffeic acid 3-O-methyltransferase [Morella rubra]

MPTTNPEAPRMLASHSVFRCSVVADGSESFQRLYSLSPVSKHFVRDEVGSHWDLLWRCFKTRSQLKDAILEGGIPFNRVHGTHPFEYPGLDPMFNQVCNKAMFNHTTMVIMKILQSYKGFEQLEQLVDVGGGGDMFSSVPEGDAIFMKWILHDWSDEHCLKLLKNCHGAIPNHGKVIVLEAVLPVMSEISTSVKSTSQLDVLMMTQTPGGKERTREEFLTLVTEPGFKGIRYGCFVRNFWVWSF

>KAB1202984.1 Caffeic acid 3-O-methyltransferase [Morella rubra]

MASQTNSSPCPSLLNDHPKEEEDSFSHAMQLANSLVLPMALQSAIELGVFDILAKAGPEAELSSSQIVAQMPNTNPEAPKMLDRILRMLASHSVFRCSVVADDSESFQRLYSLSPVSKHFVRDEDGISLGPFMALLQDKVFVDSWVYGTHAFMYPGLDPRFNQVFNRAMFNHTTMVIKKILESYKGFEQLEQLVDVGGGLGVTLNLVTSRYPHIKGINFDLPHVIQDAPPFPGVEHVGGDMFSSVPKGDAIFMKWILHDWSDEHCLKLLRNCYGAIRNDGKVIVLEAVLPVMPEISTSVKSTSQLDVLMMTQNPGGKERTREEFLTLATEAGFKGIRYECFVCNFWVMEFLK

>KAB1205223.1 Caffeic acid 3-O-methyltransferase [Morella rubra]

MGSTGETQMTPTQVSDEEANLFAMQLASASVLPMVLKSAIELELLEVISKAGPGAYLSSSEIASQLPTTNPDAPVMLDRILRLLASYSVLTYSLRTLPDGRVERLYGQGPVCKFLTKNEDGVSIAALCLMNQDKVLMESWYYLKDAVLEGGIPFNKAHGMTSFEYHGKDMRFNKVFNKGMADHSTITMKKILDTYKGFEGLASVVDVGGGTGAVLSMIVSKYPSIKGINFDLPHVIEDAPSYPGIERVAAGVEHVGGDMFVSVPKGDAIFMKWICHDWSDEHCLKFLENCYKALPDNGKVIVAECILPVAPDTSLATKGVIHIDVIMLAHNPGGKERTEKEFEALAKGAGFQGFRVMGCAFNTYIMEFIKKL

>KAB1205353.1 Caffeic acid 3-O-methyltransferase 1 [Morella rubra]

MDSMGKQTTDHMASTLNEVEEAIIHDFVVSGSFLVPMVLNACVELNVLEIIHKAGPNMQLSSHAITSHLPTSNPDAPHLLDRMLYLLCSYSLLTCSVETLEDDRVQRRYGLAPAGKFYLKNTETGSLSTFALLTSHRAIMDMRFHFKDAVLEGGYPFEKANGVSIFKHREKDPRFGEAYNSGMSEHSTFFMKQILNTYHGFEGLSSLVDVGGGNGAMLHLIMSKYPSIKGGVNLDLADVIRHAQPYKGIEHVDGNMFEDVPKGRDAILVKQVFHNWSDADCLRILRNCHKALPSNGKVIIIDLIMSTAPDTTIMGKFICHYDNLMFGLFGARERAENEFKALAIGAGFSKFRLVCCVCGFGVMELHK

>KAB1205360.1 Caffeic acid 3-O-methyltransferase 1 [Morella rubra]

MDSMGKQTTDHMASTLNEVEEAIIHDFVVSGSFLVPMVLNACVELNVLEIIHKAGPNMQLSSHAITSHLPTSNPDAPHLLDRMLYLLCSYSLLTCSVETLEDDRVQRRYGLAPAGKFYLKNTETGSLSTFALLTSHRAIMDMRFHFKDAVLEGGYPFEKANGVSIFKHREKDPRFGEAYNSGMSEHSTFFMKQILNTYHGFEGLSSLVDVGGGNGAMLHLIMSKYPSIKGGVNLDLADVIRHAQPYKGIEHVDGNMFEDVPKGRDAILVKQVFHNWSDADCLRILRNCHKALPSNGKVIIIDLIMSTAPDTTIMGKFICHYDNLMFGLFGARERAENEFKALAIGAGFSKFRLVCCVCGFGVMELHK

>KAB1206012.1 (R,S)-reticuline 7-O-methyltransferase [Morella rubra]

MALKCAVELRLADIIHSHNGPIILHQIASGIDSPSPDILYLSRIMRSLVRKKIFSEHCPTDGGETIYELTHVSRWLLHDVELSLAPMVLMQNHPWVVAPWYYLSQCVKEGGIAFKKAHACDVWEFASQNPEFNKLVNDSMACTTKIVMMAILAEYKAGFDCIGSLVDVGGGTGGMISEIVRSHPQIRGIDFDLPHVIATAPLHEGVSHVGGNMFEAIPCADAIFMKFVLHDWDHEDCIKILRNCRKAILEKTGKLIIVDIVLEKDSHDLFDDTRMVFDLMMMAHSSGGKELTELEWKEFLKGGFPGYKITKIPAIPFIIEAYPM

>KAB1206013.1 (R,S)-reticuline 7-O-methyltransferase [Morella rubra]

MGVVMAKYKDGFDGVGSLVDVGGGTGGMIAEIVKSHPHIRGINFDLPHVVATAPWVLHDWGDEDCIKILWNCRKAIPEKRKKGRLIIVDIVLEKDSHDLFDETRMVFDLSMMAHTASGKEKTELEWKEILKEGGFPRYKINKIPTIPSIIEAYPI

>KAB1206016.1 (R,S)-reticuline 7-O-methyltransferase [Morella rubra]

MVLAEYKDGFDCVGSLVDVGSGGTGGMIAEIVKSHPHIRGINFDLPHVVATAPVRERVSHVGGDMFEAGAIPDADAIFMKGKLIIVDIVLEKDSHDLFDKTRMVFDLLMMAHTASGKERTELEWKELLTEGGFRCYKIIKIPTIPSIIEAYPIQSLVQRFSN

>KAB1207631.1 (R,S)-reticuline 7-O-methyltransferase [Morella rubra]

MGETQIREAKWQSEEEQAEVGIWRCIFGFTEMAVVKCAIDLGIADAIESHASPMTLSELSTALGCAPSSLYRIMRFLMHRGIFKEKINSQGSLVYTQTCLSRRLTRHGEQSMAPLILLESSPVMLAPWHCLSARVRATETPPFDVAHGGDIWRYSATNPGHSQLINEAMACDARLVVPSMIRGCPEVFDGLSTLVDVGGGTGTTLQVLVKAFPWLRGINFDLPHVVSVAAEFTGVEHVGGDMFEGVPEADAVFLKWVLHDWGDDECIQILKKCREAVPDDKGKVIIVEAVIEEADQGDKLTEVRLALDMVMMAHTTTGKERTSKEWGFVLGKAGFSRYTVKPLIRTVQSVIEGFP

>KAB1207632.1 (R,S)-reticuline 7-O-methyltransferase [Morella rubra]

MEKTPRRAPWHEEEEQGEVGIWKYAFGFSEMAVLKCAIELGIAEAIESHGSCPMTLSELSSALGCAPSALFRIMRFLVHRGMFKEELTAQGSLGYAETPLTRRLMKHGEYSMAALILLESSPVMLAPWHSLSASCVLANESSPFDVAHGEDLWRFAAANPGHSQLIDEAMACIARSTVRLMVQGCPEVFDGLSSLVDVGGGNGTTLQKLVKACPGIRGINFDLPHVVSVAEEFTGVEHVGGNLFKSVPKADAALLMSVLHDWGDDDCIDILKKCREAIPVDKGKVIIVEAVIEEGDQTDKLTDLRLGLDMIMMAHTTAGKERTLKEWGFVLGKAGFSRYTVKPLPAMPSVIEAFP

>KAB1209855.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MSGFRQLSFKLVPGRQGTELLHAQAHTWNHILSFAKSMSLKCAVQLGIPDIIHNHGKPMTFSELIAALPIHPSKAGNVYRLMRFLVHSGVFAEEKSTEIDQEEGYLLTGVSRLLLKDDPLSLTPLLLFVLDPDMTKPWHHLTSWLQNDDPMPFDTAHGMTMWDYEGCDPKMAHLFQDAMASDTRLVISVVIDKCSDVLEGLESLVDVGGSSGTMTKAITDAFPNIECTVLDLPHVVAGLQDNANLKYVGGDMFEAVPPADAVLLKWILHDWNDEECVKILQKCKEAITRNGKKGKVIIIEMMVGNQKGDKDSTETQLFFDMLMMALVKGKERNEKEWAKLFYDAGFTDYKIKPILGLRSLIEVYP

>KAB1209856.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MKHEGRRSGAERLLLKDDPLSLTPLLLFVLDPDMTKPWHHLTGWLQSDDPMPFDTAHGMTVWDYEGRDPKIAHLFQDAMASDTRLVISVVIDKCNEVFEGLGSLVDVGGSSGAMAQAINDAFPNIDCTVLDLPHVVAGLQGRKKLKYVGGDMFEAVPPADAVLLKWILHHWNDEECVKIQKCKEAITRNGKKGKVIIIEIMTVENQKGDKDSTETQLFFDKLMMALAKGKERNEKEWAKLFYDAGFSYYKINPILGLRSLIEVYP

>KAB1209896.1 (R,S)-reticuline 7-O-methyltransferase [Morella rubra]

MALTEAKVLQDGQTKLWKHTFSFAVSMALKCAVDLRVADIINSHGVPISLSQIAAKIDSPSPNIPNLERIMRLLVRKEIFSAHQRPNSEETLYGLTASSRWFLHDSELSLAPFISLQNSEWLMAPWYRLAQFVKESVPGGSTGFSKCYGSEIFDFASKNHEFNKLFNAGMESTATVMVDAILTGYKDGFSSIGSLVDVGGGNGHMISKIVKAHPHIKGINFDLPHVIAAAPKHKGVANVGGNIFEAIPKADAIFMQRVLASFNDEDSIKVLKNCLKAIPKETGKVVIIDPLLDLENEGPFDEMIAALDLSMMMLCKGGQERTKLEWQKILEASGFLLNRVIKIPAVLTIVEAYPA

>KAB1210045.1 (R,S)-reticuline 7-O-methyltransferase [Morella rubra]

MESTEACKALMQKGQAQLWQHIFAFAESMALKCVVELRVADIIQSHGVATSLSQIAAGIDSPSPNIPYLSRIMRLLGRKGIFSAHQSSTSGETLYGLTDVSRCLLSESELDQTPLVLMQNHEWVMATWHRLAECVKEGGNAFVKVHGCELFDLAAKNPEFNKLFNDAMTCSAKGFARSLVVGYKDGLDSINGSLMDVGGGSGELIANIIKEYPHIKGVNCDLPHVIATAPAHKGVSHVEGDMFGALPKADAIIMQRILHGFDDEDCIKILRNCLKAIPKKGGKLIVVDHVRKADGNGAYDAMGVTIDLLMMTLGTGQGGKQRTAPEWKKLIEKGGFSVQRIIELHNLPSVIEAFPA

>KAB1215422.1 Isoflavone-7-O-methyltransferase 9 [Morella rubra]

MASDSGMMNLVVRDCKPVFKGLDTLIDVGGGTETCARIISKAFPHLKCRVFDLPLVVKLFFSSSLNLDYVAGEMFQSIPPADAILLKQC

>KAB1215426.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MRLLVNSGFFTRSIKGQENQEAEEEEEEEAYALTPSSKLVLKENVTTLSPFVLAMLDPALVNSWQFLGDWFRAGSELTPFGEAHGMGFWDYCDQNAEYGNMFNEGMASDSRLMSLVLMDYAPIFEGLGSLVNVGGGTGTMARIISEAFPHMSCTVFDLPHVVANLPDSSNLIYVGGDMFQSIPSADAILIKASNRFSLLKDLQYFILKWILHDWNDDECVSILKRCKEAITSNGKKGKVIVIDVVIDEEKDEQGIIKTKLLFDALMMVLLTGKERNKKEWEKLFLDAGFSRYKIAASFGMKSVIEIYP

>KAB1215429.1 Isoflavone-7-O-methyltransferase 6 [Morella rubra]

MLDPALVNSWQFLGDWFRAGSELTPFGEAHGMGFWDYCDQNAEYGNMFNEGMASDSRLMSLVLMDYAPIFEGLGSLVNVGGGTGTMARIISEAFPHMSCTVFDLPHVVANLPDSSNLIYVGGDMFQSIPSADAILIKASNRFSLLKDLQYFILKWILHDWNDDECVSILKRCKEAITSNGKKGKVIVIDVVIDEEKDEQGIIKTKLLFDALMMVLLTGKERNKKEWEKLFLDAGFSRYKIAASFGMKSVIEIYP

>KAB1219935.1 Caffeic acid 3-O-methyltransferase [Morella rubra]

MAKNRRGKGRKRQKRMASFDTDTQIPPLQTGEDLAFSKAMELVYGSALLMAMHAAIDLGVFDILASAGPEAKLSAADIAAKMPTENPEAPAMLDRICTLLVHDCVLDYAISIPKCAFADTNWLYCLNPVSEYFVRNQDGVSLAPILTLIQDNVDMDTWSRLKDAVLEGGVPFHRVQGMDAYYKYLGEDARLSQIFNTAMSNHTTIIVKTFLENYDGFEKVKQVVDVGGGIGAALSLITSEYPQIKGINFDLPHVIDCAPRYPRVKHVAGDMFESVPKGDVIILKWILRDWGDEQCLKLLKNCYDALPKDGRVIVMDQFLPIKPGAAGKSSFLLDTLLMTQNLGGKQRKPDEFSRLAREAGFTYSLSDQHFVLDIWVIEFRKISNHEYRSH

>KAB1220994.1 Caffeic acid 3-O-methyltransferase 1 [Morella rubra]

MNDRSTSRVLLEGVDGGDKLDSGSFDGLGGEEDGEDPSTETGEGDLRMREPKKKWRSSTEIEGKNGNKKKRKSVESPTTKRTTEKERRDHLKQLCVESQRILRGLAQDGCRMDASAVLYTSVKSAHASVAMLHQKKIRGGDGLGTSAGWGGLILQLAIDMVQIDVDNMSPDVVKFLRFNRAPLGKNEQLQTHLPEPDFSTARARRRRRGGQIGRPLANAVALPMVLKSALELNLIDIIAESGTGALLPVSEIAARLRTKNPDTSVMLDRMLGLLASYDILKCSLRTRKDGEVERLFGVGPICKFLVRNSDGASVGPLFLLHHDKVFMESWFHMNEAILEGGIPFKRAYGISIFEKLGTDERFNRVFNQAMSHHSTLIMKKILDVYKGFEGLKVLVDVGGGIGATLNSIISKYPQIKGINFDLPHVLVDAPPFPGVEHVGGNMFDSVPSGDAIFMKWMLHGCSDEQCLQALKNCWKVLPNSGKVIVVESIRPVAPENNVSSQIVYEQDLMMLTQSPGGKERTQNEYEALALKSGFSGSEVICCAYNTWVMEFRK

>KAB1221202.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MDPVQAQAGASNELLEAQSHLYQHVFNYISSMSIKCVVQLGIPDIIHNHGKPITLPELASALEIHDPTKAGAIHRLMRLLVHNGFFAQTEVHGNQQQEEELYDLTPSSRILLKDNVMSLSKSVLASLHPAIMDPWHVLESWVRGDKVTPFENAHGMDFWNYAVQNPAFGTLYDEALASDSGMVNLVLRDCKSVFEGLDTLIDVGGGTGTCAKIISEAFPNLKCTVLDLPRVVSDLRDSSNLKFVGGDMFELIPSADAILLKSVLNNWGDEDCLKVLKKCREAISNNGNWGKVVIIDIVLNDKKDKHELTEAKLYFDLLMMIVVSGRQRYEKEWEKLFLEAGFSHFKIIPLFGLRSLVEVYP

>KAB1222015.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MANQLLFHSWSLSFTFLPQKTSSLHRLMRLLVHFGFFTKTKVRENQEEEEAYGLAPSSRLVLRDNVASFSWLVLLISEPFLVNPCHFWADWFRGSDEFTPFENAHGMGFWDYCDQHPDLGNMFNKAMASDSQLMSLVVKDYKPIFEGLGSLVDVGGGTGTAARIISEAFPQIKCTVFDLPRVVANLPDSTNLKYVGGDMLQSIPPVDDILMKWVLHDWCDEECIKILQRCKEAITSEERNKTEWEKLFLEAGFSHYKMVASFGVRSVIEVYP

>KAB1222016.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MRLLVNSGFFTRSIKGQENQQEEEEEAYALTPSSKLVLKENVTNSSPFILAMLDPALVNSWQYLGDWFRGSELTPFGEAHGMGFWDYCDRNAEYGNMFNEGMASDSRLMSLVVKDYKSIFEGLGSLVDVGGGTGIMARIISEAFPHMNCTVFDLPHVVANLPDSSNLIYVGGDMFQSIPSADAILIKVSNRFSLLKDLQYFISKVHGILFSYISNYILQWILHDWNDDECVSILKRCKEAITSNGKKGKVIVIDLVIDEEKDEQDIIKTKLLFDALMMVLVTGKERNKKNGKSSSWMLALAASKLQHHLA

>KAB1222017.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MDLTRDQGASELFHAQSHLYRHIFSFISSMFLKCAVQLGISDIIHNHGQPITLPELVLELQINPTKAGFLHRLMRLLVHCGLFATTRVHKNQEDEEEAYDLTPSSRILLKDNITSLSPFVVAMLDPALVTPWQVLGNWFRCDQVTPFEGAHGVGFWDFGDQNPEFNKLFNEAMASDSGMMNLLSETASQFLRVWIH

>KAB1222018.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MDPVQSQGASHELLEAQTHLYQHVFNYISSMSIKCVVQLGIPDIIHNHGKPITLPELASALEIHDPTKAGAMHRLMRLLVHNGFFAQTEVHGNQQQKQEEAYDLTPSSRILLKDNVMSLSKSVLASLHPAVMDPWHVLESWVRGDKVTPFENAHGMDFWNYANQNPAFGTLYDEALASDSGMVNLVLRDCKSVFEGLDTLIDVGGGTGTSAKIISEAFPNLKCTVLDLPRVVSDLPDSSNLKFVGGDMFELIPSADAILLKSVLNNWGDEDCLKVLKKCREVISNNGNRGKVIIIDIVLNDKKDKHELTEAKLYFDLLMMIVVSGRQRYEKEWEKLFLEAGFSHYKIIPLFGLRSLVEVYP

>KAB1222738.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MDPVQAQAGASNELLEAQSHLYQHLGIPDIIHNHGKPITLPELSSALEIHDPTKAGAIHRLMRLLVHNGFFAQTEVHGNQQQEEELYDLTPSSRILLKDNVMSLSKSVLASLHPAIMDPWHVLESWVRGDKVTPFENAHGMDFWNYAVQNPAFGTLYDEALASDSGMVNLVLRDCKSVFEGLDTLIDVGGGTGTCAKIISEAFPNLKFTVLDLPRVVSDLRDSSNLKFVGGDMFELIPSADAILLKSVLTIGRRGLLEKMPRSYFKQRKLGKSVIIDIRYEKEWEKLFLEAGFSHYKIIPLFGLRSLVEVYP

>KAB1222739.1 Trans-resveratrol di-O-methyltransferase [Morella rubra]

MDPVQAQAGASNELLEAQSHLYQHVFNYISSMSIKCVVQLGIPDIIHNHGKPITLPELSSALEIHDPTKAGAIHRLMRLLVHNGFFAQTEVHGNQQQEEELYDLTPSSRILLKDNVMSLSKSVLASLHPAIMDPWHVLESWVRGDKVTPFENAHGMDFWNYAVQNPAFGTLYDEALASDSGMVNLVLRDCKSVFEGLDTLIDVGGGTGTCAKIISEAFPNLKFTVLDLPRVVSDLRDSSNLKFVGGDMFELIPSADAILLKSVLTIGRRGLLEKMPRSYFKQRKLGKSVIIDIRYEKEWEKLFLEAGFSHYKIIPLFGLRSLVEVYP

>KAB1222917.1 (S)-scoulerine 9-O-methyltransferase [Morella rubra]

MLLFFSGKEIVESMNMLKDSVLDPGRSAFYRTHGVHPYEYMEKKPTLKRSFNGFIESTSRAILDEVLKVYGGFEDVKELLDVGGCAGASLGKILSVHPHIRGLNLDLAHVIADAPTFPGMEHIAGDLFRSLPHTQTILLQGILHNWDDDHCKKLLRNCWEALPDDGKVIVVESVIPQVLANDIETRYAVTSDLCMMLLLVGGKERTISEIDILAKAVGFVETKDFPVAKSIHDIELRKKVMHHP

>KAB1222918.1 (S)-scoulerine 9-O-methyltransferase [Morella rubra]

MAARAAIELNVFSIIAEAGPGAHLSAAEITSKMETTNPKSASTNLDRLLRFLGANSLLTMAQRPFKNGEDIHHEWTYGLTKPTCSPETSSEAGISSTHGVHFYEYMEKKPTLKRLFNGFLESTSQAILDEVLKVYGGFEEVKEMLDVGGGVGASLVKILSVYPHIRGMNLDLAHVIADAATFPGVEHIAGDMFRSLPHTQTILLQRILHNWDDDHCKKLLRNCWEALPDDGKVIVVESVVPQVLANDPETRYAVAYDLGMMLLLAGGKERTISEFDNLAKAVGFVETKAFPIATSIHVIELRKKVMRHP

>KAB1223611.1 Caffeic acid 3-O-methyltransferase 1 [Morella rubra]

MVLKSALELNLIDIISEAGTGAFLSPSEIAARLPTRNPDSPVLLDRMLRLLASYSILKCSIATREDGEIERLYGVGPICKFLVRNSGGGSVSPLFLLHRDKVFMESWYHLNDAILDGGIPFNRAYGMTAFEYPGTDERFNQVFNQAMSNHTTLIMKKILEVYKRFDGLKVLVDVGGGLGVTLKSITSKYPQIKGINFDLPHVLADAPSYPGTDFVLSLAQEFYDMFKIDNSYPMTQYVANSHHGPLLFTSRPAWILHDWSDEHCLKLLKNCWKALPNSGKVIIVESILPVVPDSNVSSNIVFEQDLFMLAQNPGGKERTQKEFEALAEKCGFSGYEVVCSAYNSWVMEFHKRADP

>KAB1228317.1 (R,S)-reticuline 7-O-methyltransferase [Morella rubra]

MGVVMAKYKDGFDGVGSLVDVGGGTGGMIAEIVKSHPHIRGINFDLPHVVATAPWVLHDWGDEDCIKILWNCRKAIPEKRKKGRLIIVDIVLEKDSYDLFDETRMVFDLSMMAHTASGKEKTELEWKEILKEGGFPRYKINKIPTIPSIIEAYPI

>KAB1228320.1 (R,S)-reticuline 7-O-methyltransferase [Morella rubra]

MFEAIPCADAIFMKFVLHDWDDEDCIKILRNCQKAIPEKGGKLIIVDIVLEKDSHDLFDETRMVFDLMMMAHSSGGKERTELEWKELLKKGGFPCYKITKIPAIPFIIEAYPM

>KAB1228322.1 (R,S)-reticuline 7-O-methyltransferase [Morella rubra]

MACTAKIMMAVVLAEYKDGFDCVGSLVPDVGSGGTGGMIAEIVKSHPYIRGINFDLPHVVAAAPVRERVSHVGGGMFEAGAIPDADAIFMKGKLIFVDIVLEKDSHDLFDKTCMVFDLLMMAHTAGGKERTELEWKELLTEGGFRCYKIIKIPTIPSIIEAYLIRSLVQRFSN

>EXB31255.1 8-hydroxyquercetin 8-O-methyltransferase [Morus notabilis]

MEKRLRSFRNLDTDLQINEEKATELLGAQAHIWNNIFNFINSMSLKCAVQLGIPDTIHKHGKPMTLSKLIGALPVHQNKAPYVYRLMRILVHSGFFSLQTIGESDHQEEEGYVLTDASKLLVGDNPLSVAPFLLAMLDPVLTKPWDFLSTWFQNDDPTAFDTVNGLPFWKYGGQEPKMANFFNDAMASDARLVISVVIENCKWVFDELESFVDVGGGTGTVAKAIAATFPKMECTVFDLPHVVGDLQGKDNLKFVGGDMFQQVPPADAILLKWILHDWSDDECVKILKKCKEAITSKGSKKGKVIIIDIMIENKDEDDKSYETQLFFDMMMMVLATGQERNEKEWAKLFQDSGFSDYKIIPILGLRSLIEVYP

>EXB37024.1 (RS)-norcoclaurine 6-O-methyltransferase [Morus notabilis]

MDSADDENLRGQAEIWKYMFRFVDSMALRCVVELRIPDIINSHGGPITLAQIVSSIPEASSPDISCLARIMRFLVRRNIFTAHHPSNGSEDITLYGLTHLSRWLLTCEQTLAPMLLWQTDPTLMTPMHYFSGCVKGGGVPFEKAHGRGMFAFMSENEEFGKACNDAMECTARIILKEILSDSQCGDHVFGCLGSLIDVGGGTGGALSEIVKSYPHIKGINFDLPHVVSKAPVYAGVSHVAGDMFESIPSADAWIMHDWMDEDCVKILKNCRKAVPEKSGKVIIVDVVLDLKGNGLFDDMGLILDLLMAAHSLGGKERTEKEWKKILKEGGFSCYKIIRISTFLSIIEAYPE

>EXB38591.1 Caffeic acid 3-O-methyltransferase [Morus notabilis]

MDYGGDTGVEHVGGDMFVSVPKADAVFMKLNMKGFYIDVESCQTIVMQWICHDWSDEHCLKFLKNCYDALPENGKVIVAECILPDAPDSSLATKGVVHIDVIMLAHNPGGKERTEKEFEALAKGSGFQGFRVLCDAFNTYVMEFLKKPF

>EXB54962.1 Isoflavone-7-O-methyltransferase 8 [Morus notabilis]

MSKSDDNEMMSSSELLQAFSLLRSCSISHIKSMSLKCAIELGIPYIIHNHGQRAITFSKLIESLPVHPSKTHCIYRIMRLLVHSGFFATQKPDQEEEEEAYTLTNASRLLLTDTPVNMESYFLLPLLPQMIGPWQSLSTWLQSNDHTLFKTVYGGTIWDQLADDPELNYRFNEAMASDSRLISKVILDSEYIRVFEGLKCLVDVGGGSGTLAKAIANTFPHMKCTVFDLPHVVANVQGTTDNLSFIGGNMFSDPIPPADAILLKMIMHNWNDEDGSRILKRCREAILSNGNGGKVIVIDTVIGNEKTQDLTETKLCNDVIMMTLTGKERSLMQWEKLILTAQFSHYKITPIFGSVNSIIEVYP

>EXB54963.1 Myricetin O-methyltransferase [Morus notabilis]

MSSSDELIMSSNELVEAHSLLWHSGLDYMKSMSLKCAIELDIANVIHKHGQPIPFSKLVDSLKIPPSKANFLYRIMRILVHHGFFTAQKVNGGKTQEEEEAYSLTNASRLLLTDEPALIMNMKSLSLFFLLPAVVNSWQSWSTWLKNSDDMTLFETAEGKTWWEYASQEPGLNHLFNDAMANDSKLTAKIILEECKEVLEGLKNLVDVGGGTGTMAKAIVNAFPHIKCTVLDLPHVVANVQETSTDNLNFIGGDMFSEQIPPADAILLKNVLHDWTDEACVTILKRCREAVLSNGNKGKIILIEIVVETQKTTNKETTELQLLNDVFFMGLSAKERTLLEWEKLFSAAGISHYKIIHTFGIRSVIEVYP

>EXB54964.1 Tabersonine 16-O-methyltransferase [Morus notabilis]

MEVFSEEVMSSSELLQAHSLLWSNSVHIVRNLSLKCVIELGIPDIIHKHDQPISLSKLISALPIHPSKAHCIYRIMRILVHSGFFSTRKLNGEEEESYSLTNVSRLLLSDGPAFIKMKSFFLFHLLPEVAAPWHSLSTWLQHSDGTTFEHGNGKNFWDCLADEPKHIHLFNEAMANDSQLIAKVILTEYKNVFEGLETLVDVGGGTGTMAKAIASTFPHIKCTVFDLPHVVANLEATDNLNFIGGNMFTDTIPPTDGILLKWILHDWNDEDSVSILKRCREAILRNGKGGKVIVIEMVIENQNTNEITGIQLSYDVMMMGSFFGKERNLVEWEKLFFEAGFSHYKINAKMGARSLIELYP

>EXB54965.1 Tabersonine 16-O-methyltransferase [Morus notabilis]

MDVGDEVSANELLQAHGLIWNCSLNFIKPMSLKCAVELGIPDIINNHGQPITLSKLISSLPIHSSKAHCIYRLMRILVHSGFFATQKVDNKIDEGEEEEEEEAYSLTIASRLLLKDGPWRATPFFLVQLEPHLMTPWHFVSTWLQNSDPTPFEMVHGKTFWDGVGDEPRLKYLFTEAMATDSQLMVKVIVEECKQVFEGLTSLVDVGGGTGIVAKAIAKTFPNIMCTVLDLPYVVANSQGAKNLNFIAGDMFKEIPPANAILLKWILHDWSDEEAVMILKRCREAIWSKEKGEKVIIIDMVIENPKMDKKSAETQLYFDMLMMVNLTGRERNQKEWESLFVAAGFSHYKITPIVGLRSLMEVYP

>EXB55622.1 3'-hydroxy-N-methyl-(S)-coclaurine 4'-O-methyltransferase [Morus notabilis]

MKLDEASLRGQAEVWKYMFSFADSMAVKCAVELRIPDIIKSNGGPMSLAEIVAAFPRASSPDISCLSRIMRLLVRLKIFTARQSSDGSGDSATLYGLTQSSRWLLRDTSDDQLTLAPMLLLENHPLLMAPWHCFSQCVKDGGLPLEKAHGPEIWDFVTGNGEFNKMFNRGMECASRIVMRAVLSEYYKDGFGCLGSLLDVGGGTGGDVAQIVKSCPHIIKSINFDLPDVVAKAPEHPGVSHVGGDMFKSWIMHEWSDEDCVKILKNCRKAIPEKSGKVIIVDIVLEPEGTGVFDETGLVFDLVMVAHTSGGKERTENEWKNILKEGGFPRYKVTKIPALTSIIEAYPQ

>EXB55624.1 (RS)-norcoclaurine 6-O-methyltransferase [Morus notabilis]

MQTHPWLMAPWHCFSRCVKEGGSAFQKAHGREIWDFASENPEFNKLFNDGMECTARIILKAILSEYRDGFSSLGSLIDVGGGTGRALSEIVKSHPHINGINFDLPHVVAKAPVYPGVSHVGGDMFESIPNADAVFMKASLATDLNQLSTWIMHDWGDEDCVKILKNCRKAIPEKSGKVIIVDLVLNPEGNTLFDDMSLIWDLVMVAYASGGKERTENQWKKILIEGGFPRYKIIKIPSLTSIIEAYPE

>EXB55626.1 (RS)-norcoclaurine 6-O-methyltransferase [Morus notabilis]

MESNEASLRDREEIWKYMLNHADSMAIKCAVELRIPDIINSHGGPMSLAQIAAAIPDTSSPDISCLARIMRLLVRRNIFTAHQSSDGSGDSTTLYGLTHSSRWLLSDTSDDQLTLAPFFLMETHPWLMAPWHCFSRCVKEGGSAFQKAHGREIWDFASENPEFNKLFNDGMECTARIILKAILSEYRDGFGSLGSLVDVGGGTGRALSEIVKSHPHINGINFDLPHVVGTAPVYPGVSHVGGDMFESIPNADAVFMKWIMHDWGDEDCVKILKNCRKAIPEKSGKVVIVDLVLNPEGNTLFDDMSLIWDLVMVADASGGKERTENQWKKILKEGGFPRYKIIKIPSLTSIIEAYPE

>EXB55629.1 (RS)-norcoclaurine 6-O-methyltransferase [Morus notabilis]

MESDEASLRGQAEIWKYMFNFADSLALRCAVELKIPDIINSHGGPITLAQIASSIPNTSSDPDISCLARIMRLLVRRKIFTAHQPSDGSGNSTILYGLTHSSKWLLRDTLGDDQHTLAPIFLMETHPWLVSPWHCFSRCIKEGGIAFEKSHGREIWDFASENPEFNKLFNDGMECTAKIILKAILSEYKDGFDYLGSLVDVGGGTGGALSEIVKSHPHIKGTNFDLPHVVATAPAYPGVSHVGGDMFESIPNADAWIMHDWGDEDCVKILKNCRKAIPEKSGKVIIIDVVLNPEGNGLFDDTGLIFDLVMVAHASGGKERTENEWKKILKEGGFSRYKIVKIPALTSIIEAYPQ

>EXB57403.1 Caffeic acid 3-O-methyltransferase [Morus notabilis]

MDSKETQIQSSLSQEDEACLKAMLLCSSHVLHLVLNAAIELDLFGIMAGAGPGPEAKMSPSDIASLLPIETPNGPSMLDRMLRLFASYSLLTCSTSTSQDGKVERLYGLTPTAKFFIRGRDKNELASLYRLHCHPTTLEVWFHMKDVILEGGSTFEKAHGMSIFKYMDSNESFRNIFHSAMVARSTIIMEKVLEIYNGFQGLTSLVDVGGGTGHCLHMIISKYPSILATNLELPHAIQNAPPYPGIKHVAGDMFESIPNSDAIMIKDVLHNWEDVDCIKLLRNCHEALPQENGKVIIIDIIMPETPDSSMASKYASELDNIMLTQPGGRERSRRELQALCEESGFSRFRIACFALSVWAVVEFYK

>EXB57805.1 Tabersonine 16-O-methyltransferase [Morus notabilis]

MDYFSEDVMSSSELLQAHSLLWSNSVHIVRNLSLKCVIELGIPDIIHKHGQPITLSKLISALPIHPSKAHCIYRIMRILVHSGFFSALKVNGEEEESLSLTNVSRLLLSDGPASIKMTSFFLFHLLPEVAAPWYSLSTWLQHSDGTTFEHGNGKNFWDCLADEPKHIHLFNEAMANDSQLIAKWILHDWNDEDSVSILKRCREAILRNGKGGKVIVIEMVIENQNTNEITGIQLSYDVMMMGSFFGKERNLVEWEKLFFEAGFSHYKINAKMGARSLIELYP

>EXB57807.1 Myricetin O-methyltransferase [Morus notabilis]

MAKAIASSFPHIKCTVFDLPHVVANLEGTDNLNFIGGNMFTDTIPPTDGILLNLKGGSASDYPRPSFDLHLPFKTCALPFPSMVKAGEEISRSIRSVRRIPKDQASEASKEEALLSEYDPSVRAYHKQARKKRRQPGEAAKLQRQGGSLSAYERKSVCRLALRRETLVEVGSCSVILSLGISALMLDIIDGLLFLSELPDPRASWRGSTNGTSYDDMVYIPVVRTEERVTPVTPPPAAPTMAVLSPLPSSFPAPVEITHATNATTSAASSIAGDSITIPAIAVETAPDGTEFNKSFNPSLNPSYQKRENLRYMPSVG

>EXB58750.1 Tabersonine 16-O-methyltransferase [Morus notabilis]

MDYFSEDVMSSSELLQAHSLLWSNSVHIVRNLSLKCVIELGIPDIIHKHGQPITLSKLISALPIHPSKAHCIYRIMRILVHSGFFSALKVNGEEEESLSLTNVSRLLLSDGPASIKMKSFFLFHLLPEVVAPLHSLSTWLQQSDGKTFEHGNGKNFWDFLADEPKHIHLFNEAMANDSQLIAKVILTEYKNVFEGLETLVDVGGGTGTMAKAITSSFPHIKCTVFDLPHVVANLEGTDNLNFIGGNMFTDTIPPTDGILLKVRVYSTII

>EXB67902.1 8-hydroxyquercetin 8-O-methyltransferase [Morus notabilis]

MSLKCAIQLGIPDAIYSHGKPMTLSQLISAFPIHQNKKPDSHLIYRLMRILVNSGFFALQEVVVGKTDLLEEGYVLTNASKLLLRDNPLSVTPFLLLGNLFNEAMASDARLVTSVVIDKCKSVFEGLESLVDLAGGTGTVAKAIADAFPHVACTVFDLPHVIADLQGSKNLKFVGGDMFDKIPPADAIFMKWILHDWSDEDCVKLLERCKVAITCKGNEKGKVILVDIVIVEDQNNKDIGYDNHAHDHDHQSYETQLFFDMLMMVLVRGRERKETEWAKLFLDAGFSTYKITPILGVKSLIEVFP

>EXB67905.1 8-hydroxyquercetin 8-O-methyltransferase [Morus notabilis]

MEKVVRNSGHDLEIHSTELVKAQAHIWNYIFNFINSMSLKCAVQLGIPDAIHSHGKPMTLSQLISALPIHQNKKSDSRLIYRLMRILVNSGFFVLQEVVVGETDLLEEGYVLTTASKLLLRDNPLSVTPLLLSMLDPIMTKPWHSLSTWLQSDDPTPFAATHGMGIWDYNEYDPRLGNLFNEAMASDARLVTSVLIDKCKSVLEGLESLVDLAGGTGTVAKAIAYAFPHLACTVFDLPHVIADLQGSKNLKFVGGDMFDEIPPADAIFMKWILHDWSDEDCVKLLERCKVAITCKGNKNGKVILVDMVIVEEQNNKDIGHDHHAHDHDHQSYETQLFFDMLMMVLYPGRERKETEWAKLFSDAGFNTYKITPILGVRSLIEVFP

>EXB68019.1 8-hydroxyquercetin 8-O-methyltransferase [Morus notabilis]

MPDWSDEDCVKLLEGCKKAITCKGNFKKRNKVIIVDMIVMENQKSKDIIDHVHDDRSYETLLFFDMIEMIFLPGTRDRTEKEWAKLFSNAGFTTYKITPLSGVRSLIEVFP

>EXB75147.1 (RS)-norcoclaurine 6-O-methyltransferase [Morus notabilis]

MEGIDHHVDEMQRGQADIWQVMYSHMDSLVLKCAVELRIADIIHSHGCPVTLSQIASSISGSTSPNIHYLERILRLLVCKKIFTAHRDDHDSSSGDHPHHHQTRYGLTEKSRWILWESEPSLAPVIMMQNRRLVIDAFDHLSDSVRHGVVPYKAAFGHDFVGESTVDPKSKKWFKDGMINLANMVMDPVLSALKNEFSCMGSLIDVGGFTGETIYEIVKAHPHIKGFNFDLPDIIAMAPSYDGVTHVAGDMFEAIPCADAIFMKKVLNNWTDEQCIKILRNCRQSIPEKTGKVIIVDIVLESLESNDVVFLYDEMRIRFDLGLLAFRGVGRERTELEWKKLLEEAGFPRNKIIRIPAMPSIIEAYPV

>EXB75933.1 Caffeic acid 3-O-methyltransferase [Morus notabilis]

MEDESSEKRNQARLKVLELANMISVPMSLNAVVRLGVPDAIWQSGSNSPLSASQILTRVLPSSSSSAASADPDNLQRLLRTLTSYGVFSEHISGEIRKYSLTDVGKTLVTDSDGLSYAPYVLQHHQDALMRAWSLLHEAVVDPTTEPFAKANGEPAYKYYGKMPEMNGLMQRAMSGVSVPFMKAILNGYDGFEGVRRLVDVGGSAGDCLRMILQKYPNVTEAINFDLPEVVARAPHVPGVTHVGGDMFKLIPEADAIFMKWILTTWTDDECQAIMESCCKAVPGGGKLIACEPVLPKETDDSHRTRALLSGDIFVMTIYRAKGKHRTEDEYRKLGLAAGFPHFQAFYIDYFHTVLEFTK

>EXB83827.1 Anthranilate N-methyltransferase [Morus notabilis]

MENNPNVLNDVYRREEEENYSFAMQLATAPALSMSLHAAIELGVFDIIAKAGEGAKLSPAEIVEQLAANNPEAPIMLDRILRMLASHSILSCSVVGDGSSEPKFRRLYGLRPVSKYFVTNEYDGSFGPMLALVHDKILMDSWFQLKDAILEGGVPFKRVHGTHSFEYLGLDQRLNQLFNKAMDNASTIIVKKLLKYYKGFNHLQKLVDVGGGLGVTLNLITSKFPHVKGINFDLPHVVEHAPSYPGVEHVGGDMFDKVPIGDAILLKSVLHDWNDEHCLKLLKNCSEAIPTNGKVIVVDVIFPVKPETSSHAKSNSQLDVLVMAEHQLGAKERSREEFLALATGAGFREIKFEYFMGDYWIMEFFK

>EXB93812.1 3'-hydroxy-N-methyl-(S)-coclaurine 4'-O-methyltransferase [Morus notabilis]

MEEIQRDELIKWGIPEEEIEEEERAKVEIWKYIFGFVEMAVVKCAIELGIADVIATHGRPMTLLELSSALDCDPQNLHRIMRFLVNRAIFKEILIRNDAVPTAYYAQTPISRRLMRTGENSMAAFILLESSPPMLAPWHGLSARVMARGTSAFEAAHGEDIWKYAEANPGHARLIDEAMACDARVAVPAIIDGCSDVFDGVRTLVDVGGGNGTALRMLVKGCPWISKGINFDLPHVASVAEKCEGIEHVGGLEVFGRKCTASRKDFVVHFEDEWCSLDNAIKEIQHGGNNVKEEVFECISPIGVSNSLELSELFIVWWVLHDWADDECIHILKKCRAAIPKDIGKVIIAEAVIGNKEQQKEDNKLKDVGLVLDMVMMAHTTKGKERTLDEWAYVIREAGFSRHTVRSIAAVQSVIEAFPA

>EXB94570.1 3'-hydroxy-N-methyl-(S)-coclaurine 4'-O-methyltransferase [Morus notabilis]

MGEAQRNHDHLTCGLSKEEKEEEEERARVDISKYIFGFVEMDVVKRSIELGIADAIANHGRPMTLLGLSSSLDCDPQNLQRIMRFSVNRGIFKEMTRNDAVPAAYYSQTAISRRLRRTGEDSMAALILLHSSPPMLAPWQGLRACVMAKGSSAFEAAHGGDVWRYAEVNPAHGRLINGTMACGARATVPEIINGCSDVFDRVETLVDVGGGNGTTLRMLVKACPWISKGITFDLHHVVSIAEELEWSRQVSSPSPIDAVSLVDSSASQFQFIFSIKYCTRIRRRDDRGANFNLNIVHVYGDATIVE

>EXB94571.1 3'-hydroxy-N-methyl-(S)-coclaurine 4'-O-methyltransferase [Morus notabilis]

MEETQRDHLTWGLLEEEREEEKQKKFDMSKYYFGGDVEMAVVKCAIDLGMADAIANHGRPMTLLELSSALDCDLQNLHRVMRFLVNHGIFKEIIIRNEDTVPTAYYAQTHSSRRLMRTGENSMAAFILMQSSPPAKAAWHCLSACVKGKATSAFEVVHGEDVWKHAEANPAQSQLINEAMACLARVIVSAIIDGCLDMFEGVETLVDVGGGTGTIMRRLVKACPWISKGITFDLPHVVSLAEQCEGIEYVGGDMFEFIPKADAVLLVAVLHDWGDDECIRILKKCRKAIPKDKGKVIIVEVVIGNKEQQKEDNKLNDVGLVLDMAMMALTHKGKERTLDEWAYVLREAGFSRHTVRSIAAIQSVIEAFPA

>EXB95356.1 3'-hydroxy-N-methyl-(S)-coclaurine 4'-O-methyltransferase [Morus notabilis]

MKETQRDHLTWEEREEEKHEKVDMSKYYFGGVVEMAVVKCAIELGMADAIANHGRPMTLLELSSALDCDLQNLHRVMRFLVNHGIFKEIIIRNEDTVPTAYYAQTPSSRRLMRTGENSMAALILMQSSPPAMATWHCLSACVKGKATSAFEVVHGEDVWKYAEANPAHGQLINEAMACKARVMASAIIDGCLDVFEGVETLVDVGGGTGTIMRRLVKACPWISKGITFDLPHVVSLAEQCEGIEYVGGDMFEFIPKADAVLLVTVLHDWGDDECIRILKKCREAIPKDKGKVIIVEAVIGNKEQQKEDNKLNDVGLVLDMVMMAHTYKGKERTLDEWAYVLREAGFSRHTVRSIAAIQSVIEAFPA

>EXC02140.1 Caffeic acid 3-O-methyltransferase [Morus notabilis]

MAPLMFLMQDKVYMDIWHHVKDAVMEGGHPYERAHGMNMVEYVRKDDRFGELFKCSMKEFNPILMKRILEIYQCFEGIEHCAGDMFVAIPKGDAIFMKWMLHAWDDENSLVILQNC

>EXC13656.1 Caffeic acid 3-O-methyltransferase [Morus notabilis]

MASSLKLANGGPKVLCHDRKEEEEAFSQAMCLVMSSGMPVCLKTAFELRVFDIIAKAGEGAKLSSAEIVAQMPTNNPDAATMLDRILRLLASHSVLSCSVVSDDNGCNVQRLYGLSPVSKYFVTNEDGVSLGHFIAMVQDKVFVDTWPQLKASILEGGNAFNITYGMHAFEYIGTDLRFNKVFSKAMHSHSTVVMKSILEHYKGFENIKQLVDVGGGLGVTLNQITSKYPHIKGINFDLPHVVENAPSYPGVEHVGGDMFQNVPCGDAIFMKWILHDWTDEHCLKLLKNCYKAISNDAKVIVVDSILPIMPETNFAVKSVEHVGGDMFQNVPCGDAIFMKWILHDWTDEHCLKLLKNCYKAISNDAKVIVVDSILPIMPETNLRASWHLIRACWLHIQGERSGANKSS

>EXC13658.1 Caffeic acid 3-O-methyltransferase [Morus notabilis]

MASSLKLANGGPKVLCHDRKEEEEAFSQAMCLVMSSGMPVCLKTAFELRVFDIIAKAGEGAKLSSAEIVAQMPTNNPDAATMLDRILRLLASHSVLSCSVVSDDNGSNVQRLYGLSPVSKYFVTNEDGVSLGHFIAMVQDKVFVDTWPQLKASILEGGNAFNITYGMHAFEYIGTDLRFNKVFSKAMHSHSTVVMKSILEHYKGFENIKQLVDVGGGLGVTLNQITSKYPHIKGINFDLPHVVQNAPSYPGVEHVGGDMFQNVPCGDAIFMKWILHDWTDEHCLKLLKNCYKAISNDAKVIVVDSILPIMPETNFAVERLGI

>EXC13660.1 Caffeic acid 3-O-methyltransferase [Morus notabilis]

MASPLELGNTRKVVDDQRKEEEQEEHFFSYAMQLATSTVLSMSLQSAFELGVFDIIAKAGEGAKLSSVEIAAHLPTTNPEAPIMLDRILRLLASHSVLNCSLDGDNGDIGSNFQWLYSLSPVSKYFVTNEDGVSLGPFVALVQDKVSFESWPQLKNAVLEGGIPFNKVHGMHAFEYTGVDSRFNSVFNAAMYNHTTIVIKSILNLYKGFEHLKQLVDVGGSLGVTLNQIISKYPHIKGINFDLPHVIGQAPSYPGVEHVGGDMFESVPCGDAIFMKWILHDWTDEHCLKLLKNCYEAIPDDGKVIVVEAILPVSGTSSAAKTAFQFDVGMMTQNPGGKERSQQEFVALAVGAGFSGIRFECFVTNYWVMEFFK

>EXC22153.1 Tabersonine 16-O-methyltransferase [Morus notabilis]

MAFSEEVMSSSELLQAHSLLWSTSVNYAKYVTVKCAIELGIPDIIHKHGKPITLSKLINALPIHPSKTHCICRIMRILVHSGFFSTGRQVEEEEEEEEESYSLTNASRLLLSEGSDFTKMKSFVLFHLLPEAAAPWHSMSTWLQSSDGSTFEHQKGKTFWDCLADEPSQNRLFNEAMANDSQLIAKLTLTECKDVFEGLTTLVDVGGGTGTMAKAIASTFPHIKCTVFDLPQVVANLEGNDNLNFIGGNMFSDTIPTADAILLKWILHDWNDEESLAILKKCREAILKNEKGGKVIVIETVIDSKNTDEITGIQLCNDMIMMVSFSGKERNLREWEKLFFSAGFSHYKINRKLGVRSLIELYP

>EXC27579.1 8-hydroxyquercetin 8-O-methyltransferase [Morus notabilis]

MEKVRSSGHDLQVGATEQLKAQAHIWNQIFNFINSMSLKCAIQLGIPDAIHSHGKPMTLSQLISALPIHQNKKLDSHLIYRLMRILVNSSFFSLQEVVGETDQLEDGYVLTNSSKLLVRDNPFSLTPILLTVLDPIMTKPWHSISTWLQSDDPTPFATTHGMEFWDYTVRDPRFGNVFNEAMASDARLVVSVLFDKRISVFEGLESLVDLAGGTGTVGKAIADAFPHVECTVFDLPHVIADLQGSTNLKFVGGDMFDEIPPADAIFMKWILHDWSDEDCVKLLKRCKVAITCKGNKNGKVILVDMVIVEKQNNKDIGHDHDHQLYETQILFDMLMMVSFPGRERKETEWAKLFSDAGFSTYKITPILGVRSLIEVFP

>EXC27580.1 8-hydroxyquercetin 8-O-methyltransferase [Morus notabilis]

MEKVVRSSGHDLEINATELVKSQAHIWNQIFNFINSMSLKCAIQLGIPDAIYSHGKPMILSQLISSLPIHQNKRPDSRLIYRLMRILVNSGFFALEEVVVGETNLLEEGYVLTNASKLLLRDNPLSVTPFLLSMLDPIMTKPWHSISTWLQSDDPTPFATTHGKEFWDYNEYDPRLGNLFNEAMASDARLVTSVVIEKCKSMFEGLESLVDLAGGTGTVAKAIAYAFPHLACTVFDLPHVIADLQGSKNLKFVGGDMFDEIPPADAIFVKWILHDWSDEDCVKLLERCKVAITCKGNKNGKVILVDMVIVEEQNNKDIGHDHHAHDHDHQSYETQLFFDMLMMVLLSGRERKETEWAKLFFDAGFSTYKITPILGVRSLIEVFP

>EXC30549.1 Tabersonine 16-O-methyltransferase [Morus notabilis]

MLSFISSMSIKSAVQLSIPDIINNDGQPITLSELASALDIHPTKAGFIHRLMCLLVHHGFFNSAKIGHDEEAYDLTPSSRLLKDKIPSLSPFVMSLLDPALITPWHLLGNWFQKEEKMPPFESAHGMSFWAYVNKNSDFNNHFNQAMAIDSGMMNLVVKDCKPVFEGLSSLVDVGGGTGTISKIIIETFPHIKCTVLDLPHVVANLPATENLKFIGGDMFQGIPSADAILLKLMLHCWSDEECLKVLKICRVAIPSNGGKVIITDIVINKDKDDPELTEGKLYFDLLMMILVTGRERSEKDWEKLFLEAGFSHYKITPLFGLRSLIEVFPRKQLSSNESVHLRTSLISMVARNSMQLFVFLPYVYELLK

>EXC30550.1 6a-hydroxymaackiain methyltransferase 1 [Morus notabilis]

MDLLQGQGSNELFQAQSHLYSHIFRFISSMSLKCAVQLGIPDIISNHGQPITLSELVSALDIHPTKAGFIYRLMRLLVHDGFFTSTKIGENEEEEEEEASYDLTPSSRLLLKDKIPSLSPFLVAMLEPAITTPWHSLGNWFQREEDMTPFESAHGISFWAYGNKNSEFGNLFNQAMASDSGMMNLVVKDCKLLFEGLSSLVDVGGGTGTVSKIITEAFPHLICTVLDLPHVVANLPDTENLKFVGGDMFQDIPSADAIFLKWLVHAWSDEEGLKVLKKCREAIPSNGRLHAWSDEECLKVLKKCREAIPSNGRGKVIIIDIVINKEKDERELTQGKLYFDLLMMVAVSGRERSKKEWEKLFLEAGFSHFKITPLFGLRVKNWTEIGDEVEISSGPSRPDTGVIVGMGLM

>EXC30551.1 Chavicol O-methyltransferase [Morus notabilis]

MLDPILFAPCHVLTKRLQDDTAVTSFDSFHGLNISDYIKKSFEFEDLIDSAMDSDSSKMNLAIKDLKKVFDGVTSLVDARGKRSVFCSIIIDAFLYMQCTVLDLPHVVANLEPIQGNHGKKVIIIDIVMSENDGTELMETKLYYDIMAMMLMNGKERSERDWQKLIAKAGFSLCEITVKVRIRSLPRFFLDGEGAWLDWQRTVCRVGPTRCLKSTLSMCFWLYVVYCVPCIPVCGDWIGSGICFMNLEL

>EXC32921.1 Caffeic acid 3-O-methyltransferase [Morus notabilis]

MASPLELGNDRKFLDSEGRNKEEEDKENFSYAMQLVFSTVLSMSLQTAIELGVFDIIAKAGEGAKLSPAEITAQMTTDNPEAPIMLDRILRVLASHSILRCSVVGDVNSESDFQRLYSLGPVAKYFATNEDGVSLGPLMALIQDKIFLDSWPQLKEAVLKGGIAFNRVYGTHAFEYPGLDPRFNHVFNKAMYNQTTIVIKNILKFYKGFKDLAKLVDVGGGLGVTLNLITSKYPHIKGINFDLPHVIEHAPSYPGVEHVGGDMFEKVPTGDAIFMKWILHDWSDEHCLKLLKNCYKATPENGKVIVVESVLPVEAETNTAVKSTSQLDVLMMTQNPGGKERSTQQFLALATDAGFRGIKFEYFICNFWVMEFFK

>EXC61661.1 (RS)-norcoclaurine 6-O-methyltransferase [Morus notabilis]

MQKVLNNWTDEQCIKILRNCRQSIPEKTGKVIIVDIVLESLESNDVVFLYDEMRIRFDLGLLAFRGVGRERTELEWKKLLEEAGFPRNKIIRIPAMPSIIEAYPV

>MD00G1100700

MKNAIIEGGIPFEMAHGSHAFKYVGYDQRFNQAFNIGMNSITTMLVKKILEVYMGFENLKKVVDVGGGLGVAISLITTTYPHIKGINYDLPHVVKDAPKYPGVEHVGGDMFASILDADVVFMKGILHDWFDEDSIKLLKICYKALPVDGKVIVVDAVLPSIPDSKSITKSNYLLDVHMMVQTPGGKQRSAEEFMDLATAADFSAIKLACFAAHLGVVEFYK

>MD01G1048300

MPFWELSAKKQTFGDLFNEAMEANSKLIARVAVEECGGVFEGSKSLVDVEGGTGTMAKAIAYGFPNINCTVFDQPHVVADLEGTAHNLGFVGGDMFDKIAPANAILLKIKYLHLILDYWNDEESMKILNKCRESKLLSKNEGRKKIIIIDIVVGYNKKSIETQLMFDMLMMSIVTSKERSKS

>MD01G1048400

MGLNNGEVGAISHELLGAQAHVWNHMFQFINSMSLKCAVQLGIPDVIHNHGQPISLSELVARLNIHPSKAHFMSRLMRILVHSDFFAQHDHVHHDRDDAEEEVAVVLYSLTPASGLFLKDGPLNTTPFLLMILDQVITDPFHSMGNWLQMNCGDDLVPCTPFEVANGMPFWELSAKKPRFGDLFNEAMEADSKLIAGVVVEECGGVFEGLKSLVDVGGGTGTMAKAIANAFPNINCTVFDQPHVVADLEGMTHNLGFVGGDMFEEIPPANAILLKWILHDWNDEESVKILKKCREAIFLNKNEGRKKKIIIIDIVVGYADNKTKVDKKSIETQLMFDMLMMSTITGKERSESEWEKIFLAAGFSHYNITHMLGLRSLIEVYP

>MD01G1051800

MGLSNGEVGATSHELLGAQAQIWNHMFQFINSMALKCAVQLGIPDVIHNHGQPISLSELIAALNVHPSRAHFVSRLMRILVHSDFFAQHHHVHRGCDDMEEEEAVVLYSLTPTSRLLLKDGPSNTTPLILMILDPVLTTPFHLMGAWLQMNGGDDPATICTPFKMENGMPFWDLAAQEPRFGNLFDEAMEADSKLLGREVVEECGGVFEGLKSLVDVGGGTGTMAKAIANAFPSINCIVFDQPHVVANLLGSTHNLGFVGGDMFVEIPPANAILLKWILHDWSDEESVKILKKCREAILLSKNDEGNKKIIIIDIVVGHVDKKEKMVDKKSIETQLMFDMLMMSTVTGKERSESEWKKIFLAAGFTHYNITHTFGFRSLIELYP

>MD01G1051900

MSLSNEVGATSHELLGAQAQLWNHIFQFINSMSLKCAVQLGIADVIHNHGQPISLSELMAGLKVHPSKAHFVSRLMRILVHSNFFAQHHHVHHDRADVEEEETVVLYSLTPASRLLLKDGSLNTTPFLLMILDPVVTTPFHLMGAWLKINGGDDPAATCTPFEMENGMPFWELGAREPRFGNLFNEAMEADSKLIGRVVVEECGGVFEGLKSLMDVGGGSGTMAKAIANAFPNINCTVFDQPHVVAGLQGTTHNLGFMGGDMFEEIPPADAILLKWIMHDWNDEESVTILKKCREAISLSKNEGGNKKIIIIDIVVGYVDNKKKMMDKKSIETQLMFDMLMMSILPGKERSKSEWEKIFFAAGFTHYNITHTLGFRSLIEVYP

>MD01G1089600

MALQLEEEENFCYAMQLVFSSVLSMSMQSAIELGIFDIIAKAGPGAKLSSSEIAAHIGSGTRNSEAPMMLDRILRLLASHSILSCSAVANEEDGSDSQRLYSLGPVSNYFVTNEDGVSLGPLMALIQDKVFLDSWSQLKDAVVEGGIPFNKVHGTHAFEYPGLDARFNQVFNTAMFNHTTIVMKKILHLYKGFEKLTQLVDVGGGLGVTLSLITSKHPHIKGINYDLPHVVKHAPSYPGVEHVGGDMFASVPSGDAIFMKWILHDWSDQHCLKLLKICYNAIPEDGKVIIVEAVLPVMSETSTAVKSTSQIDVLMMTQNPGGKERSREEFMALATGAGFSGIKYECFVCNFWVMEIFK

>MD01G1089800

MFNHSTIVMKRILKLYKGFEHVTQLVDIGGNLGGAISLITSKYPHIKGINFDLPHVIKHASSYPGVENVGGDMFESIPNGDAIFLKFILHDWLDKDCIKLLKNCYNAIPDNGKVIVVEALLPIKPDSNLSVRTNGQLDLHMMTQTPGGMERSQEEFMALATASGFSGIRYECFTANLWIMEFYK

>MD01G1090400

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>MD01G1090500

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>Mapoly0136s0036|Mapoly0136s0036.1

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>Mapoly0337s0001|Mapoly0337s0001.1

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>Mapoly0003s0058|Mapoly0003s0058.1

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>Mapoly0055s0090|Mapoly0055s0090.1

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>Mapoly0055s0089|Mapoly0055s0089.1

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>Mapoly0013s0033|Mapoly0013s0033.1

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>Mapoly0044s0122|Mapoly0044s0122.1

MSSVWQKEDSSWADPSLLVGLPMAVRAALMLNVPKIIDSAYPKLSLSAEEICKHVPTTREHTPKSENLEKILDWLCCNGIFSLIIEEGDDGSKAKRYAHSPKSRCLSRDHTADMLLMYTSPELTRVWPHAHEIVLSPDVSPFEIVTGKNMYTYLAVDAPQVQKLYVRGLNATAIPSLSLLEKYDETFKALKGRVVDVGGQEGTMCAGLVAKYPHLQFVNFDQPEVVRGAPQIPGVEHVGGSFKESVPEGNLLIMKFCLLNWDDETCIGILTNCRKALPVAEGGKMLILERLDRSTEATDAHNEVARTGSLWSNFHGTVLLSGARTRTVEQFRRLALAAGFSQLEFVNHCPGFDLLEASLSPSGHSQ\*

>Mapoly0044s0123|Mapoly0044s0123.1

MSSVSQKEDASWADPSLLVGLPMAVRAALMLNVPKIIDSAHPKLSLSAEEICKHVPTTREQIPKAENLEKILDWLCCNGIFSLIIEEGDDGSKVKRYAHSPKSRCLSRDHTADMLLMYTSPELTRVWPHAHEIVLSPDVSPFELVTGKNIYTYFAVDAPQVQELYVRGLNGTAGPSLSLLEMYDETFKALKGRVVDVGGQEGTICAGLVAKYPHLQFVNFDLLEVVRGAPQIPGVEHVGGSFKESVPDGNLLIMKFCLLNWDDETCIGILTNCRKALPVAEGGKMLILERLDRSTEATDAHNEVARTGSLWSNFQSTVMLSGARTRTVEQLRSLALAAGFSQLEFVNHCPGFDLLEASLSPSGHSQ\*

>Mapoly0044s0121|Mapoly0044s0121.1

MSSVSQKEDASWADPSLLVGLPMAVRAALMLNVPKIIDSAHPKLSLSAEEICKHVSTTREHTPKSENLEKILDWLCCNGIFSLIIEEGDDGSKVKRYAHSPKSRCLSRDQTADMLLLYTCPELTRVWPHAHEIVLSPDVSPFELVTGKNIYTYLAVDAPHVQELFVRGLNRTAGPALGLLEKYDETFKALKGRVVDVGGQEGTMCAGLVAKYPHLQFVNFDLPEVVKGAPQIPGVEHVGGSFKESVPDGNLLIMKFCLPNWDDETCIGILTNCRKALPVAEGGKMLIMEPLDRSTEATDAHNEVARRGSLCTNFQSTVMFSGARTRTVEQLRSLALAAGFSQLEFVNNFTGFDLLEASLSPSGHSQ\*

>Mapoly0681s0001|Mapoly0681s0001.1

MELDSMTKGKLSNKEMPEIRTIYKAFDFATSFALKSTMTMGIPDVLARSKEPMTADNIVEKLPCKNPAAAAGYLDRIMDILIVPGFYSKTPVSNADGKSHKAAYGLTPVSRMLVKDDVEFTLLPIALLHVHRVFTDSFQHLHKSVLEDRAPMEVALGKPFYEYFAENQELRSTFQEALSCHSNYWIKIIAQEYDGFDHTKTLVDVGGCDGESLKELVAVHPHIHGINFDLPAVIQNAPQIPGVDHVGGDYFASVPAGDTIFLKLVLHNNGDEECLKILKNCYQALPERGGKVVIGESVYDHDSKEDEAQFVKHLDVMMLSVFLNGRERSFDAYKALLTSCGFGDCKLIKLSGSVALIEAYKY\*

>Mapoly1374s0001|Mapoly1374s0001.1

MIEPTPQSLIDLDWVATSDLNHIKVIASSQNPKENYSWPDYKRSPLILGIPDILPMSKEPMTAENIVKKLPCKNPAAAAGYMKRIMDILIIPSKPLDSTEDENLMKLAPVSRLLVKDDHRFTALPLALMHLYLFFIVGLVASRICIRLCWKIDRRCHELPLKVLKKVIAHEYNGFKITKTLVDVGGDEGEAIRELVAAHPHIHGINFDLPDVIKNAPPIPGVDHVGSNFFQSIPSEKPSFECWRFPHSSPIC\*

>Mapoly0015s0026|Mapoly0015s0026.1

MSPQQNFGDDEAGMLQALQMSVMVTLPFTLKAAINLGVPKILMDAGPGAELTAEEIATSIAKVSDCRADSKNLDRILRILASHNVVTEIVSKDANDSDSAQRSCGPTSTLKYFTDNEDGVSLVPFVFMHIDPVFLASYQNLHLPVLDVNVEPHTLDHGMNLFEYIATDAKLDKLFNKAMHDHSNIKMSALLKTYRGFETLTSLVDVGGGLGSTLAMILSKYPNLRGINFDQPHVVANGLQVPNLEHVGGDFFASVPEADAVFMKWILHDWDDERCVKILKNVWRALPPHGKVINLDALMSDISDPSPATKISLYMDMIMMACTPSGRERTLSQFKKLAADAGFKRVELVAKTSHMSILEFYKN\*

>Mapoly0015s0025|Mapoly0015s0025.1

MSPQQNLGDDEAGRLKALQIAMMLALPFSLKAAVNLGVPKILVDAGSGADLTAEDIATSIAKLLDRCADATNLDRILRVLASHNVLTEIVSKNGNDSDCPQRSYGPTSTLKYFTDNEDGVSLAPFLLMATDTVILPTFQYLHLPVLDYAATDARFDKLFNKAMHDHTHIEMSALLKKYRGFETLTSLVDVGGGLGATLAMILSKYPKIRGINFDQPHVVADGLQVPNLELVGGDFFASVPEADAVFMKWILHDWDDEQCVKILKNVWRALPPHGKVINLDYVLSDNSDPSPATKISLCTDISMMAVNSNGRERTLAQFKRLAADAGFRRIECVAQIDDLSLLEFYKN\*

>Mapoly0015s0023|Mapoly0015s0023.1

MSQQQNLGDDEAERLKALELVMMLALPFSLKAAVNLGVPKILLDAGSGAELTAEDIATKLSDRCPDATNLDRILRVLASNNIVTEIVSKNGNDSDCPQRSYGSTSTLKYFTDNEDGVSIAPFLLLCTDPVFVPTFQYLHMPVLDENVEPHVLVHGMKSFEYAATDTRFDKLFNKAMHDHTHIEISALLKKYRGFETLTSLVDVGGGLGATLAMILSKYPKIRGINFDQPHVVAEGLQVPNLEHVGGDFFASVPEADAVFMKWILHDWDDERCVKILKNVWRALPPHGKVINLDYVLSDNSDPSPVTKISLCMDISMMAINSNGRERTLSQFKRLAADAGFKRVELVAQTDNLSLLEFYKN\*

>Mapoly0002s0063|Mapoly0002s0063.1

MTLQQNIGDDEAGRLQALQLAEIVALPLSLKAAVTLGVPKILVDTGPGAGLTVEEIAASISKLSDRCADPANLDRILRVLASHNVVTEIVSKIPNDSDSPQRRYGPTSTLKYFTDNEDGVSLAPLLLLLTDPIFLAPCQYLHLPVLDVKLEPHVVVHGMNCFDYCPTDARFQSVFDKAMHDHSHIEMTALLEKYRGFETLTSLVDVGGGLGASLAMILSKYPNLRGINFDQPHVVTDGLKVPNLEHVGGDFFASVPEADAAFMKWILHDWDDERCVKILQNIWRALPPHGKLLNLDSLLSDVSDPSPATKTSLYLDMFMLAVSPRGRERTLSQFKKLASDAGFKRVEVVAQVDNLSLLEFWKN\*

>Mapoly0002s0334|Mapoly0002s0334.1

MNCFEYCPTDARFQTVFDKAMHDHSHILMSALLEKYRGFETLTSLVDVGGGLGASLAMILSKYPNLRGINFDQPHVVADGLKVPNLEHVGGDFFASVPEADAAFMKWILHDWDDERCVKILENIWRALPPHGKLLNLDSLLSDISDPSPATKISLYADMIMLAVTPRGRERTLSQFKKLAAGAGFQKVEVVAQVDNLSLLEFCKN\*

>Mapoly0015s0024|Mapoly0015s0024.1

MSPQQNFGDDEAGMLQALQMSVMVTLPFTLKAAINLGVPKILVDAGPGAELTAEEIATSIAKVSNCCADPKNLDRILRVLASNNIVTEIVSKNGNDSDCTQRSYGPTSTLKYFTDNEDGVSLAPFLLLSTDPVFVPTFQNLHLPVLDVNAEPHTLDHGMNLFEYIATDAKLDKLFNKAMHDHSNIKISALLKNYRGFETLTSLVDVGGGLGATLAMILPKYPNLRGINFDQPHVVADGLQVPSTVVSPFLAHYILQTYSMHCYLQLYFHRNCGNTLFCFFAEFKQF\*

>Mapoly0040s0105|Mapoly0040s0105.1

MTAEECSGDEREGRLAALQLAGMCAVPLSLKAAILLGVPEILNEAGPDAKLTSEEISKLIVSPGGTSADAENLDRLLRVLACHNIVTETCVAACPSNPQATERRYGVTPVLKYLIASNETGMSLSPLFLLRTDSVYTSAFQYLHAPVLDRNAEPFVIANGKKIIDVLETDSRLSELFDTSMAHHTHMWVSMLLETYRGFEGLTSLVDVGGGVGANLAMILSRYPDLRGINFDLPHVVAKGIQSPRLEHVAGDFFQSVPRGDAVWMKWILHCWSDESCVKILKSVNRALPPRGKLINMDSVLPETSDSSVETQINVCADMLMMAANKGGKQRTLTQFRKLAQDAGFSSVHLVATVDTLSVLEFHKG\*

>Mapoly0002s0065|Mapoly0002s0065.1

MTLPENIGDDAAGRLQALQLTDIVALPFCVKAAVLLGVPKILVDAGPGTGLTVEEIAAAISKLSNCCADPANLDRILRVLASFNVVTETLSKNVNDSDSPQRRYGSTSTLKYFTDNKDGVSMAPLLLMVTDPIFLAPYQCLHLPVLDAKSEPHVVVHGKNCFDYYATDARFQTVFDKAMHDHSHIAMSALLEKYRGFETLTSLVDVGGGLGASLAMILSKYPNLRGINFDQPHVVAEGLKVPNLEHVGGSFFESVPEADAVFMKWILHDWDDERCLKILENIYRALPPHGKLLNLDALLSDVSDPSPATKVSLCADIAMLACTPKGRERTLSEFKQLAADAGFKRVEVVAQVDHLSLLECYKN\*

>Sobic.001G354200.1 (SbASMT1)

MALVQESSQDLLQSYVELWHQSLCFAKSMALAVALDLRIPDAIHRHGDDGATLAQILAETALHPNKLRALRSLMRALTVFGTFSVQQPPTSVVVDASSGEAAVYRLTAASRFLVGDDEVSSSSTTLAPFVSLALHPIAVAPHTQGMCKWFRQEQNEPTAYALAFRQPTPTIWEHADDVNALLNKGMVADSRFLMPVVIRECGEVFRGIDSLVDVGGGHGGATATIAAAFPHIKCSVLDLAHVVAGAPSDVNVQFIAGNMFQSIPPATAVFLKTTLHDWSDDNCVKILKKCKQAISPRDAGGKVIILDMVVGYGEPNIKLLKTQVMFDLYIMTVNGAERDEQEWKKIFIEAGFKDYKILPVVGALSVIEVYP

>Sobic.001G354400.1 (SbASMT2)

MAPAEESSQDLLQAYVELWHQSLCFAKSMALAVALDLRIPDAIHRHGGGGATLTQILAETKLHPNKLRALRSLMRALTVLGTFSVQQPPPTIADASGEAVYRLTAASRFLVSDEVSSSTLAPFASLALHPIAVAPSTVGMCKWFRQEQNEPSAYALAFCQPTPTIWEHADDVNALLNKGMVADSRFLMPIMLRECGEVFRGIDSLVDVAGGHGGATATIAAAFPHIKCSVLDLPHVVAGAPSDVNVQFVAGNMFESIPPATAVFLKTTLHDWSDDNCVKILKKCRQAISPRIAGGKVIILDMVVGYGELNTKHLETQVMFDLYIMTVNGAERDEQEWKKIFTEAGFKDYKILPVLGALSVIEVYP

>Sobic.002G077700.1 (SbASMT3)

MAQSKSVPVPPTSTTTTTGAELLQQAEAELWCHNFGYLKSMALRCAIKLGIPNAIHRRGGAASLSHCRSCMPPSPSPKRPCLSRIITFLAATGIFREEEISADDGEAAAGPRYHLTAASRLLIVVDDDDDARGGGRGCVAQLFILCSSPSYFTASQHLPEWLQQEDGTTDDDGAPAAARTTPFTMAHGAGFYDVVRRDAAFGVVFDEAMGSDSRFVADIVVRECGEVFAGLTSLVDVGGNNGTTARAIAKAFPHVRCSVLELPRVVDAMPADATVEFVAGDMMKFIPPADAVLLKFTLHNWSDEDCVQILKRSKEAISTREPKGKVIIIDIVSGSPSNKRTLEAQLLMDLCMMVVLEGKERTEETWHKIFLDAGFTRYKVTPILGTTRSLIEVYP

>Sobic.002G079300.1 (SbASMT4)

MDVGGGDGTMAAAIAKAFPQIRCSVLELPHVVDAAPADCGVQFIAGDMMEFIPPADVLLLKWILHNWSDEDCVRILKRCKEVVSTREPKGKVVIIEVVVGSQSKQMLEAQFVSDLCMMLLTTGEERDRDKWQRIFQDAGFTQYKISPVLGFRSLIELYP

>Sobic.003G298500.1 (SbASMT5)

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>Sobic.004G128400.1 (SbASMT6)

MALSKEQSTGSDEQAVLDAQLQLWHHTVGYVKSMALKAALDLNIPNAIHLHGGSATLPQIVTKVTLHPSKIPCLRRLMRVLTFTGVFSVHDGDGGDEPVYGLTPASRLLIGSGMNLTPLLTLMLGAVFVSSFLDIGEWFRHEMPGPSPFEMANGRDIWDLCNHDAGFGKLFDDGMVADSDFIMDVVVKECSDVFQGISSLVDVAGGHGGAAQTIAKAFPHVECSVLDLSHVIASAPTNTNVKYIAGDMFESIPSANAVFLKWIMHDWGDAECVKILKNCKKTIASQGGGKVIILDMVVGTGSSSDEKHVETQILFDLLVMCIYTKGAERDELEWKKIIFEAGFSHYKIIPVLGTRSIIEVYP

>Sobic.004G341500.1 (SbASMT7)

MAFLGEYSSQELLQGQLLLWHQSLGFFKSLALAVAMDLRIADAIHRLGGAATLPQIIAEAGIKIDPRNNKLRDLRRVMRALTVSGIFTVQRPASAVVAAAADGGAEAEGPVYKLTAASRLLVVGEKKSSTTTTMPTPSLTVQVQLFLETCRGSAFSRGMRAWFRPQDEQHQHQEQPAGLSPFAMACGGQTIWERAERDADAFPFDDAMASDTAFLMPIVLRECGDEVFRGLTSLVDVAGGLGGAAANIAAAFPDLKCTVLDLPQVVAKAAAGSNEKVQYVGGDMFESIPPADAVLLKWILHDWSDDECVKILKKCKQAIPPRAAGGKVIIIDMVVGSADEPSPESDVRHVETQVLFDLLIMCINGVERDELEWKKIFSEAGFHDYRIIPVLGVRSIIELYPN

>Sobic.004G341600.1 (SbASMT8)

MAFLGEYSSQELLQGQLLLWHQSLSFFKPVALAVAKDLRIADAIHRLGGAATLPQIIAEAGINPCKLRALRRVMRVLTVSGIFTAVQQPATATAAAASGGGGTEGPVYKLTAASSLLVVGEKSSTAAAAATTKSQLPPSLSVQVQLFLDPCRGSAFSSGIRAWFRQDEHQQPAGLSPFALACDGQTIWERAERDADVFPFDDAMASDNAFLMPIVLKECGDVFRGLTSLVDVAGGLGGAASTIAAAFPDLKCTVLDLPQVIAKAPSAAGTSVQYVAGDMFQSIPPADAVFLKWILHDWNDDDCVKILKNCKQAIPPRDVGGKVIIIDMVVGSESSDNRHVETQVLFDLLVMTIDGAERDEQEWKKIFLEAGFEDYKIIPVLGVRSIIELYP

>Sobic.005G045600.1 (SbASMT9)

MGSITEQQQCTDQQGLLDAQLELWHSTFAFIKSMAFKSALQLGIADAIHCHGGTATLTQIATKAALHPSKTPCLRRLMRVLTVAGIFSIAAKTSSDDDDDDDGGDHVYGLTPASRLLVGSSQNLTPTLSLILDNVFVSPFLDLGTWFEHELPAADLPLFELSHGKNVWDVVGHDPSMSQLFNAGMVADTSFLMDIAIRECGGVVFQGISSLVDVGGGHGAAAQAISVAFPGIQCTVMDLAHVVATAPACAGLSFVAGDMFEAIPPANAVFLKWIMHDWSDTECVTILRNCKKAIPPRDAGGKVIIVDTVVGAGPPNLKNRETQVMSDIFFMIVNGTERDEQEWRKIIFEAGFSDYKIIPVLGVRSIIELYP

>Sobic.005G086600.1 (SbASMT10)

MALSSEDTRELLQAHVELWNQTYSFMKSVALAVALDLCIADAIHRCGGAATLSQILGEIGVRPCKLPALHRLMRVLTVSGTFTIVQPSAATMSLESDGNELVYKLTTASRLLVSSESSATASLSPMLNHVLSPFRDSPLSMGLTAWFRHDEDEQAPSPCPFTLMYGTTLWEVCSRDDAINALFNNAMAADSNFLMQIVLREFGKVFHGIDSLVDVGGGVGGATMAIATAFPSLKCTVLDLPHVVAKAPSSSIGNVQFVGGDMFESIPPANVVFLKWILHDWSNDECIKILKNCKQAIPSRDAGGKIIIIDVVVGSESSDTKLLETQVMYDLHLMKIGGVERDEQEWKKIFLEAGFKDYNIMPVLGLRSIIELYP

>Sobic.005G129100.1 (SbASMT11)

MAGAEDSTQDLLQAHLQLLHQSLGYISSTALAVALDHGIPDAIQHHGGSATLSQILAKIDVSPTKRRGLHRLMRMLTVTGAFSVDQRPAVAVAAAPHDGGRRGDPVYQLTAASRLLLSDDDDGIRHPASLTPLLTMLLGPLLASPLAAVVSALVREDRQPDLSAFGIAHGQTVWDDVADHEAAFNVSLHDAIAADTRFLMPIVLKECGEVFRGIDSLVDVGGGPYGSAAASIAAAFPRLKCSVLDLPHVVAQAPPDSSVQFVAGNMFECIPRANAVFLKWILHDWGDDECIKLLKRCKQAIPPRDAGGKVIIIDMVLGSGPADDVKHKETQVLFDLLMMALNGVERDEQEWKKIFLEAGFKDYKIIPVLGVRSIVELYP

>Sobic.005G216100.1 (SbASMT12)

MAFVHGEQEGEDMVGAFALVYQHVFSYIKTMALKCAVELAIPDAIHGRGGAATLAEIAADTGVHESRLADLRCLMKLLTTSGLFRATAADGGEEVASSYALTAASSLVVGPRGLSNMVRFDCGPVSLTPFFDMPTWLRTAPGPEAPKSLFELTHGRTRWDPANADNDTMIVSAFIESQLLIEAVLGGHADVFRGLTSLVDVGGGQGSFAKAIAAAFPGIKCAVMDLPHVVADAPVAAGGGDDVQFVAGDMFESIPPADAVLLKYVLHCWDDDNCVKILKNCKEAIPARDAGGKLVITEMVLGSGPRRDRNVAETEEMHSLFLTCITGVGREEHEWKKIFVDAGFSDYKITPVMGPLSVIEVYP

>Sobic.005G216200.1 (SbASMT13)

MAFVHGEQEGEDMVGAFALVYQHVFSYIKTMALKCAVELAIPDAIHGRGGAATLAEIAADTGVHESRLADLRCLMKLLTTSGLFRATAADGGEEVASSYALTAASSLVVGPRGLSNMVRFDCGPVSLTPFFDMPTWLRTAPGPEAPKSLFELTHGRTRWDPANADNDTMIVSAFIESQLLIEAVLGGHADVFRGLTSLVDVGGGQGSFAKAIAAAFPGIKCAVMDLPHVVADAPVAAGGGDDVQFVAGDMFESIPPADAVLLKYVLHCWDDDNCVKILKNCKEAIPARDAGGKLVITEMVLGSGPRRDRNVAETEEMHSLFLTCITGVGREEHEWKKIFVDAGFSDYKITPIMGPLSVIEVYP

>Sobic.006G007900.1 (SbASMT14)

MVLISEDSRELLQAHVELWNQTYSFMKSVALAVALDLHIADAIHRRGGAATLSQILGEIGVRPCKLPGLHRIMRVLTVSGTFTIVQPSAETMSSESDGREPVYKLTTASSLLVSSESSATASLSPMLNHVLSPFRDSPLSMGLTAWFRHDEDEQAPGMCPFTLMYGTTLWEVCRRDDAINALFNNAMAADSNFLMQILLKEFSEVFLGIDSLVDVAGGVGGATMAIAAAFPCLKCTVLDLPHVVAKAPSSSIGNVQFVGGDMFESIPPANVVLLKWILHDWSNDECIKILKNCKQAIPSRDAGGKIIIIDVVVGSDSSDTKLLETQVIYDLHLMKIGGVERDEQEWKKIFLEAGFKDYKIMPILGLRSIIELYP

>Sobic.006G008000.1 (SbASMT15)

MVHISEDSRELLQAHVELWNQTYSFMKSVALAVALDLHIADAIHRRGGAATLSQILGEIGVRPCKLPGLHRIMRVLTVSGTFTIIQPSAETMSSESDGREPVYKLTTASSLLVSSESSAAASLSPMLNHVLSPFRDSPLSMGLAAWFRHDEDEQAPGMCPFTLMYGTTLWEVCRRDDAINALFNNAMAADSNFLMQILLKEFSEVFHGIDSLVDVAGGVGGATMAIAAAFPCLKCTVLDLPHVVAKAPSSSIGNVQFVGGDMFESIPPANVVLLKWILHDWSNDECIKILMNCKQAIPSRDAGGKIIIIDVVVGSDSSDTKLLETQVIYDLHLMKIGGVERDEQEWKKIFLEAGFNDYKIIPILGLRSIIELYP

>Sobic.007G074800.1 (SbASMT16)

MALISEESKDLLQAQAELYNQVFSYMKSVALAVALDLRIADAIHHHGGAATIFQIAGEIGVNPCKIPRLRRLMRALTVAGIFTIQPSDEQTVKASSAGHEPAAVYKLTTASRILISKSSPSLFPTLSQQLNSFRDSVLSMGLSTWFRHDEQPGPCPFTLKQGITFWEKSERDHAANVSFNNSMAAHSRFLMQIVLKELSNIFHGMGSLVDVGGGAGGASISIAAAFPCMKKCSVLDLPHVVAKAPSAASVSNNVQFVAGDMFRSIPPANAVFLKWILHDWGDDECIKILKNCKQAIPSRDAGGKAIIIDIVVGSKPSDTKLLETQVLCDLNMMKIGGAERDEQEWKKLFLEAGFKDYNIMPVLGLWSIIEVYP

>Sobic.007G170500.1 (SbASMT17)

MTLRLLAEVSPQDLLVALSELQTHVLSYIKSMALKCAVDLSIHDTIHRHGGAATLADIAADAKIHPAKVPDLQRVMELLAATGIFTATASKKDDGSAETVYGLTTACRFLVGHRNLSPMVPFLVSPLVVSSFFSLSDWLRKEPAAAGAGGAGSLFELAHGCSHREMAKQDAAFSSVVNDSMAADSQLFLEVVIMDKGRIFRGLSSLVDVGGGHGAAAQVIARAFPRIKCMVLDLPHVVNEATASDGNMHFIAGDMFESIPPADAVLLKNILHEWGDENCVKILQRCKQAIPSRTAGGKVIIIEMVRGSSQGDSKINEMEVIRNMFMLCINGVERDINEWKKIFSDAGFSDDYKIMPVLGPFSVIEIYP

>Sobic.008G013900.1 (SbASMT18)

MHQAAPPPRRRLTCRRCSASWRALARPSPPSSAWKSGSDFRDGGATTLFEMALGVPPWTLTKNDDAYNRAMNEACVVDTTMSMDIMLKDTSSSIFSGLTSLVDVGGGHGAAAMAIATAFPHIKCSVLDLEQVIIKVPQQAGTDHIHSTVQFIAGDMFESIPPTDAVFLKHVLDCWDDDHCVKILQQCKRAIPARDAGGKVIIMNVVIGYGSLDKIVKEAQVLFDMYMMRYGGSEREEHEWRKIFSKAGFSDYKITPILGFHSIIEVFP

>Sobic.008G014000.1 (SbASMT19)

MSPPSAHAEQQEPDAHNHLLHQTYVELYHHGLHHIKSSALLCAVGLGIPGAIRGGAATISDLVTDTGVRPAKRSHLRRLMRMLTCFGIFGAASEQREGSAATDDGESETVIYTLTPVSSVLVGDKDASGAAAAASPSLDMSALLRLVARPSTSVSTFFSLEEWFRDGGGATTLFEMALGVPPWTLTKNDAAYNRAMNEGCVADTSLAMDVMLKDTCRGASSIFSGLTSLVDVGGGHGAAAMAIATAFPHIKCSVLDLEQVIIKVPTTDLIHSTVKFIAGDMFESIPPADAVFLKHVLHCWDDDHCVKILRQCKRAIPSRDAGGKVIIMSIVVGYGTLDKVVKETQVLFDMYMMRYGGSEREEHEWRKIFSKAGFSDYKITPILGFHSIIEVFP

>Sobic.009G197000.1 (SbASMT20)

MALTTSTNQALLDAQLELWNTTFSHIKSMALKSALDLRIADAIHNHAGAATVPDIVATVKLHPSKIPCFRRLMRVLAATGVLSAGNPSGSSTELVYALTPLSRLLVGSHNLVPITAMILHPSFVSPFLELGTWFQQELPGPCVFKQTHGQTVWEQAARDASFDALVNDGMVSDSHFIMDIVFEECADAFQGISSLVDVGGGLGAAAQAISKAFPDVKCSVLDLDHVVAKAPSGTDVQYIAGDMFESVPPANAMFFKWVLHDWSHEECVKILKNCKKAIPPKEEGGKVIIIDIVIGEESSNLKHKETQALFDLYIMLVNGIERDEQEWKKIFFEAGFSDYKILPVLGARSIISVYP

>Sobic.009G197400.1 (SbASMT21)

MALTTSTNNQALLDAQLELWHTTFAYMKSMALKSALDLGIADAIHSHGGNATLPQIVSRATPTLHPSKIPCLRRLMRVLTATGIFSAAHHDDAGGGGELVYGLTPASQLLVGGSSSLTPFMSLALHGIFVSPFLGLGTWFQQEHSDPSLFEMTHGQTAWDLNDHNPAFGKLFNQGMVCDSSFIMDIVVKDCGDVFRGLSSVVDVAGGLGGAAMAISIAFPDVQCSVLELPHVAANAPTSTDVKYVAGDMFESIPPANAVFLKWVLHDWGDADCIKILKNCKNAIPSRDAGGKVIILDMVMGGQSSNIKHKETQVLFDLFIMFVNGVERDEQEWKKIIFEAGFSDYKIIPVLGVRSIIEVYP

>Sobic.009G197600.4 (SbASMT22.1)

MAPVKAQDASTDQQTMLDAQLQLWHHTFGYIKSMALKAALDLRIPDAIHQHGGSATLPQIATKATLHPSKIPCLRRLMRVLTLTGVFQHSTTTDDDGGELVYELTPASRLLVGSVTTNVSPFLNMVLGTVFVSSFLDLGEWFQHELPDPSPFKLTHGRHVWDLAIHDASFAKLCDNGMVADSGFIMDVMVKECGDVFQGISGSLVDVAGGLGGATQAIAKAFPHIECSVLDLPNVVAVAPTDTDVKYIAGDMFESVPSANVVFLKWVLHDWGDAECVKILKNCKKAIPSEGGKVIIMDIVVGAGSSDQKNVETQVLFDLFIMTINGAERDEKEWKKIIFEAGFRSYKIMPVLGVRSIIEVYP

>Sobic.009G197600.5 (SbASMT22.2)

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>Sobic.009G197800.1 (SbASMT23)

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>Sobic.009G198000.1 (SbASMT24)

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>Sobic.010G230800.1 (SbASMT25)

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>Sobic.010G231000.2 (SbASMT26)

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>Sobic.010G234400.1 (SbASMT27)

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>Sobic.010G234500.1 (SbASMT28)

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>VIT\_203s0038g03090|VIT\_203s0038g03090.1|Vvinifera\_v2.1

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>VIT\_203s0038g03080|VIT\_203s0038g03080.1|Vvinifera\_v2.1

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>VIT\_215s0045g01490|VIT\_215s0045g01490.1|Vvinifera\_v2.1

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>VIT\_212s0028g02860|VIT\_212s0028g02860.1|Vvinifera\_v2.1

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>VIT\_212s0028g02950|VIT\_212s0028g02950.1|Vvinifera\_v2.1

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>VIT\_212s0028g02740|VIT\_212s0028g02740.1|Vvinifera\_v2.1

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>VIT\_212s0028g01880|VIT\_212s0028g01880.1|Vvinifera\_v2.1

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>VIT\_212s0059g01750|VIT\_212s0059g01750.1|Vvinifera\_v2.1

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>Zm00001d038702\_T001

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>Zm00001d038699\_T001

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>Zm00001d010736\_T001

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>Zm00001d049303\_T001

MRRHMAPIKEQKHTTSAEQQVMLDAELQLWNHTFGYVKSMALKAAIDLGIPEAIHQHGGTATLPQIVTRVKLHPSKTPCLRRLMRVLTLTGVFGAQEPHDDDGGCDDELVYTLTPASRLLVGSPGQNVGPFLTLMLGPIFVSSFLDLRGWFQHETPDPSPFKMTHGRDIWELAAHDAAFGRLFDAGMVADSSFIMDVVVRECGGVFEGISSLVDVAGGLGGATQTIAKAFPNLECSVLDLPNVVASAPADTAVKYVPGDMFESVPAADAVFLKWIMHDWGDADCVKILKNCKKAIPAQGGKVIILDIVVGAGSSCDRKNVETQCLFDLFIMFINGAERDERQWKKIIFEAGFTSYKIIPVLGIRSIIEICL\*

>Zm00001d053156\_T001

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>Zm00001d047192\_T001

MALSTQDLLEAHVELWHQSLCYAKSLALAVALDLRIPDAIHHHGGSATLPQILAETAAHPSKLRALRRLMRVLTVSGTFSVEQQPPAGGDDSTVDAPDEAVYRLTAASRFLVSDEVSSSTLAPFVSLALHPIAVSPHTMGICAWFRQEQREPSPYGLAFQQTFPTIWEHADDVNALLNKGMVADSRFLMPIMLRECGEVFRGIESLVDVGGGHGGATAAIAAAFPHLKCSVLDLPHVVAGAPSDVNVQFVAGNMFQSIPPATAVFLKTTLHDWGDDECVKILKNCRQAISPRDAGGKVIILDMVVGYGQPNITHLETQVMFDLYIMTVNGAERDEQEWKKIFIEAGFKDYKILPILGALSVIEVYP\*

>Zm00001d038700\_T001

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>Zm00001d029359\_T001

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>Zm00001d029356\_T001

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>Zm00001d052683\_T001

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>Zm00001d004921\_T001

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>Zm00001d047194\_T001 MAFTEESSQDLLQAHDELWHQSVSYLKSLALTVALDLRIPDAIHHHGGGATLLQILDKTALHQSKLRALRRLMRVLTVSGTFSVVQQPPCGDDDSTVYRLTAASRFLVSEEVSSATLAPFMSVVLHPISQSSHARGICAWFRQEHHDPSAFGLAFGQAPTIWEHADDTNAILNKGLAAQSRFLVPVMLRECGEAVFRGIDSLVDVGGGHGGAATAIAAAFPHLKCSVLDLPHVVAGAPSDGNVQFVAGDMFQSIPPATAVFLKTALHDWGDDECVKILKNCRQAISPCDEGGKVIIMDMVVGYDESNTKRLEVQILFDLFIMMVNGAERDEQEWKKIFIQAGFKDYKILPVVGSLSVIEVYP\*

>Zm00001d023254\_T001 MSPCAHAEQQEPDAPPLHNDHHRHQTYVELYHHGLHHVKSSALLCAVGLGIPGAIHRRGGAATVSDLVSGTGVHPAKRAQLRRLMRMLACFGIFGAAGGDEGESETVYTLTPVSSVLVGDKDKEASATSSASSPDMSALLRLLARPSTSVSTFFDMEEWFRDGGTTTLFETALGVASWSLTKSDAAYNRAMNEACVADTSLSMDIMLKDTGGCCGGGGASSVFGGGRLTSLVDVGGGHGAAAIAIANAFPHIKCTVLDLKQVIDKVPPAAATGTDRIINSTAATAVQFVAGDMFESIPPADAVLLRHVLDCWDDEHCVKILGQCKRAIPGREAGGKVIIINVVVGYGSPDKLVKETQVLFDMYMMRYDGSEREEHEWREIFSRAGFSDYKITPTLGFHSIIEVFP\*

>Zm00001d049181\_T001 MGHQAQHATDDTEELLAAHRELWCHALGYVKSMALKCALDLRIPDIIQRCGGSATLGQLLAASEVPASNLGYLRRVMRTLTAMRIFAVVGHGHGPDKADDPADDDATAVSYRLTPASRLLATSDDDDDASKNNLSIHPNISSHVRPKNVSLLFSMAEWMKDEQALSVSLYETVNRKCMWACVEDDAATRACFYESMDADTRLVMQAVIRKCPAVFDDGLTSLVDVGGARGTAAAAVVAAFPHIQKCTVMDLPHIVAEAPAGTGLCFHGGDMFEHIPSADAVMLKVYIYTNWYQMDWILHDWDDDKCVKIMERCKEAISGKEGRGGKVIIIETVLGSRPDDDATCKETYVLDLQILSFVNGAEREEHEWRRIFLAAGFRDYKITHTRGIPSIIEVFP\*

> LOC\_Os01g54969.1 (OsASMT1)

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> LOC\_Os04g11970.1 (OsASMT2)

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> LOC\_Os05g43930.1 (OsASMT3)

MELTESKCDGGQEVSLLDAQLELYWNTFAVIKSMALKSALDLRIADAVHLHGGAATLAEIASEVALHPSKIPCLRRLMRALTVSGVFAAAVKPGDGGGGEPVYELTPSSRLLVGSSNLSGIMSMILHPTLVVPFLGVGEWLRRDREPPEEDPYCIFKQAHGRSLWELAGRDAAFDALINDGMVSDSRVIMDYVVREHGEVFRGIASLVDLAGGLGAAAQVISKAFPEVRCSVMDLGHVVAKAPAGTDVEYIAGDMFESVPPADAVFLKWVLHDWGDDDCIKILKNCKKAIPPRDKGGKVIIMDIVVGAGPSDQKHREVQALFDMYIMFVNGIERDEQEWKKVFMGAGFSGYKIMPVLGFRSMIEVYP

>LOC\_Os05g43940.1 (OsASMT4)

MGSLELSKNKCNGGQEVSLLDAQLELYSNTFAVIKSMALKSALDLGIADAVHRHGGAATLAEIASEVALHPSKIPCLRRLMRALTVSGVFAAAVKPGDGGGGEPVYELTPSSRLLVGSSNLSGIMSMILHPTLVVPFLGVGEWLRRDREPPEEDPYCIFKQAHGRSLWELAGRDAAFDALINDGMVSDSRVIMDYVVREHGEVFRGIASLVDLAGGLGAAAQVISKAFPEVRCSVMDLGHVVAKAPAGTDVEYIAGDMFESVPPADAVFLKWVLHDWGDNDCIKILKNCKKSITPRDKGGKVIIMDIVVGAGPSDQKHREVQALFDMYIMLVNGIERDEQEWKKVFVEAGFSGYKIMPILGFRSMIEVYP

> LOC\_Os06g13280.1 (OsASMT5)

MSCHAEQELSTPDMLQGHIELHHHLFSYLKSKALRCAADLGVPSAIHRRGGAATISDIAADTGVHPAKLPHLRRIMRVLTVAGIFAANDEPSSSADQDGDAAGETAYTLTPPSRLLVGDRATCNMDPMMRFLAAHGGVPAWEMTKRDNSYSRALNEACAGDTSFVMDIAVREGGDVFRGLSSLVDVGGGHGAAAMAVARAFPHIKCSVLDLPQAISEAPADGTVNFVAGNMFEYIPPANAVFLKYVLHCWGEEDCIKILQQCKKAIPARGDGGKVIIINTVVGSGEPQDNALKETQVLFDVYMMGIGGGEREEHEWKKIFFEAGFSDYKIKPILGFISVIEVYP

>LOC\_Os06g16960.1 (OsASMT6)

MALKCAAELGIPAAIHRRGGAATLRDIVADVALRQAKVPHLRRLMRVLTVSGIFAMKQQQPASSGEAVYTLTPASRLLVAGAGGGHDMSPMLRFLVHPTALTPFFSLHAWFRVDDEEEEEEPVAAGGGAAMSLFEMAHGFPRWEMTGRDAAYGAVLNDAMAADSRFVMEVVFREGGGDVFRGIGSLVDVGGGHGAAAAAVAAAFPHVKCSVLDLPQVVRKAPPDAGDVRFVAGDMFEYVPPADAVLLKYVLHCFGDDDCVKILRRCKEAIPARDAGGKVIIINMVIGSGSQRDIFKETQVLFDLYMMYIDGVEREEKEWENIFSKAGFSAYKIMPILGFLSIIEVYP

> LOC\_Os07g27880.1 (OsASMT7)

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> LOC\_Os07g27970.1 (OsASMT8)

MEHEQLLQASTELMNHSLGYIRSMALGCAAKLGVADAIHHAGGRATMDDLRAALSLHPSKLPYFLRRVMRVLVASGVFAHDEEEDDDDIYRVTPVSSLLVTATGGNGGRSLLPFVLLQLSPPIYVTPATSMAEWLTSGEEETPFEMTHGAGLWTVCSRDPELGELFNDAMAADSAFIMDVAIRGAGRQVFDKITSLVDVAGGTGTAARVVAAAFPHIKCTVLDLPHVIDSIPADHRGRDVVKFVAGDMMDFIPRADALLLKFVLHDWSDEDCMKILKRCKEAIPSREAGGKVIVIDVVVGSSTQAMCHGTQLLFDLLISTTLPGMQRGEKEWCKVFKEAGFTDYKISPVLGIRSIIEVFP

> LOC\_Os07g28040.1 (OsASMT9)

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> LOC\_Os08g07260.1 (OsASMT10)

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> LOC\_Os08g19420.1 (OsASMT11)

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> LOC\_Os08g35310.1 (OsASMT12)

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>LOC\_Os09g17560.1 (OsASMT13)

MAQNVQENEQVMSTEDLLQAQIELYHHCLAFIKSMALRAATDLRIPDAIHCNGGAATLTDLAAHVGLHPTKLSHLRRLMRVLTLSGIFTVHDGDGEATYTLTRVSRLLLSDGVERTHGLSQMVRVFVNPVAVASQFSLHEWFTVEKAAAVSLFEVAHGCTRWEMIANDSKDGSMFNAGMVEDSSVAMDIILRKSSNVFRGINSLVDVGGGYGAVAAAVVRAFPDIKCTVLDLPHIVAKAPSNNNIQFVGGDLFEFIPAADVVLLKCILHCWQHDDCVKIMRRCKEAISARDAGGKVILIEVVVGIGSNETVPKEMQLLFDVFMMYTDGIEREEHEWKKIFLEAGFSDYKIIPVLGVRSIIEVYP

>LOC\_Os10g02840.1 (OsASMT14)

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> LOC\_Os10g02880.1 (OsASMT15)

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> LOC\_Os11g12760.1 (OsASMT16)

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> LOC\_Os11g33300.1 (OsASMT17)

MALIHGSEEVISHEEDMVGAFALLYHHVFSYIKPMALKCAVELGIPDAIHRRGGAATLANIAADTGVHASRLTDLRCLMKLLTTSGMFAATAATTDGGEGEPAVATSTMYTLTAASGLVVGPRGLSTVVRFAAGPVAVSPFFDMHAWLRAAPAAAPPAARSLFELAHGRSRWDAANADNDTMNAHSFVESQLLIEAVLRDHAGVFRGLRSLVDVGGGHGAVAKAIAAAFPDIKCTVMDLPHVVADAPVSDDGNLHLVAGDMFQSIPPADAVLLKYVLHCWGDDDCVRILRNCREAIPAREAGGKVIITELVLGSSAASRDANVAEAEDMHSLFLMCISGVGREEREWRAIFSDAGFGDYKITPVLGPISVIEVYP

>LOC\_Os12g25450.1 (OsASMT18)

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> LOC\_Os12g25490.1 (OsASMT19)

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>ESW14071 pep chromosome:PhaVulg1\_0:8:56528565:56529849:-1 gene:PHAVU\_008G250700g transcript:ESW14071 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

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>ESW14037 pep chromosome:PhaVulg1\_0:8:56237670:56239124:1 gene:PHAVU\_008G247600g transcript:ESW14037 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

MESREEDQSAKLLRAQTHVWNHIFSFINSMSLKCIVDLGIPDIIHNHGQPMSLSNLISSLPIHSSKTHFIHRLMRIMVHSGFFSQHNPTENELELKYALTDSSLLLLKSNAMSVTPFLQAMLDPVMTNPWNQFSNWFKNGNPTTFEMENGKPFWEYASCDPRFNILFNDAMASDAQLVTSLVTEKCKGVFMGLESLVDVGGGTGIMGKAIAKSFPQLECTVFDLPHVVSGLQGSENLKYVGGDMFEAIPPADAILLKWILHDWSDEECVNILKKCKEALSRKGKEGKVIIIDMVVDKEMKDDESFETQLFFDILMMVLLTGKERNKKEWVKLFSSAGFNNYKITPFVGSRSLIEIYP

>ESW13098 pep chromosome:PhaVulg1\_0:8:43437752:43438483:1 gene:PHAVU\_008G1678001g transcript:ESW13098 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

METQGEEHASKLFRAQTHIWNHMFKFINSLSLRCAIDLSIPNIIHNYGQPMPLSKLISSLPLHPSKTCFISRLMRILTHSGFFSEHHATQNEPEVMYVLTDASKLLLKDQPSSMASLLQLIVDPVYINTWYQLSTWFTNEDPTPFHAENGMTFWDFARCKREFNNLFNDAMASDSHWVSSVVIEKCEGVFNGSKSFVDVGGGTGTMAKAIAKSFPQLNCIVLDLPHVVADLQETENIKICWRGY

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METQGEEHASKLFRAQTHIWNHMFKFINSLSLRCAIDLSIPNIIHNYGQPMPLSKLISSLPLHPSKTCFISRLMRILTHSGFFSEHHATQNEPEVMYVLTDASKLLLKDQPSSMASLLQLIVDPVYINTWYQLSTWFTNEDPTPFHAENGMTFWDFARCKREFNNLFNDAMASDSHWVSSVVIEKCEGVFNGSKSFVDVGGGTGTMAKAIAKSFPQLNCIVLDLPHVVADLQETENIKICWRGYV

>ESW11471 pep chromosome:PhaVulg1\_0:8:2707004:2717150:1 gene:PHAVU\_008G032800g transcript:ESW11471 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

MVSNDGSKASEIFRGQVHLYKHLFAHTIDAMSLKWMVELSIPDIIHNHGQPITFQKLVSILQVSPTKVRGVQSLIHYLAHTGFFEIVSVHENMEEKEAYALTAASQLLVKDSDLCLAPTVEGFVDPGLTGVWSNLKKWTYEDDLTLFGVSVGSNLWEFLDKNPASDEAFNETLAADSKMMNMALKGCNWVFEGVESIVDVGGGTGITAKILCEAFPNMKCIVLERPGVIENLSGTNNLTYVGGDMFKSIPKADAVLLKSQVAFAHSLYFVAKLFLLFASFCTSHHILTVSSSSQSHPSPRPPHSQMALQTATPPTTPSAQVVGNAFVEQYYHILHHSPDLVYRFYQDSSVISRPDSNGVMTSVTTMKGINEKIVSLNFKEFKAEIKTADAQKSYQEGVTVLVTGCLTGKDNMRRKFAQSFFLAPQDNGYFVLNDVFRYVEDDEPSELPPVNGDGDAAAVKIIPEPESSHVADSPAPDSTNSIVNKGQIVVEKAYAPSNHHERQIPAENEDNVESHFQSNGNDDSQATEVDSLAQEDAPKQSYASIVKVQKGSSVPTKVYVPTNTLKSGSNKTESLVAEPVESSEVPEAASDSVNDPESSDAHEEVEGHSIYIRNLPLNVTVGQLEVEFKKFGSIKPDGIQVRNNKQQGYCFGFVEFLSLNSMNSAIQASPIPIGGRQAVVEIKRTTTRVGSGISNTGRPRIPPGRGGLRNDSFRGRGNYGGGRGYGRNDYGNRGGEFSGRGRSHGDGEFSGRGRSHGDGEFSGRGRSHGESYHQGRGRGGRSSGPKQNAVVSN

>ESW11472 pep chromosome:PhaVulg1\_0:8:2707004:2717206:1 gene:PHAVU\_008G032800g transcript:ESW11472 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

MVSNDGSKASEIFRGQVHLYKHLFAHTIDAMSLKWMVELSIPDIIHNHGQPITFQKLVSILQVSPTKVRGVQSLIHYLAHTGFFEIVSVHENMEEKEAYALTAASQLLVKDSDLCLAPTVEGFVDPGLTGVWSNLKKWTYEDDLTLFGVSVGSNLWEFLDKNPASDEAFNETLAADSKMMNMALKGCNWVFEGVESIVDVGGGTGITAKILCEAFPNMKCIVLERPGVIENLSGTNNLTYVGGDMFKSIPKADAVLLKSQVAFAHSLYFVAKLFLLFASFCTSHHILTVSSSSQSHPSPRPPHSQMALQTATPPTTPSAQVVGNAFVEQYYHILHHSPDLVYRFYQDSSVISRPDSNGVMTSVTTMKGINEKIVSLNFKEFKAEIKTADAQKSYQEGVTVLVTGCLTGKDNMRRKFAQSFFLAPQDNGYFVLNDVFRYVEDDEPSELPPVNGDGDAAAVKIIPEPESSHVADSPAPDSTNSIVNKGQIVVEKAYAPSNHHERQIPAENEDNVESHFQSNGNDDSQATEVDSLAQEDAPKQSYASIVKVQKGSSVPTKVYVPTNTLKSGSNKTESLVAEPVESSEVPEAASDSVNDPESSDAHEEVEGHSIYIRNLPLNVTVGQLEVEFKKFGSIKPDGIQVRNNKQQGYCFGFVEFLSLNSMNSAIQASPIPIGGRQAVVEIKRTTTRVGSGISNTGRPRIPPGRGGLRNDSFRGRGNYGGGRGYGRNDYGNRGGEFSGRGRSHGDGEFSGRGRSHGESYHQGRGRGGRSSGPKQNAVVSN

>ESW14070 pep chromosome:PhaVulg1\_0:8:56521938:56523290:-1 gene:PHAVU\_008G250600g transcript:ESW14070 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

MESCGEDQSAKLLRAQTHVWNHILSFINSMSLKCIVDLGIPDIIHNHGQPMSLSNLISSLPIHSSKTHFIHRLMRIMVQSGFFSQHNPTENELEVKYALTDSSLLLLKSHAMSMTPYLQAKLDPAFTNPWNQFSNWFKNDSPTTFEMAHGKPFWEYAGSDPRFNILFNDAMASDAQLVTSVVIEKCKGVFMGLESLVDVGGGTGTMGKAISKSFPQLECTVFDLPHVVSGLQGSENLKYVGGDMFEAIPPADAILLKWILHDWSDEECVKILKKCKEAISRKGKEGKVIIIDMVVDKEMKDDESFETQLFFDLMMMVLFNGKERNKKEWVKLISSAGFNNYKITPVMGIRSLIEIYP

>ESW11469 pep chromosome:PhaVulg1\_0:8:2695482:2698133:1 gene:PHAVU\_008G032600g transcript:ESW11469 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

MASNDGSKASEIFRGQVHLYKHLFAHTIDAMSLKWMVELSIPDIIHNHGQPITFQKLVSILQVSPTKVRGVQSLIHYLAHTGFFEIVSVHENMEEKEAYALTAASQLLVKDSDLCLAPTVEGFVDPGLTGVWSNLKKWTYEDDLTLFGVSVGSNLWEFLDKNPASDEAFNETLAADSKMMNMALKGCNWVFEGVESIVDVGGGTGITANTICEAFPNMKCIVLERPHMFKSIPKADAVLLKMVLHNWNDKDCRKILENCKEAISDKGKRGKVIVVDIVMNESEDEEELNELKLLYDVRMTCLINGKERKEEEWKKLFVEAGFQSYKISPFTGYLSLIQIYP

>ESW13099 pep chromosome:PhaVulg1\_0:8:43439020:43439316:1 gene:PHAVU\_008G1678000g transcript:ESW13099 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

WIMHNWKDEECVKILKNCKEAITNQGRVIIIDMIMENKKEEDELTETQFFFDMQMMMLFGGKERNEKEWANLIFSAGFTDYKIITNTPGILSIIEIYP

>ESW11470 pep chromosome:PhaVulg1\_0:8:2701370:2702913:1 gene:PHAVU\_008G032700g transcript:ESW11470 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

MASNDGSKASEIFQGQVHLYKHLFAHTIDAMSLKWMIELGIPDIIHNHGQPITLPKLVSILQVSPTKVRGVQSLIHYLTHTGFFERVSILENMEEKEAYALTAASQLLVKDNNLCLVPMVEGFVDPCLAGVWSHLKKWTYEDDLTLFDVSVGSNMWEFLDKNPASNRLFNEIFAADSKMMNMALRGCNWVFEGVESIVDVGGGTGITAKTICEAFPNMKCIVLDRPSVVENLSGTNNLTYVGGDMLKSIPKADAILLKLVLHNWNDKDCRKILENCKEAISDKGSRGKVIVVDVVMNASEDEEELTGLKLLIDVRMRCFINGKERKEEEWKKLFVEAGFQSYKISPFTGYLSLIQIYP

>ESW11557 pep chromosome:PhaVulg1\_0:8:3377029:3379244:-1 gene:PHAVU\_008G040200g transcript:ESW11557 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

MGSCFSEKENHVVVEREDTETTLSAMVLGSNVVFPAALNAAIELNVFDIIAKEGSAESGGFMSPSEIASKLLIPTQQQHRCELANRLERLLRLLASYSLLAVSSRSDGDGGSVRVYGVSPSGKYFVRDVSGEGYLASFTSFLCHPALSGVWVNFKEAIIDPEIDLFKKVHGMSKFEYFGKYPEINHGISTLVDVGGGTGQCLKMIISKHPSIKGINFDLPHVIENSPPVPGVEHVGGNMFEGVPQGDAIMLKAICHNWSDEKAVELLSNCHKALPPKGKVIVGDFILPEDPEPTNEHKMISILDNIMFITPGGRERTEKEFESLGKSSGFSRFQVVCRAFSTMALMEFYK

>ESW20997 pep chromosome:PhaVulg1\_0:5:2973815:2975036:1 gene:PHAVU\_005G0323000g transcript:ESW20997 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

SEIASQLPFQHKKLPQRLDRMLSLLASHSLLTCSTRANQDGKLQRLFQLSPSGKYFLNAEATASLAFFSKFMSHPKLVQALFNFKEVLLDCDNGLYMKVHGMPIYEGIQSDPPWNHIFNQAMANICTAEMTKILQMYTGFEGISLLIDVGGGVGQSLNMIISKYPSIKGVNFDLPQVIQQAPPYPGIEHVEGDMFESVPKGDAILLKGILHNWSDENCLRVLNNCHKALPENGKVVVVDFIMPEEIGCTEADKMVTSFDNLMFLDGGSERTEKEFMNLCQSSQFSSFKVVSRAFTVLGVMEFYK

>ESW21431 pep chromosome:PhaVulg1\_0:5:11532987:11536578:1 gene:PHAVU\_005G070300g transcript:ESW21431 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding description:hypothetical protein

MEEESTDSRKQSRLAIMELANMISVPMALNAVVRLNVADAIWNGGANAPLSAAQILPRILPVGDGDAENLQRLLRILTSYGVFHEHLAAGERKYSLTDVGKALVTDEQGLSYGAYVLQHHQDALMRAWTLVHEAVVDPTKEPFERANGEGAYAYYLKQAEMNELMVKAMSGVSVPFMRAMLEGYDGFQGVERLVDVGGSGGDCLRMILLKYPNIKEGINFDLPEVVAKAPPTPCVTHVGGDMFKSIPQGDAIFMKWVLTTWTDEEIKQIMQNCHKALPEGGKLIACEPVLPEHSDESHRTRALLEGDIFVMTIYRAKGKHRTEEQFRQLANDAGFPRFRAFNVDHFYTVLEFQK

>Pp3c21\_990|Pp3c21\_990V3.1

MPGKVIDSSYLGGMLRLASSVKVLREVATMSEDGSTELRYGLEPIGKFLVGDAEKGSLVHLLLMYQVPVLLSTWNHLPESVVDDSVQPFAIFNKAMAGHSKLYMRAFLDVYEGFEGVRVLIDIGGGFGSAITTITCETTGLLSGVEHTSGDMFESIPTGGDAISLKIRKLGLDAGFMRVDVVCKVDQLSVTEFVKAWLGSGDRSPMFACDWRFLSIPKVSIPLSSTSTGFKARNHYILHLNKAGIA\*

>Pp3c5\_16200|Pp3c5\_16200V3.1

MIARLSIVHLVRFVSSWIVWQTVILDYNVKVFTEFVAFFNLLMAEATARSSDVDHKDCASAAQNGMRVLSPLLFGHAAAMTLKTAVVLNIPDILARAEPERGALSVHEISKELPSDSVDEQVLHRVMRTLVHLKVFSAERVSESGTTVARYGLTPASRRLVQENNSRSLAPLLMYLNYISSHVPWQHLHESVLYGKDAWGTAYGMTSWEYSDVDPEYGALWNAFNKVQGAPTIEALKRYDGFKDVNVLVDVGGYQGATVAAIVAAHPHIRGINFDLPHVIAEAPEFPGVEHVSGHLLEGGVPSGDAMLMKNIVHLFKDEEAVKVLQNCKKALTANGKLLIYDPVIPSEFDEGGSPYDGVPPLMDLGLLVYGKVDRTEEQWRALLASGGFPNASFVCLQPQH\*

>Pp3c11\_12200|Pp3c11\_12200V3.1

MDLEGRAIEELAKAQLEVLGLAVSVVFPAALNAVVKMQVAEVLATAAEEGHRSLSADEIVARMPNRPSQPNSKNLERLLRVLSFKGVFKEEARHDKRRTFRLTPMSSALIRNLPEGTMANYVLLTSLGQEFIESCKHLTAAVLESKVPFAMAHGGKHQFQYCAANPDYSNVFQAAMTDHSHQLVDLMLAKFEGFKDVQRMADVGGGVGTTIGRIVEQYPHIQGINFDLPHVIAHAPQREGVEHIAGDMFESVPPDCDAFFLKNIIHDWDDELNIQILMNCHKALPSRGRVIMVDAVLPATTLLRESSLDDMCAFEADITMMAVSAHGRERDAEEWENLATTSGFTNITFVKLDYMYVIEAMKP\*

>Pp3c12\_5860|Pp3c12\_5860V3.1

MACGEGHDHVGEDVYSTNQQKATTHIDKVRLAAIELVGQAAIPGTLASLARLNVFEALARAGDGVELTPQELGNQAMPGKVINLSYLGRMLRLASSVKVLREVATMSEDGSTEHRYGLEPIGKFLVDDAEKGSLVHLLLMYQDPVFLSTWNHLPESVLDDSVQPFARAHGGLHAWEYGMQNPEFDEKFNKAMAGHSKLYMRAFLDVYQGFEGVRVLIDVGGGFGSAISTITARYPHIKGINFDQPHVIKACPELPGVEHMSGDMFESIPSGGDAIFLKYILHDWDDESCIKLLKNCHKVLPANGKVIAVDSVLTDTINFEGGDRMAFMVDMNMMAFNHSGARERNEGEMRKLGLYAGFLRVDVVCKVDQLSVTEFIKA\*

>ONH92375.1 hypothetical protein PRUPE\_8G171000 [Prunus persica]

MEDKQRELGGEEKEEEHAKLEIWKYVFGFVEIAVVKCAIQLGIADAIESHGSPMTLLELSSALRCDPSPLYRIMRVLVHLKIFKEKPATQLGPKVYAQTPLSKWLLKSGKNSMAALILLESSPVMLAPWHGLSARIQGVNNSAFEAVHGEDVWSYAAANPNHSKLINEAMACDARVAVPAVLESCLEVFKGLETIVDVGGGDGTTLRLLVEACPWIRGINFDLPHVVSVAQECDRIENVGGDMFDCVPKADAAIIMWVLHDWGDDECIRILKKCREAVPEDKGQVIIVEAVIEEDNEKQDKKLTNVRLMLDMVMMAHTNTGKERTMKEWGYVLGEAGFSRHTITPIHAVQSVIQAFP

>ONH92376.1 hypothetical protein PRUPE\_8G171100 [Prunus persica]

MLSTFDSNLFLQITYTPKTLGQTHTHKDMEDKQSRELRSEEEEEEEHAKVDVWKYVFGFVEIAVVKCAIELGIADTIESHGSPMTLLELSSALRCDPSPLYRIMRVLVHLKIFKEKPATQLGPKVFAQTPLSKWLLKSGETSMSALILLESSPVMLAPWHGLSARIQGISNPAFEAVHGEDVWSYAKANPDHSKLINEAMACDARVAVPAVIESCLEVFKGIATIVDVGGGDGTTLRLLVEACPWVQGINFDLPHVVSVAQECDHIKNVGGDMFDSVPKADAVIMKWVLHDWGDDECIRILKKCREAIPENKGKVIIVEAVIDEKDEKEDIKLTNVRLMLDMVMMAHTNTGKERTLKEWGYVLGEAGFSRHTITPIHAVQSVIQAFP

>ONH92379.1 hypothetical protein PRUPE\_8G171400 [Prunus persica]

MEDKQREIGGEEKEEEHAKVQIWKYVFGFAEIAVVKCAIQLGIADAIESHGSPMTLLELSSALRCDPSPLYRIMRVLVHLKIFKEKPATQLGPEVYTQTPLSKRLLKSGQNSMAALILLESSPVMLAPWHGLSARIQGNIRNPVFEEVHGEDLWSFGAANPDHNKLFNEAMACDARVHVPAVIESRLEVFKGIETIVDVGGGDGSTMRLLVEACPWIQGINFDLPHVVSVAQECDRIENVGGDMFDCVPKADAVIIKGVLHDWGDDECIRILKKCREAIPEDKGKVIIVEAVIDEKDEKADIKLTNVRLMLDMVMMAHTNTGKERTLKEWGYVLGEAGFSRHTITPIHAVPSVIQAFP

>ONH92381.1 hypothetical protein PRUPE\_8G171600 [Prunus persica]

MEVKQRELGGEKEEEEHSKVEIWKYMFGFVELASGRKVYAQTPLCKRLLKSGQNNMAAFILPESSPVMLAPWHGLSARIQGNIRNPVFEEVYGEDLWSFGAANPDHSKLFNEAMACDARVVVPAVIESCINSDLPHVVSVAQEYDRIENVGGDMFDYVPKADVVIIKWVLHDWEDDECIRILKKCREAIPEDKGKVIIIEAVIDEEDEKEDSKLTNVRLMLDMVMMAHTNTGKERTLKEWVYVLDDGP

>ONH92385.1 hypothetical protein PRUPE\_8G171900 [Prunus persica]

MTLLELSSALRCDPSPPYRIMRVLVHLKIFKNKPATQLGPKVYAQTPLSKRLLKSGQNSMAAFILLENSPVMLAPWHVLSTRIKGNIRNSVFEEVHGEDIWSFGAANPDHNKLFNEAMACDARVVVSAMTESCIEVFEGIETIVDVGGGDGTTLRLLVEACPWIQGINFDLPHVVPVAQECDRIENVGGDMFDCVPKADAVIIKSVLQDWGDDECIRILKKCREAIAEDKGKVIIVEAVIDEKDEKEDIKLTNVRLMLDMVMMAYTNTGKERTLKEWEYVLEEAGFSRHTITPIHAVCSVIQAFP

>ONH92386.1 hypothetical protein PRUPE\_8G172000 [Prunus persica]

MEDKQRELGGEEKEEEHAKVEIWKYVFGFVEIGVVKCAIELGIADAIESHGSPMTLLELSSALRCDPSPLYRIMRVLVHLKIFKEKPATQLGPKVYAQTPLSKQLLKSGENSMAALILLGNSPVVLAPWHGLSARIQGISNPAFEAERGEDIWSYAAANPDHSKLFNEAMACDARVAVPAVIESCSEVFKGIEKIVDVGGGDGTTLRLLIEACPWIRGINFDLPHVVSVAQECDRIENVGGDMFDFVPKADAVIMKWVLHNWGDDECIRILKKCREAIPADKGKVIIVEAVIDEKDEKEDIKLTNVRLMLDMAMMAATQIGKERTLKEWGYVLADAGFSQHTITPIHAVQSVIQAFP

>ONH96362.1 hypothetical protein PRUPE\_7G123600 [Prunus persica]

MENHVSHVTTTAEQPSNEARLGILELANMISVPMSLNAVVRLNVPDAIWQGGSNSPLSASAILSHVLPDGGGDAENLQRILRMLTSYGVFAEHLVSADDDGGSHQRKFSLTEIGKTLVTDQNGLSYGPYILQHHQDVLMGAWPMVHEAVVDPTIEPFVKVNGEPAYEYYGKKPEMNGLMQRAMSGVSVPFMKAILDGYDGFEGVGRLVDVGGSAGDCLRMILQKHPSVREGINFDLPEVVAKAPTIAGVSHVGGDMFKSIPSGDAIFMKWVLSTWTDSECKLIMENCYKALPVGGKLIACEPVLPTKSDDSPRTRALLENDIFVMTIYRAKGKNRTEDELRQLGLSAGFSHFKPIYIDYFYTVLEFQK

>ONI07667.1 hypothetical protein PRUPE\_5G134400 [Prunus persica]

MKEKQVTKMATNEEEEIHSQYAMQLASASLVPMVLKAAIELGVFDILHRAGPGALLSATQIASLLPSNNNPGADLVLDRMLRLLSAYSVLACSVTSHQTDGEALRLYGLSPVSKYFIKNQDGVSLAPLLYLCNDKVTIDSWFHLKDAVLEGGLPFSQAYGMNVVEYVGKDERFRGVFKDSMKEFNPIFMKKILETYKGFVGLKTLVDVGGGDGTILNMIISMYPAIKGFNYDLPSVVEKSPSHPGIEHIAGDMFVRIPKGDAVFMKWMLHGWDDKHCLMILKNCYEALPDHGKVILVDMVVPEAPETSLSASSLFQFDVYLMNTNAMGKERTEKELESLAKEAGFSNIRVACSAFTFSVVELFKNV

>ONI07668.1 hypothetical protein PRUPE\_5G134400 [Prunus persica]

MKEKQVTKMATNEEEEIHSQYAMQLASASLVPMVLKAAIELGVFDILHRAGPGALLSATQIASLLPSNNNPGADLVLDRMLRLLSAYSVLACSVTSHQTDGEALRLYGLSPVSKYFIKNQDGVSLAPLLYLCNDKVTIDSWFHLKDAVLEGGLPFSQAYGMNVVEYVGKDERFRGVFKDSMKEFNPIFMKKILETYKGFVGLKTLVDVGGGDGTILNMIISMYPAIKGFNYDLPSVVEKSPSHPGIEHIAGDMFVRIPKGDAVFMKVSGCYMAGMTNIA

>ONI10568.1 hypothetical protein PRUPE\_4G054200 [Prunus persica]

MDGDEARDLFQAQSHLYKHIFNFISSMSLKCAVQLGIPDIINSHGQPITLPDLVTALQIHPARTGHVHRLMRLMVRSGFFAIKQVRNNQEEEEEEEEEAYDLTPSSRLLLKDKVPSLSPFVLAMLDPALATPWQFLGNWFRGNELTPFESAHGMGFWEYGDQNPEFNSLFNEAMTSDSGMMNLVIKDCKPIFEGLSSLVDVGGGTGKVARILCEAFPHLKCTVLELPQVVANLTDTENLKFIGGDMFQAIPPADAILLKLTLHALSDEECLKVLKKCREAIPGNGQGKVIIIDIVIDDTKDEHEITEAKLFFDLLMMVVVTGRERSEKDWKNLFLEAGFSNYKLTPIFGLRYLHLPHTTVIGFENNDKRAWVERIMQVDKRDIGTALNVISSNISAATFLCSISLTLSSLIGAWLGSSSSNEVFTSELIYGNVSPSILTIKYITLLTCFLLAFACFVQSARHFVHANYLISTPDSNIPAWYVELAVIRGGDFWSLGLRALYFALTLLLWFFGPIPMFLSSIVMVILLHYMDKNTRPLHDHQLPGRQLVKNVGQRITEVAVNIHQHTEAVEATV

>ONI11083.1 hypothetical protein PRUPE\_4G086200 [Prunus persica]

MENTRSLENIVSARGLINFIPIQMTLKAAIELNVFSIIAKSGPASHLTAKEIASQIPTSNPNAAGNLERILRLLAAHSLLSTTLNPCPNDETLQERAYGLTNETLCLVPDENGVSLAPFIILNSELEIVKSLYMLKHTVLEPDFLPFCKAHGITIYEYMSKKPEMSQLFNKSMAETSNLNFSEVLKVYKGFEEVKELMDVGGGIGTSMSEVVSMYPHIHGINFDLPNVVAQAPTYQGVNHVGGNMFETIPNAQSIMLKWVLHNWGDDQCKKVLRNCWEALPKSGKVIVVEFAIPEELEKTKAVLNIVTLDITMMACPGGKERTTTEFANLAKHVGFVETKFFPISYGIYVLEFLKIEEA

>ONI13891.1 hypothetical protein PRUPE\_4G252900 [Prunus persica]

MDLSNEMSSANLLQAQAHIWNCIFSFINPLSLKCAVQLGIPDIIKKHGNPMSLSELISALPIHPTKSNCVYRLMRILVHSGFFGRQKLSELDEEEGYVLTDASRLLLKDDPLSARPFLLGQLDPFMTKPWHYFSTWFQNNDPTACFTAHGTTFWDFGYLEPSLSHIFNDSMASDARLISKVVSNEYKGVFEGLESLVDVGGGIGTMAKAIADVFPHVECIVFDLPHVVADLKGSKNLKFFGGDMFEAIPHTDAILMKWILHDWSDEECIKILQRSKEAITRKEKKGKVIIIDMVMKQKGDDQSIETQLFFDMLMMVLVTGKERTEKEWAKLFSDAGFSDYKITPICGLRYLIEVYP

>ONI13894.1 hypothetical protein PRUPE\_4G253200 [Prunus persica]

MDLSNEMSSANLLQAQAHIWNCIFSFINPLSLKCAVQLGIPDIIKKHGNPMSLSELISALPIHPTKSNCVYRLMRILVHSGFFGRQKLSELDEEEGYVLTDASRLLLKDDPLSARPFLLGQLDPFMTKPWHYFSTWFQNNDPTACFTAHGTTFWDLGYLEPSLSHIFNDSMASDARLISKVVSNEYKGVFEGLESLVDVGGGIGTMAKAIADVFPHVECIVFDLPHVVADLKGSKNLKFFGGDMFEAIPHTDAILMKWILHDWSDEECIKILQRSKEAITRKEKKGKVIIIDMVMKQKGDDQSIETQLFFDMLMMVLVTGKERTEKEWAKLFSDAGFSDYKITPICGLRYLIEVYP

>ONI13895.1 hypothetical protein PRUPE\_4G253300 [Prunus persica]

MDLSNEMSSANLLQAQAHIWNCIFSFINPLSLKCAVQLGIPDIIKKHGNPMSLSELISALPIHPTKSNCVYRLMRILVHSGFFGRQKLSELDEEEGYVLTDASRLLLKDDPLSARPFLLGQLDPFMTKPWHYFSTWFQNNDPTACFTAHGTTFWDLGYLEPSLSHIFNDSMASDARLISKVVSNEYKGVFEGLESLVDVGGGIGTMAKAIADVFPHVECIVFDLPHVVADLKGSKNLKFFGGDMFEAIPHTDAILMKWILHDWSDEECIKILQRSKEAITRKEKKGKVIIIDMVMKQKGDDQSIETQLFFDMLMMVLVTGKERTEKEWAKLFSDAGFSDYKITPICGLRYLIEVYP

>ONI16744.1 hypothetical protein PRUPE\_3G118900 [Prunus persica]

MSLKCEVQLGIPDVIHNHGQPISLSNLIFGHNVHPSKAHFIACLMRILVHSNFFAQDQQVQLPLRPNNNNSNENIVHQDLDDEAEEKTVVAYSLTPASGLLLKEGTLSTTQFLLMILDPVVTDPFHLMGTWCQMNNHGNLDHPASPFEMAHGRPFWGLAAQQPKFARAVVEECEGVFEGLNSLVDVGGGTGTTAKAIAKAFPNINCTVFDQPHVVANLQGTHNLDFVGGDMFEKIPPANAIFLKWIMHDWSDEERVKILKKSREAILSKNEVGKVIILDINVSADNTKMDKKSIETQLINIMMMVDLSGKKRSEAEWEKLFLTAGFSHYKITHTLSLRSLIEVYPRKKESLF

>ONI16746.1 hypothetical protein PRUPE\_3G119100 [Prunus persica]

MGSEVRATHELLQAQAHIWNHIFSFINSMSLKCAVQLDIPDVIQKHGQPMTLSELVSALPISPTKAHFIPRLMRILVHSGFFARESLNGGEQGYVLTEASALLLKDNPISARPFLLAMLNPILTDPWQYLTPWFQNDNPTPFHVVHGMTFWDYGSQDPTLSHFFNDAMPSDARLISSLMIDDCKGVFQGVESLVDVGGGTGTVAKSIADAFPYMKCTVLDLPHVVADQKGSKNLEYVAGDMFEAVPAGGAIFLKWILHDWSDEECVKILERCKEAITREGKKGKVIIVDMTVENKKTDKESGETQLFFDMQMMVMTTGKERNEKEWAKLFSDAGFSHYKITPCLGLRSLNEVYP

>ONI16752.1 hypothetical protein PRUPE\_3G119700 [Prunus persica]

MRATHELLQAQAHIWNHIFSFINSMSLKCAVQLDIPDVIQKHGQPMTLSELVSALPISPTKAHFIPRLMRILVHSGFFARESLNGGEQGYVLTDASALLLKDNPMSARPFLLDMLNPILTDPWQYLTTWFQNDNPTPFHVGVFQGVDSLVDVGGGTGTVAKSIADAFPHMKCTALDLPHVVADLKGSKNLEYVAGNMFEAVPAADAIFLKWILHDWSDEECVKILKRCKEAVTREGKKGKVIIVDMKVENKNTNKESGETQLFFDMLMMVMATGKERNEKEWAKLFSDAGFSHYKITPCLSLRSLIEVYP

>ONI16753.1 hypothetical protein PRUPE\_3G119800 [Prunus persica]

MNNHGNHDHPASPFEMAHGRPFWGLAAQQPKFGSLFNEAMEADSQLIARAVVEECEGVFEGLNSLVDVGGGTGNMAKAIAKAFPNINCTVLDQPHVVANLQGTHNLDFVGGDMFDKIPPANAIFLKWILHDWSDEESVKILKKSKEAILSKNEGGKVIILEINVSPDNKKMDKKSIETQLMWDMLMMVNLNGKERSEAEWEKLFLTVGFSLYKITHTLGLRSLIEVYP

>ONI16758.1 hypothetical protein PRUPE\_3G120200 [Prunus persica]

MGGGTGTVAKSIADAFPHMKCTVLDLPHVVADLKGSKNLEYVAGNMFEAVPAADAIFLKWILHDWSDEECVKILERCKEAITREGKKSKVIIVDMTVENKNTDKESGETQLFFDMLMMVMATGKERNDKEWAKLFSDAGFSHYKITPCLGLRSLIEVYP

>ONI16760.1 hypothetical protein PRUPE\_3G120400 [Prunus persica]

MSLSNDKVSATSHELLQAQAHVWNHIFQFINSMSLKCAVQLGIPDVIHNHGQPISLSNLISGLNVHPSKAHFIARLMRILVHSNFFAQDQQVQLPLRPNNNNNNENIVHQDLDDEAEEKTVVVYSLTPASRLLLKEGTLSTRQFLLMILDPVMTDPFHLMGTWCQMNNHGNLDHPASPFEMAHGTPFWGLVAQQPKFGSLFNEAMEADSQLIARAVVEECEGVFEGLNSLVDVGGGTGTMAKAIAKAFPNINCTVFDQPHVVANLQGTHNLDFVGGDMFEKIPPANAIFLKWILHDWSDEESVKILKKSREAILSKNEGGKVIILDINVSADNTKMDKKSIETQLMWDMLMMVELSGKERSEAEWEKLFLTAGFSHYKITHTLGLRSLIEVYP

>ONI16892.1 hypothetical protein PRUPE\_3G127600 [Prunus persica]

MDSEVRASHELLQAQAHIWNHIFSFINSMSLKCAVQLGIPDVIQKHGQPMTLSELVSALPISPTKAHFIPRLMRILVHSGFFARESLSGGGEQGYILTDASALLLKDNPMSARPFLLAMLSPILTDPWQYLTTWFQNDNPTPFHVVHGMTCWEYGNQDPTLAHFFNDAMASDARLISSLVIDDCKEVFQGVNSLVDVGGGTGTMAKSIADAFPHMKCTVLDLPHVVADLKGSKNLEYVAGDMFEAVPAADAIFLKWILHDWSDEECVKILEQCKEAITREGKKGKVIIVDMTVENKNTDKESGETQLFFDMHMMVMTTGKERNEKEWAKLFSDTGFNHYKITPCLGLRSLIEVYP

>ONI16909.1 hypothetical protein PRUPE\_3G129000 [Prunus persica]

MGLSNDKVSATSHELLQAQAHVWNHIFQFINSMSLKCAVQLGIPDVIHSHGQPISLSNLISGLNVHPSKAHFIERLMRILVHSNFFAQDQQVQLPLLPNNNNNENIVHQDLDDGEEEKAVVVYSLTPASRLLLKEGPLSTTQFLLMILDPVVTDPFHLMGTWCQMNNHGNHDHPASPFEMAHGRPFWGLAAQQPKFGSLFNEAMEADSQLLARAVVEECEGVFEGLNSLVDVGGGTGTMAKAIAKAFPNINCTVFDQPHVVANLQGTHNLDFVGGDMFEKIPPANAIFLKWILHDWSDEESVKILKKSREAILSKNEGGKVIILDINMSADNKKMDKKSIETQLMFDMLMMVDLNGKERSEAEWEKLFLTAGFSHYKITHTFGLRSLIEVYF

>ONI16910.1 hypothetical protein PRUPE\_3G129100 [Prunus persica]

MGSEVRASHELLQAQAHIWNHIFSFINSMSLKCAVQLGIPDVIQKHGQPITLSELVSALPISPTKAHFIPRLMRILVHSGFFAQESLSGGEQGYVLTDASALLLKDNPMSARPFLLAMLNPILTNPWQYLTTWFQNDNPTPFHVDPTLAHFFNDAMASDARLISSLMIDDCKGVFHGVDSLVDVGGGTGTMAKSIADAFPHMKCTVLDLPHVVADLKGSQKLEYVAGDMFEVVPEADAIFLKWILHDFSDEECVKILERCKEAITKEGKKGKESGETQLFFDMLMMVLATGKERNEKEWAKLFSDLGFSHYKITPCLGLRSLIEVYP

>ONI16911.1 hypothetical protein PRUPE\_3G129200 [Prunus persica]

MGLSNDKVSATSHDLLQAQAHVWNHIFQFINSMSLKCAVQLGIPDVIHSHGRPISLSNLISGLNVHPSKAHFISRLMRILVHSNFFAQDQQVQLPLLPNNNNNNENIVHQDLDDEEEEKAVVVYSLTPASRLLLEESPLSTTQFLLMILDPVVTDPLHLMGTWCQMNNHGNHDHPASPFEMAHGRPFWGLAAQQPKFGSLFNEAMEADSQLLARAVVEECEGVFEGLNSLVDVGGGTGTMAKAIAKAIAKAFPNINCTVFDQPHVVANLQGTHNLDFVGGDMFEKIPPANAIFLKWILHDWSDEESVKMLKKSREAILSKNEGGKVIILDINVSADNKKMDKKSIETQLMWDMLMMVDLNGKERSEAEWEKLFLTAGFSHYKITHTLA

>ONI16913.1 hypothetical protein PRUPE\_3G129400 [Prunus persica]

MGSEVRASHELLQAQAHIWNHIFSFINSMSLKCAVQLDIPDVIQKHGQPMILSELVSALPISPTKAHFIPRLMRILVHSGFFAKESLSGGSEQGYVLTDASALLLKDNPMSTRPFLLAMLNPILTDPWQYLTTWFQNDNPTPFHVVHGMTFWDYGNQDPTLAHFFNDAMASDARLISSLMIDDFKGVFQGVDSLVDVGGGTGTVAKSIANAFPHMKCTVFDLPHVVADLKGSKNMEYVAGDMFEAVPAADAIFLKWILHDWSDEECVKILERCKKAITREGKKGKVIIVDMTVENKNKDKESGETQLFFDMLMMVLVKGKERNDKEWAKLFSDAGFSHYKITPYLGLRSLIEVYP

>ONI16915.1 hypothetical protein PRUPE\_3G129600 [Prunus persica]

MCINLNSHHILSQQQGMGSEVRASHELLQAQAHIWNHIFSFINSMSLKCAAQLGIPDVIQKHGQPMTLSELVSALPISPTKAHFIPRLMRILVHSGFFARESLSGGEQGYVLTDASALLLKDNPMSARAFLLAVLNPILTDPWQYLTTWFQNDNPTLFHVVHGMTFWDYGNQDPALAHFFNDAMASDARLISSLVIDEYKGVFQGVDSLVDVGGGTGTMAKSIADAFPHMKCTVLDLPHVVANLKGSKNLEYVAGDMFEAVPAADAIFLKWILHDWSDEECVKILEKCKEAITREGKKGKVIIVDMTVENKNTDKESGETQLFFDMEMMVLATGKERNENEWAKLFFDAGFSHYKITPCLGLRSLIEVYP

>ONI16919.1 hypothetical protein PRUPE\_3G129800 [Prunus persica]

MGSEVRASHELLQAQAHIWNHIFSFINSMSLKCAVELDIPDVIQKHGQPMILSELVSALPISPTKAHFIPRLMRILVHSGFFARESLSGGSEQGYVLTDASALLLKDNSMSTRPFLLAMLNPILTDPWQYLTTWFQNDNPTPFHVVHGMTFWDYGNQDPTLAHFFNDAMASDAQLISSLMIDDFKGVFQGVDSLVDVGGGTGTVAKSIADAFPHMKCTVFDLPHVVADLKGSKNLEYVAGDMFEAVPAADAIFLKWILHDWSDEECVKILERCKVAITREGKKGKVIIVDMTVENKNKDKESGETQLFFDMLMMVLVKGKERNEKEWAKLFSDAGFTHYKITPCLGLRSLIEVYP

>ONI18734.1 hypothetical protein PRUPE\_3G235300 [Prunus persica]

MAMLEVKEEEAILQGQVDILRYTYNFVESMALKCAVELGIADIINSHGQGQPITLSQIAPQIASPSTDLDLLSRLLRFLVHMNLFEATIDPKTGDALYGLTSSSKWLLSNEEQSLAPLVLMANQPHHLASWHYLSQCIKEGGCGFQKANGFSLYDIPSEKSELGNYFKEGMACTSRIVMKAILSTYKQGFDGVGLIVDVGGGLGTAVAEIVKAHPHIRGINFDLADVVATAPKYPGVIHVGGDMFDVIPKADAIFMKWILHNWNDEKCTQILKNCRKAIPEKIGKLVIVDGVLLPDNGLWDSFVQRYDLTMMVQTINGKERSEVEWKKLLREGGFGRYKIIKIPSFLSIIEAYPE

>ONI18736.1 hypothetical protein PRUPE\_3G235500 [Prunus persica]

MEATEAEAMLRGQADIWKYMFGFADSMALKCAVELRIADIIHSHAPTDHMITLSQIASHLIAPSPDITCLTRIMRLLVRRNIFAVHHPSEGGEPVYGLTYSSRWLLHDSEMSLAPMLVMENHPSLMAPWHYFSQCVREGGPWAFKKAHGLEIWDFASENPGFNKLFNDGMACTARIVMKAILTEYGRWFDGVGSLVDVGGGTGSAVADIVQAYPNIKGFNFDLPHVVATAPAYHGVSHVGGDMFEDHIPNADAVFMKWIMHDWNDSDCIKILKNCRKAIPERGGKIMIADIVLEPSGDGVLDDTRLVFDLVMIAHASGGKERTENEWEKILKEGGFPRYKIIKIPALLSIIEAYPV

>ONI23621.1 hypothetical protein PRUPE\_2G199000 [Prunus persica]

MAFPLERKIHPKINHAEPEDEITKEEEEESFCYAIQLPERVQAPSSLRLILQPRLAPMMMDRILRLLTSHSVLHSSLAAANEDENGGSDFQRWILHDWTDEHCLKLLKNRYRAIPDDGKQCCGSTSQLDVIMMTEIPGGKERSEQEFMALATGAGFSGIRYECFVCNFWVMEFFK

>ONI23622.1 hypothetical protein PRUPE\_2G199100 [Prunus persica]

MASSLERKIHPKINHAEPEDEITKEEEDESFCYAIQLVGSSVLSMSLQSAIELGVFDIIGKEGPGAKLSSSEIAAKIGAKNPEAPMMIDRILRLLTSHSVLHCSLVSANEDENGGGSDFQRVYSLGPVSKYFVNDEEGGSLGPVLTFTQDKVYMESWSQLKDAVVEGGIPFNRVHGTHAFEYPGLDPRFNQAFNTAMFNHTTIVIKKLLHIYKGLEDKNLTQLVDVGGGLGMTLNLITSRYQHIKGINFDLPHVVNHAPSYPGVEHVGGDMFASVPNGDAIFMKWILHDWSDEHCLKLLKNCYKAIPDNGKVIVVEALLPAMPDTSTAVKSTSQLDVMMMIQYPGGKERSEEEFMALATGAGFNGIRYECFVCNFWVMEFYK

>ONI23623.1 hypothetical protein PRUPE\_2G199100 [Prunus persica]

MASSLERKIHPKINHAEPEDEITKEEEDESFCYAIQLVGSSVLSMSLQSAIELGVFDIIGKEGPGAKLSSSEIAAKIGAKNPEAPMMIDRILRLLTSHSVLHCSLVSANEDENGGGSDFQRVYSLGPVSKYFVNDEEGGSLGPVLTFTQDKVYMESWSQLKDAVVEGGIPFNRVHGTHAFEYPGLDPRFNQAFNTAMFNHTTIVIKKLLHIYKGLEDKNLTQLVDVGGGLGMTLNLITSRYQHIKGINFDLPHVVNHAPSYPGVEHVGGDMFASVPNGDAIFMKVIFEFLKH

>ONI23625.1 hypothetical protein PRUPE\_2G199300 [Prunus persica]

MASSLERKSHPKINHVEPGDEITREEEEESFYYAMQLVGSSVLSISLQSAIELGVFDIIDKEGLGAKLSSSGIAAKIGTKNSEAPMMMDRILRLLTSHSVLHCSLVAANEDENEGGSLGPLMALDQDKVFMKSRSQLKAAVVEGGIPFNKVHGMHAFEYPCLDPRFNQVFNTAMFNHTTIVTKKLLHIYKGLEDKNLTQLVDVGGGLGVWNMFASVPSGDAIFMKWILHDWSDEHCLKLLKNCYKAIPDNGKVIVVEALLPAMPETS

>ONI23626.1 hypothetical protein PRUPE\_2G199400 [Prunus persica]

MASSLERKSHPKINHAEPEDEITKEEEDESFCYAIQLVGSSVLSMSLQSAIELGVFDIIAREGPGAKLSSSEIAAKIGTKNPEAPMMVDRILRLLTSHSVLNCSAVAANGGSDFQRVYSLGPVSKYFVNDEEGGSLGPVLTLIQDKVFMESWSQLKDAVVEGGIPFNRVHGTHAFEYPGLDPRFNQAFNTAMFNLTTIVIKKLLRIYKGLEDKNLTQLVDVGGGLGVTLNLITSRYQHIKGVEHVGGDMFASVPSGDAIFMKWILHDWSDEHCLKLLKNCYKAIPENGKVIVVEGLLPAMPDTSTAVKSTSQLDVMMLTQNPGGKERSEQEFMALATGAGFSGIRYECFVCNFWVMEFFK

>ONI23627.1 hypothetical protein PRUPE\_2G199400 [Prunus persica]

MASSLERKSHPKINHAEPEDEITKEEEDESFCYAIQLVGSSVLSMSLQSAIELGVFDIIAREGPGAKLSSSEIAAKIGTKNPEAPMMVDRILRLLTSHSVLNCSAVAANGGSDFQRVYSLGPVSKYFVNDEEGGSLGPVLTLIQDKVFMESWSQLKDAVVEGGIPFNRVHGTHAFEYPGLDPRFNQAFNTAMFNLTTIVIKKLLRIYKGLEDKNLTQLVDVGGGLGVTLNLITSRYQHIKGINFDLPHVVNHAPSYPGVEHVGGDMFASVPSGDAIFMKWILHDWSDEHCLKLLKNCYKAIPENGKVIVVEGLLPAMPDTSTAVKSTSQLDVMMLTQNPGGKERSEQEFMALATGAGFSGIRYECFVCNFWVMEFFK

>ONI23628.1 hypothetical protein PRUPE\_2G199500 [Prunus persica]

MASSLERKSHPKINHVEPGDEITKEEEEESFCYAMQLVGSSVLSISLQSAIELGVFDIIAKEGPGAKLSLSEIAAKIGTRNSEAPMMMDRILRLLASHSVLHCSLVAANEDENGGSDFQRVYSLGPVSKYFVNDVEGGSLGPLMALDQDKFVLIIILIGSQLKDAVVEGGIPFNRVHGMQTFEFLGLDPRFNQVFNTAMFNHTTIVIKKLLHIYKGFQDKNLTQLIDVGGGFGVTLNLVTSRYPHIRGIYYDLPHVVNHPLPILVWNMFASVPIPSGDAIFLKWILHNRSDEHCLKLLKNCCKAIPDNGKVIVVEELLPAMPDTRDTSTAVKSTSQLDVIMMTQIPGAKERRTRNHGPGNWC

>ONI23629.1 hypothetical protein PRUPE\_2G199600 [Prunus persica]

MASSLERKSHPKINHAEPEDEITKEEEDESFCYAMQLVGSSVLSMSLQSAIKLGIFDIIARKGPGAKLSSSEIATKIGTENPEAPVMVDRILRLLTSHSVLNCSAVAANGGSDFQRVYSLGPVSKYFVNDEEGGSLGPLLTLIQDRVFLESWSQLKDAVVEGGIPFNRVHGMHAFEYPGLDPRFNQVFNTAMFNHTTIVIKKLLHIYKGLEDKNLTQLVDVGGGLGVTLNLITSRYQHIKGVEHVGGDMFASVPSGDAIFMKWILHDWSDEHCLKLLKNCYKAIPDNGKVIVVEALLPAMPETSTATKTTSQLDVLMMTQNPGGKERSEQEFMALATGAGFSGIRYECFVCNFWVMEFFK

>ONI23630.1 hypothetical protein PRUPE\_2G199600 [Prunus persica]

MASSLERKSHPKINHAEPEDEITKEEEDESFCYAMQLVGSSVLSMSLQSAIKLGIFDIIARKGPGAKLSSSEIATKIGTENPEAPVMVDRILRLLTSHSVLNCSAVAANGGSDFQRVYSLGPVSKYFVNDEEGGSLGPLLTLIQDRVFLESWSQLKDAVVEGGIPFNRVHGMHAFEYPGLDPRFNQVFNTAMFNHTTIVIKKLLHIYKGLEDKNLTQLVDVGGGLGVTLNLITSRYQHIKGINFDLPHVVNHAPSYPGVEHVGGDMFASVPSGDAIFMKWILHDWSDEHCLKLLKNCYKAIPDNGKVIVVEALLPAMPETSTATKTTSQLDVLMMTQNPGGKERSEQEFMALATGAGFSGIRYECFVCNFWVMEFFK

>ONI23632.1 hypothetical protein PRUPE\_2G199800 [Prunus persica]

MASSLERKSHPKINHVETEDEITKEEEEEILCYALQLVGSFALSISLQSAIELGVFDIIAREGPGAKLSSSEIAAKIGTKNSEAPMMMDRILRLLTSHSVLHCSLVAANEDENGASDFQRVYSLGPVSKYFVNDEEGGSLGPMMALTQDKVFTESWSQLKDAVVEGGIPFNRVHGMQTFEFLGLDPRFNQVFNTAMFNHTTIVIKKLLHIYKGFEDKNLTQLVDVGGGFGVTLNLVTSRYPHIRGINYDLPHVVNHAPSYPGVEHVGGDMFASVPSGDAIFVKWILHNWSDEHCLKLLKNCYKAIPDNGKVIVVEELLPAMPDTSTAVKATSQLDMIMMTQIPGAKERSEEEFMALATGAGFSGIRYECFVCNLWVMELFK

>ONI23635.1 hypothetical protein PRUPE\_2G200100 [Prunus persica]

MASSLERKSHPKINHAEPEDEITKEEEDESFCYAIQLVGSSVLSMSLQSAIELGVFDIIAREGPGAKLSSSEIAAKIGTKNPEAPMMVDRILRLLTSHSVLNCSAVAANGGSDFQRVYSLGPVSKYFVNEEEGGSLGPVLTLIQDKVFMESWSQLKDAVVEGGIPFNRVHGTHAFEYPGLDPRFNQAFNTAMFNLTTIVIKKLLHIYKGLEDKNVTQLVNLITSRWYQFQLAPCRKSCPFLSW

>ONI23636.1 hypothetical protein PRUPE\_2G200100 [Prunus persica]

MASSLERKSHPKINHAEPEDEITKEEEDESFCYAIQLVGSSVLSMSLQSAIELGVFDIIAREGPGAKLSSSEIAAKIGTKNPEAPMMVDRILRLLTSHSVLNCSAVAANGGSDFQRVYSLGPVSKYFVNEEEGGSLGPVLTLIQDKVFMESWSQLKDAVVEGGIPFNRVHGTHAFEYPGLDPRFNQAFNTAMFNLTTIVIKKLLHIYKGLEDKNVTQLVNLITSRWYQFQLAPCRKSCPFLSW

>ONI25770.1 hypothetical protein PRUPE\_2G319700 [Prunus persica]

MGSTGETQMTPTQVSDEEANLFAMQLASASVLPMVLKAAIELDLLEIMAKAGPGVFLSPTDIASQLPTKNPDAPVMLDRMLRLLASYSILTYSLRTLADGKVERLYGLGPVCKFLTKNEEGVSIAPLCLMNQDKVLVESWYHLKDAVLEGGIPFNKAYGMTAFEYHGTDPRFNKVFNRGMADHSTITMKKILETYKGFEGLTSVVDVGGGTGAVLNMIVSKYPSIKGINFDLPHVIEDAPQYPGVEHVGGDMFVSVPKGDAIFMKWICHDWSDEHCLKFLKNCYAALPDNGKVILGECILPVAPDSSLATKGVVHIDVIMLAHNPGGKERTEQEFQALAKGAGFQGFNVACSAFNTYVIEFLKKN

>ONI25771.1 hypothetical protein PRUPE\_2G319700 [Prunus persica]

MGSTGETQMTPTQVSDEEANLFAMQLASASVLPMVLKAAIELDLLEIMAKAGPGVFLSPTDIASQLPTKNPDAPVMLDRMLRLLASYSILTYSLRTLADGKVERLYGLGPVCKFLTKNEEGVSIAPLCLMNQDKVLVESWYHLKDAVLEGGIPFNKAYGMTAFEYHGTDPRFNKVFNRGMADHSTITMKKILETYKGFEGLTSVVDVGGGTGAVLNMIVSKYPSIKGINFDLPHVIEDAPQYPGINHVGGDMFVSVPKGDAIFMKWICHDWSDEHCLKFLKNCYAALPDNGKVILGECILPVAPDSSLATKGVVHIDVIMLAHNPGGKERTEQEFQALAKGAGFQGFNVACSAFNTYVIEFLKKN

>ONI34719.1 hypothetical protein PRUPE\_1G494500 [Prunus persica]

MSSRISEKTNANPMSQQQEEEKEEEEVGKLAIRLANVVILPMVLKSAIELNIIDIISAAGDGKFLSPSEIAASLPTKNPDASVLLDRMLRLLTSHSILKCSVRTGQDGKVERLYGAGALCKFLVKDQHDGVGSVGPLLLLHHDKVFMESWCHFNDAVLEGGIPFNRAYGMTAFEYPETDERFNRVFNQAMSNHTTLILKKIFDVYKGFEGLNVLVDVGGGIGVTLNLITTKYPRIKGINFDLPHVLADAPSYPGVEHVGGDMFVSVPQGDAIFMKWILHDWSDEHCLTLLKNCCKALPSSGKVIIVESILPDIPDSSVTSNIVCEQDLLMLTVNPGGKERTKHEYEDLAVKSGFSGCEVICNAYNSWIMEFHKNANP

>Solyc01g068550.2.1 (SlASMT1)

MSSSESTSSELLHAQAQIWNYIFNFISSSAVRCAFQLGIPDVLYKHDKPMCLSDISAELSVVNSSKVSFLPILMQFLVQSGFLNQHEDHYSLTPASCLLAKDDPFNVRSLLLLNHGQAFSKAWPELSDWFQNDSPTPFHTAHGKSLWDFIGEEQPSVLGDIFNDALASDSRLNTNVLIAECKHVFEGLTSLVDVGGGTGTVSIAIAKAFPNIKCTVLDLPQVVGDLKGSGNLDFVGGDMFDMIPHTNAILLKCVLHDWNDEDCVKVLKKCKESIPSREKGGKVIIIDTVLEDPKQSNEFVRAQHNMGMLMMVLFAAKERTEKEWEKLFSEAGFTEYKIFPALGLRSLIEIYP

>Solyc02g077510.2.1 (SlASMT2)

MYFHCQTCGVPTLATSLCFYPVSFSLCGCVSGTVEALTELDAIHRLMGLLVYSGFFATTNTILLDESSENQQGYILTPSSKLLLKSEIPNLSPFVRAIVAPVSVNPWQSVGDWFLGNETTPFETPHGAPMWEFFHQNPGFNNVFNEDCKEVFQDMDSLVDVGGDTGIIANTILAAFPHLKCTVLDLPHVVANMPDTHNLKYVGGDMFHSIPSADSILFKHVLHNWSDEDCVKILKRCRGAIKDKNEGRKGKFLIIDMVLDGDDEEANMTEV

>Solyc02g077520.2.1 (SlASMT3)

MDVPMSSEMFEAQAHIYKHAFSFANSMVLGCAIQLGIPDVIHSHKQPMTLSQLVSHLKLPLEKSDAIHRLMRLLVYSGFFATTDFLDENSESQQGYVLTPSSKLLLKSEIPNLSPFARAMIDPVMVNPWQSLGDWFLGNETTPFETAHGAPMWKFCDQNPRFSNVFNEAMASDSQMMCLVVKDCKQVFQEIDSLVDVGGGTGIIANTILAAFPHLKCTVLDLPHVVANMPDTENLKYVGGDMFHSIPSADAILFMHVMHNWSDENCVKILKRCGEAIKDKNEGRKGKVLIIDMVLDRDKEEANMTEVKLIFDVLMMVLVTGRQRTEKEWEKLFLEAGFMSYKITPLFGLRSLIEVFP

>Solyc02g077530.1.1 (SlASMT4)

METNNNVERANELFKAQAHIYKHAFAYANSMALNCAIQLGIPDIIHNHKKPITLPDLLSGLKLPSSKSNAIHRLMRLLVHAQFFDIIKLEENSETEGYVLTTSSRLLLKSEIPNLLPCVRLMVDPVLVTPWQLLGEWFHKNEEATPFETAHGMPMWDFCAQNPIFDTAFNEAMASDSQMMKLVVKDCREVFEGLNSLVDVGGGTGVIAKTILEAIPHLKCTVLDLPHVVANMPQTENLIYVGGNMFQCIPHADAILLKHVMHDWSDEDCVKILKRCREAIEDKDEGRKGKVLIIDMVLGRDEEEANMTEVKLIFDVLMMVVTTGRQRTEKEWEKLFTEAGFMSYKITPLLGLRSLIQVFP

>Solyc03g097700.2.1 (SlASMT5)

MALPNNIGDETNEVLAAQAHIANHVFNYINSMSLKCAIQLGIPDIIHNHGRAMTQSDLVNALPINKSKGHDCIYRLMRILIHAGFFTQGEEGYLLTPTSRLLLKNEPLSLAPFVQAQLDPVLMDPWHSLGEWFANEDSTPFATAHGKPLFEYAGDEQRLNNLFNEAMGCDARLIMSVLIKNGKGVFEGLKSLVDVGGGIGTVAKAISNAFPELKCSVFDLPHVVEGLEGGKNLTYIAGDMFKFVPSADAILLKWILHDWSDKDCVKILKKCKEAIPSKENGGKVIVIDIVIDNQKRDNKSFETQLFSDVLMMVHVSGKERNEQEWAKLFSNAGFSDYKISPILGLRSVIEVYP

>Solyc06g060200.1.1 (SlASMT6)

MMDHTYSGVFNKAMFNHTTLMMKKILDKYKGFENIKTLVDVGGGLASNLKMITTKYPTIKGTNFDVPHVVQHAPTYKGVGHVGGDMFESVPEGHAIFMKKWILYDWSDSQCVKLLKNCYKATPAEN

>Solyc06g064500.2.1 (SlASMT7)

MASNNNICAYELIEAEAQSWDYILSYLRPSCIKCAIQLGIPDILHKNADPIMSLSDLIAALPNLNPSKTTFIPILMRVLVDFGLFNYHQQQGDGYSLTTVGRLLVENHHFGNRSFFLFAQHPVVLNTAASVGDWLKDDLRTAFETADGKSHWDYCGADPEFNGVFNDAMAGDSRLMSNLLISDCCAGVFEGLTSLVDIGGGTGAVAMAIAGAFPSLKCIVLDLPHVIADRKGSGNLEFVAGSMFDKIPHANAILLKWILHNWDDEDCVKLLKKCKESISSRENGGKVIIIDMIMEDNYNNKQLVQSQHLMDLIMRITYASKERTEKEWEKLFLEAGFSGYKIITSLGLRSLIEIYP

>Solyc06g064510.2.1 (SlASMT8)

MANKKNNMYANELIEAEALSWDYILTYLRPPCIRCAIQLGIPDILHKSAHPIMSLSDLIAALPNVNPSKTTFIPILMRVLVDLGLFNYHPQQGDGYSLTSVGRLFVESDPSNKRSIFTFLIQFEIVDSMSDWLRNDLPTAFETAHGKSIWDYCSGESEYSGVFNDAMASDSKLISNLLISDCCSGVFEGLTSLVDVGGGTGTVAMAIAGAFPSLKCTVLDLPHAIGDRKGTQNLEFVAGNMFDKIPHANAILLKWILHDWNDEDCVKILKKCKESIPSKENGGKVIIIDIVMEDNCSNNEQLVQSQHLMDLLVRITYDSKERSNKEWEKLFLDAGFSGYKIITSLGLRSLMEVYP

>Solyc10g008120.2.1 (SlASMT9)

MVVPIVGEHETEILHAQTHIWNHIFSFINSMSLKSAIQLNIPDIIHKHGKPMTLDELANALSINHSKITHLRRLMRILVHSGFFLKSVSGSGSESGSGEGGYVLAPPALLLLKDEPLTVTPFLLAMLDPILVKPWHHVSEWFTSDEPTAFEVAHGRTFWDYAGHEPRLNHFFNDAMASDAKLVMSVVMKYSKDVFEGLNSIVDVGGGTGTVAKTIAKTFPNLQCTVFDLPHVVEGLEGSDNLTYVGGDFFVSIPHAEALLLKWILHDWSDEESVKILKKCKEAIPSKEKGGKVIIIDMMVDNKIGDDESIETQIFFDMLMMVLVTGRERSERGWAKIFSEAGFSDYKVTPILGLRSLIEVYP

>Solyc10g079540.1.1 (SlASMT10)

MADHNENLTPSELLQAETQSWNQLYFFIEHVTLKCALQLDIPNVITKHDKPMTISELMSSLPISPSKYPYFHRLTRILVHYGFLILQKHDDNNVDDDKGCYSLAPADCYVVKDGPWNSMEDQDTFFFKAWSCLGDWFKNDDPSAFYTAYGDLFWSKLSSDSSTSNWFNENMSRDSRSFMNVLIGNEYKDVFKGLTSLVDVGGGTGTVAMSIAKSFPDMKCIVLDLPPVVANLQGSENLEFVAGDMFQKIPPANAVLLKSILHDWNDEECVKILKNCKEALRGSGKVIIIDMVMENTELDDESVQAQLFIDMLMMVFVGSKERNEKEWEKLFSISGFTSYKIVLTLGLRSVIELYP

>Solyc12g041960.1.1 (SlASMT11)

MALPNDNTREILAAQAHIWNHTFSYINSMSLKCAIQLGIPDIIHSHGRAMTLSDLVNALPINNNVKTLDYIFRLMRILIHGGFFNKIKVNDKEEGYLLTPASCLLLKDEPLSQVAFVQTELDQSFMDPWHSLIKWIRSDHDNSSTPFAISHGKPLFEYDETQPNINRQFNEIMASDSRLVISVLIKNCKGVFEGLKSLVDVGGGIGIVGKVLADAFREMNCIVFDLPHVIEGCEGSKNLCYVGGDMFKFIPSANAILLKWVLHDWSDEECIKILKKCKKAIPSKEKGGKVIIIDMVLMDRKIEKGDGKSYETQLFFDMLMMVHVSGKERNQQDWAKLFCSAGFSDYNIIPMLGLRSIIEVFP

>Sphmag15G072100|Sphmag15G072100.1

MAADGSSDHRAQAVEEDHHETPLRNGIVVGEQDTAAARHAAMRLATMMVVPAALKAAIELGVFEILAKARGAAPRAKSLTAKEIASQVIQPDSDGLSVINDRYLERILRLLASENVVSESAVAVASGNSSCSTSGMERCYALQPAGTYFVRSDEDAASLAPLLVQLQDRDFLEPWHHLSATVMDDSTEPFTKAHGEPVFQYTSHNPRLDKIFNTSMAHHSRLYTQAVLQVYHGFQDVKCLVDVGGGTGSSLALIAAKYPHIRGINYDLPHVTAASPAHPGVEHVGGDMFKSVPSGDAIFMKWILHDWNDSECVTILRNCFNALATSGGKVIAVESVLPDLVLQSELGAGPTVALRADLLMLACSAVGARERTLQEFRELGKTAGFASVSVVVSIDFLSVLEFRKA\*

>Sphmag02G186300|Sphmag02G186300.1

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>Sphmag02G187200|Sphmag02G187200.1

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>Sphmag02G179800|Sphmag02G179800.1

MATNSYRVAHANGTTENLGKQSSSFHQNYVARHAALDFALYSVVSGTLKAAIELGVFEIAKAGASASQKSLTAKEIAEQLVRPTANGTAVNSGYLQRLLRVLASVNIVSESVAVVAAGPGNFTSYNTHHQRSYALTPIGKYFVQGEDGFSWAPLVLMSEDWVFKKAWDHLSAAVLDDVDPFVRAHGKSEFQLNNEDPRVNKLFNTAMSSHARIYMEAMLEAYHGFQDVNCLVDVGGTGASLASITAKYPHIRGINFDLPHVVATSPAYPRVEFVGGNMFESIPSGDAIFMKSILHWNDEDCVTILKNCFKALPSSGGKVIVMESVLPDSINLQDEDGGVKSSLALRVDVVMLAYSGGAKERTLHEYQQLADATGFASLALITTVDFLSVLEFTRVAV\*

>Sphmag02G014100|Sphmag02G014100.1

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>Sphmag05G004500|Sphmag05G004500.1

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>Sphmag05G005000|Sphmag05G005000.1

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>Sphmag05G009900|Sphmag05G009900.1

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>Sphmag05G004700|Sphmag05G004700.1

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>Sphmag05G010500|Sphmag05G010500.1

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>Sphmag05G004900|Sphmag05G004900.1

MAVNGRSDHHAQAADEDHHETPLRNGLVDEQDAAARDAAMRLATIMVVPAALKAAVELGFEILAKARGAGKSLTAKEIVSQVLPPDSGSVINYAYLERILRLLASENVVRESAVTVPSYFVRSDEDAGSLAPLLVHLQDRVSLEPWQHLSATVLDDSTDPFRRAHGESVFQYINHNPSEKIFHAAMGHHSRLYMKAVLRAYHGFQDVKCLVDVGGGTGSSVALITAKYPHIRGINYLPHVAAASPAYPRVEHVGGDMFESVPCGDAIFTKWVLHDWNDSECLMILRNCFNALPASGKVIAAESVLPDLLLQSELGAGSEVALRLDLIMLAHASPGAKERTLQEFRQIAKAAGFAVSVVVAIDFLSVLEFNKA\*

>Sphmag05G011000|Sphmag05G011000.1

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>Sphmag05G004800|Sphmag05G004800.1

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>Sphmag05G010900|Sphmag05G010900.1

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>Sphmag05G010600|Sphmag05G010600.1

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>Sphmag05G016100|Sphmag05G016100.1

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>Sphmag05G011100|Sphmag05G011100.1

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>Sphmag05G009800|Sphmag05G009800.1

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>Sphmag05G005100|Sphmag05G005100.1

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>Sphmag05G011200|Sphmag05G011200.1

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>Sphmag09G101500|Sphmag09G101500.1

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>Sphmag14G045600|Sphmag14G045600.1

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>Sphmag04G137300|Sphmag04G137300.1

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>Sphmag04G006900|Sphmag04G006900.1

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>Sphmag12G011200|Sphmag12G011200.1

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>Sphmag12G001200|Sphmag12G001200.1

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>Sphmag12G011300|Sphmag12G011300.1

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>Sphmag12G011800|Sphmag12G011800.1

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>Sphmag12G011500|Sphmag12G011500.1

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>Sphmag12G011100|Sphmag12G011100.1

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>Sphmag12G011700|Sphmag12G011700.1

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>Sphmag12G011400|Sphmag12G011400.1

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>Sphmag12G012100|Sphmag12G012100.1

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>Sphmag12G011600|Sphmag12G011600.1

MAEAHGSKAQQPVADEEEFMADRAVLYPLILGFVGSSVLRTAVVLGLPNIIVRAGPDETTVKQIGAQLKSESVNEFGLQRVLTALVKWKLFRCTKAETSKMQYGLTPVSQLLEFWKYCDNPEFAKCFNDGMTAMINIESIALRKYEGFKDIKTLVDVGGGVGKTLETIISTYPHIHGTYDHHFSSTHHACVHIMRCWNCENCLKILNNCQTALPEKGKMFIYDFVLESIGGLPQIFTMMMTLTNTGMERTEQWRNLLTTAGFSAINFIQLLAEQWLIEAVK\*

>Sphmag01G164100|Sphmag01G164100.1

MAPNSYSDAQIDLNKQSSSVYYYDAARNAAMELTGYCSVSGCMKAAVELGVFEVLAKAASGRKSLTAKEIAEQLVRPGANGAVVNQGYLQRVLRLLASVNVLSESVEVVAAEPGNLTSNTHHRRSYALTQVGKHFVRGEDGVSLAPLMLMNEDWVFKKTWDHLSAAILDDSVDPFVRHGTSQFQLNNEDSRVDKVFHTAMASHSRLYTQAVLGAYQGFQDVNCLVDVGGGLGSSLAITAKYPHIRGINFDLPHVVAAAPPYPGVECVGGDMFESVPTGDAIFMKWILHDWSDEDCRILRNCLKALPASGGKVIVVDTVLPESISLESENAGARSFVGLRTDVAMLAYNSGGAKETLHEFQQLADAVGFARMELVVTVDFMSVLEFTKTAA\*

>Sphmag18G023800|Sphmag18G023800.1

MATNSYRVAHSNGTTGNFGKQSSSVHQNDVARHAAMEFTLYSVVSGTLKAAIELGVFEIAKAGASASQKSLTAKEIAEQLVRPTANGTAVNSGYLQRFLRLLASVNIVSESVAVVAAGPGNFTSYNTHHQRSYALTPIGKYFVQGEDGVSLAPFILMSEDWVFKKAWDHLSAAVLDDVDPFVRAHGKSEFQLNNEDPRVDKLFNTAMSSHSRIYMEAMLGAYDGFQDVNCLVDVGGTGASLASITAKYPHIRGINFDLPHVVATSPTYPMCMIGVEFVGGNMFESIPSGDAIFMKVLHDWNDEDCMTILKNCFKALPSSGGKVIVMESVLPDSINLQFENSGVKSLLGLRIDLVLAYNSGGAKERTLHEFQQLADATGFASLALITTIDFLSVLEFTRVAT\*

>Sphmag16G083200|Sphmag16G083200.1

MAEANYDGSKMEQSAAADQEAELMAGHDVLCSLLFGFVGSFLLRAAVVLGLPDIIARAAPDGTLTVKQIAAQMIQKSGVETVNEFELQRVLTALANYKIFRSCTQDVGSDQEMQYGLTASKLLVTENNPHNQAPGVLFQTDPVAQAPYRQLHRCVLYGEQAFQSAHGKDVWKYVNDDEYSKCFNAAMASTTTIDLIAVRKYQGFKDIKTLVDVGGGVGKALETIISTFPHIHGINYLPHVVADAPTMPGIEHVAGSMFESVPSGDAIFMKHIMHDWNDNNCIKILNNCQRALPEKKVLIYDFVVQPSGGLPQIFDVVMMAHTNGGMERTQDQWRKLLTTAGFSAINFIQLMPQQLIEAVK\*

>evm.model.chr4.2085

MGSVENGLVIANEDEWLLGMEFGNFSCLPMAMKTAIELDVLQIIANAGDGAQISPREIVHIPTTNPDAAITLDRILRVLASHSVLSSSVTTDKNGKAQRVYGLTALCKYLVQNKDGVSAPLVLMNQDKVLMECWYHLKDAVLEGIEPFTKAHGVNAFQYHAKDPRFNNVFNRGMAEHTMLMEKILDTYQGFENFHELVDVGGGIGSTLNLIVSKYPHIKGICFDMPHVVAEAPHYPLRHIGGDMFDTIPSGQAIFMKWILHDWSDEHCVKILKNCYKALPEGGKVIVVDSILPVAETSPYARQAFHCDLLMLAYNPGGKERTEQEFRDLAKAAGFAGGIKPVCCVNGMWVIEFYQP\*

>evm.model.chr4.2087

MGSMEKGLIIANEEEWILGMELGNFSCLPMAMKAAVELDVLQIIANAGPGAQISPREIVHIPTENPDAAITLDRILRVLASHSVLSSSVTTDENGKAERVYGLTPLCKYLVQNKDGVSAPLVLMNQDKVFMESWYYLKHAVLDGSQPFTKAHGVNAFEYPAKDPRFNNVFNRAMAEHTMLMQKILDTYPGFKDVQEIVDVGGGIGSTLNLIVSKYPHIKGVNFDMPHVVAEAPQYPLRHVGGDMFDSVPSGQAIFMKWILHDWSDEHCLRLLKNCHKALPEGGKVIVVDSILPVAETSPYARQAFHCDLLMLAYNPGGKERTEQEFRDLAKATGFAGGIKPICCINGMWVMEFHQD\*

>evm.model.chr4.2086

MGSMENGLIIANEDEWLLGMELGNFSCLPMAMKAAVELDVLQLIANAGPGAQISPREIVHIPTTNPDAAITLDRILRVLASHSVLSSSVTTDENGKAERVYGLTPLCKYLVQNKDGVSAPLVLMNQDKVFMESWYYLKDAVLDGSQPFTKAHGVNAFEYPAKDPRFNNVFNRAMAEHAMLMQKILDTYPGFKDVQEIVDVGGGIGSTLNLIVSKHPHIKGVNFDMPHVVAEAPQYPLRHVGGDMFDSVPSGQAIFMKWILHDWSDEHCLRLLKNCHKALPEGGKVIVVDSILPVAETSPYARQAFHFDLLMLAYNPGGKERTEQEFRDLAKATGFAGGIKPVCCINGIWVMEFHQA\*

>evm.model.chr4.1806

MGSMEKGLIIANEEEWVLGMELGNFSCLPMAMKAAVELDVLQIIANAGHGAQISPREIVHIPTTNPDAAITLDRILRVLASHSVLSSSVTTDENGKTGRVYGLTPLCKYLVQNKDGVSAPLPFTKAHGVNAFEYPAKDPRFNNVFNRAMAEHSTMLMQKILDTYPGFKDVQEIVDVGGIGSTLNLIVSKYPHIKGVNFDMPHVVAEAPQSPGLRHVGGDMFDSVPSGQAIFMKWILDWSDEHCLRLLKNCHKALPEGGKVIVVDSILPVAAETSPYARQAFHCDLLMLAYNPGGKRTEQEFRDLAKATGFAGGVKPVCCINGMWVMEFHKQA\*

>evm.model.chr7.281

MDVLSQHIDPKLQAQALKFIVPFVPGLVLKSAVLLKVPDIIAKAGPDAYLSVHQIAAQLTQNPHLNYLSRILRYLAAVGVFSTTIDTSDEVRYGLTDMTKVFYVTENNPWSLVPMLLMNHEVFMAPWQHLHECVLEGGDAFQKANGKDMWAYGRDDPQVNNIVNSAMASPSKVVMKQVASYDGFSHVKTLVDVGGGLGAALAEISGVYPHIHGINFDLPHVVATAPVLPGIEHVGGMFESVPSGDAIFMKSVLHDWDDERCLKILQNCHKALPENGKIILAERVLPRHSDPNGTMFVVDLAMMAHTNGGRERTEKQWRALLENAGFSQMKILGRADRLPIKIVEGVKITKM\*

>evm.model.chr11.1112

MNGPLETNHATMDGLRLFESEEEELEGQAQAWGHIFAFVESLAVKCAALLGIPDIIARHPRATLSLPQIAESLPSKAPDVGCLLRIMRFLVSKNVFTSEVAVTQNGVPETRYGLTPSSWLLKHNQYLSMRPMLLMQNDKRSVAPWHHFNECVLEGGIAFERANGADIWSYASKDPEYHLFNDAMACNAKMVMKAILSKYDGFTALNSLVDVGGGIGTGIAEIVSVYPHIRGINYDLHVVATAPPFPGVEHIGGDMFASVPSADAVFMKWIMHDWNDEDCIKILKECRKAIPEDRGVIIADVVLNEEGRKKRALDPVGLVFDLVMVAHSSGGKERTEEEWRKLLSRAGFNRYNIIIPALQSIIEAFPS\*

>evm.model.chr7.280

MDAHSQHIDPKLQAKALEFIVPFVPGLVLKSAVLLRIPDIIARAGPDAYLSVHQIAAQLTQNPHLDNLSRILRYLAAVGIFSAAVDSSNRVRYGLTDMAKVFYVTENNHLSLVPVLLMNHEVFMAPWQHLHECVLEGGEAFQKANGKDMWAYGRDDPHVNNIVNSAMASSSKVVMKQVASYDGFKDAKMVVDVGGGVGAALAEIIGAYPHIHGINFDLPHVVATAPVLPGIEHVGGMFESVPSGDAIFMKSVLHDWDDEECLKILENCHKALPENGKIILAEIVLPQLSNPNGARFVVDLAMIAHTSGGRERSEEQWRALLENAGFSQIEILGRADRLPIKIVEGVKIAKM\*

>evm.model.chr6.245

MAARASSTEPPSSVDAQHKLYEMILCFAKPMALKSAVLLNIPDIIASEGHGDSLSLQQIAHISPPPQSMEYLLRILRFLASYDVFTERQWKRNGADKFFCESYHHLNESVLEGGYAFNAFGKSPWDYVSEHPNYNKTFNDGMVSHTRALMASALKIYDGFKNFKSVVDVGGGVGTAIMIAKHHTHLKVINFDLPHVIDTAPAIPGVEHVGGNMFEQIPPADAVFIKSILHDWDDEHVRILNKCREAIPENGKVIIVDVIVERNEGSMRRLGLLWDMIMMAFTTGGKERTEEEFKVFEKAGFKSYTLLKLPAVQSIVELSKA\*

>evm.model.chr10.1216

MDCSGDQVREIIEEKITGHEEDMESLIELCKRMFGFMDSLGLRWAVEMGIPIRTLFPNPPNPPSRLLLICPLSTEREIVGKEGKEVEYGLTPISKWLLTENGSCMNSMVMMQTHEAVFPWYHFGECVLRGGFPFEVVHGKSMFSFAKNNPDFGKLFNDAMASHSGMLMKHILSVYGDDRFKDLKSLVDVGGGDGTTVSQIAHSFPHIKCYNYDLPQVIHQAPPYPGVQHIAGDMFMVPHADAVFMKMILHDWGDEECMQILRNCRQAIPVDGKVIIVDVVLTKDGVRRRGFEEIGMMDMVMLAHQRGKERSEEQWKELLQASGFDCYKITPLPDHLSIIEAVPADRD\*

>evm.model.chr6.356

MAANASSEPHTLDAKHKLYEMILSFAKPMTLKAAVLLNIPDIIASEGHGASLSLQQIAAISPPSQSMEYLLRILRFLASYDVFTESVHVVRGEEKQWSFGLTAISELLVQKGNQHSLAFLLLAADKFFCESYHHLDESVLEGCYAFNKVYSKSPWEYVSEHPNFNKTFNDGMVSHTRLMASALKIYDGFRDVKTVVDVGGGVGTAISIIVKHHTHLKGINFDLPHVIATAPAIPGVHVGGNMFEQIPPADAVFIKWILHDWDDEDCVRILKKCREAIPDNGKVIIVDAVVERNEGLRRLGLLFDITMMTFTTRGKERTEDEFKLLFEKAGFKSYAFLKLPAVQSIIELYKV\*

>evm.model.chr6.355

MAGNASSEPHTLDAQHKLYEMILCFAKPMALKAAVLLNIPNIIASEGHGASLSLQQIAAISPPPQSMEYLLRILRFLASYDVFTESVHVVRGEEKQWSFGLTAISELLVQKGNQHSLAFLLLVADKFFCESYHHLDESVLEGCYAFNKVYSKSPWEYVSEHPNYNKTFNDGMVSHTRLMASALKIYDGFRDVKTVVDVGGGVGTAISIIVKHHTHLKGINFDLPHVIATAPAIPGVHVGGNMFEQIPPADAVFIKWIIHDWDDEDCVKILKKCREAIPENGKVIIVDAVVERNEGLRRLGLLFDIAMMTFTTGGKERTEEEFKLLFEKAGFKSYAFLKLTAVQSIIELYKV\*

>evm.model.chr8.207

MADKYSNRDSLFENEEEELRGHAQVWKYVLAFVDSMAVRCAVLLGIPDMISREGHHATLLSEISEKLPTKSPDVGCLFRLLRFLVSKNVFSAKSVVRADNGICETRYGLTPVSKWLVTSRDVNLVPMFLMINQTNLAPWYCFNECILNGGITAFERANGAEPWSFAASHPEYSKIFNNMACNTKISMKALLSNYDGFQSLNSLVDVGGGTGTAAEEIVRAYPHIKAISYDLPHVVAAPSRPGVEYVGGDMFAGVPSADAVFLKWIMHDWNDEDCIRILNQCRNAIPETGKVIIVDVIAEESDEKENGILRETKLVLDLVMVTNTIGGKERTEAEWKRVLCGAGFGRYNIISIQAHSVIEAFPSESTIY\*

>evm.model.chr6.246

MATSSSSIEPPSSVDAQHKLYEMILCLAKPMALKAAVLLNIPDIIASEGHGDSLSLQQIAHISPPPQSMEYLLRILRFLASYDVFTESLQVVGEETQWRFRLTAISELLVQKGNQQSLPFLLMAADNFFSESFHHLHESVLEGGSAFNKAYGKSPWEYVSEHPKYNKIFNDGMVCHTTFMASALKIYDGFKNFKTVVDVGGGVGTAISLIVKHHTHLRGINFDLPHVIATAPAIPGENVGGNMFEQIPPADAVFIKWILHDWDEEQCVRILNKCREAIPENGKIIIVDAVVERNKSMRRLGLSFDIAMITFTSGGKERTEEEFKALFEKAGFKSYTLLNLPAVQSIIELSKD\*

>evm.model.chr10.1211

MDYKRGCSGHEVQEITEDKITAHAEDMEGFIELWKRMFGFMDSLGLRWAVEMGIPDIISAGPQSAQQIASHLPCESPQVDFISGILRFLAMRGVFTEIVDKEGKEEVEYGLTAISKWLTENGSCMNSMVMMQTHVAVFAPWYHFGESVLRGGFPFEVVHGKSLFPFAKDNPDFGKLFDAMASYSRMLLKHVLSVYGDEDRFKDLKSLVDVGGGDGTTVSQIAHSFPHIKCYNYDLPVIQDAPPYPGVQHIAGDMFMTVPHADAVFMKLILHDWGDEECMQILRNCRQAIPVDGKVIVDVVLTKDGVRRRGFEEIGVMMDMVMLAHQRGKERSEEQWKELLQASGFDCYKITPLPHLSIIEAVPADRN\*

>evm.model.chr10.1222

MDHSKSGSSNEHGEEEEQNKIHVRDQEDMDGFIELWKRMFGFMDSLGLRWAVEMGIPDISKSGPQSAQQIASHLPSESPHIDFISRILRFLAMRGVFTETVGEEEKEVRYGLTPISKWLTENSRCMNSVILVQTHEKDIAPWYFFGQCVLRGGFPYEIAHGKQRFSFAKDDPDFNKLNDSMASCSRTLIGNILTTYSDGFKRLKSLVDVGGGDGTTISNIAQSFPHIKCYNYDLPHIQEAPPYPGVEHIAGDMFISVPHADAIFMKTVLHDWEDEECKKILKNCRQAIGQEDGHVIVDAVLREAGKKRSGFDEIGVMMDMVMLSHQRGKERSESQWKELLEASGFDRYSFIPLPSEMSIIEAFPSI\*

>evm.model.chr10.672

MASSAEEFSSASFHPCDDGNDHENLWRSQASFWNMTFSILPAMVVKSALRLRLPDIIARGPDAALSLQDIAAHLPTQTPNLDALSRILCYLSRVGIFTQSIANDRVGDTSSETRYGLTLGKSCFVVENNPSSLAPFLLLLTHQALTTAWNHFDACVLEGPNAFEKCHGKDLWPYAESSDFNQTFNASMEALTRAVMKGILSTYDGFRDVKTLVDVGGGVGQALRDIVAAYPHIRGIFDLPHVIATAPTVPGIHHVSGNFFEDSLPCADAFFMKHVLHAWDDELCCKLLNNCHKALENGKLIVAEEVVKVSPGHADPVESGEAMDMIMLGVTRGGRERSERQWRELLAGSGFRLTIVGRAGNIVKIIEAVKF\*

>evm.model.chr10.1212

MAMDRSKSGSSNQHEEEEQNKIHVRDQEDMEGFIELWKRMFGFMDSLGLRWAVEMGIPDISKSGPQSAQQIASHLPSESPQIDFISRILRFLAMRGVFTETVGEEEKEIRYGLTPISKLLTENSDCMNSMILVQTHEKDIAPWYFFGQCVLRGGFPFEMAHGKRRFSFTKDDPDFNKFNDSMASYSRMLINNILTTYGDGFKRLKSLVDVGGGDGTTISKIAQSFPHIKCYNYDLPVIQDAPPYPGVEHIAGDMFISVPHADTIFMKTVLHDWGDEECKKILKNCRQAIGQEDGHIIVDAVLREAGKKRSGFDEIGVMMDMVMLSHQRGKERSESRWKELLEASGFDRHNIIPLNSQMSIIEAFPSISFS\*

>evm.model.ctg25062.1

MRMLGFNGLLGRRWQVEWVLRDIISKSGPQSAQQIASHLPSESPQVAFISRILRFLAMRVFTEAVGEEDQKEIRYGLTPISKWLVTDNTENGSMNLMVLMETHEALVAPWYRFGECVLGGFPFDVMHGKPFFSFSKDNPGFNKLFNDAMASYSGMLMKHILAAYSDSGFKGLKSIVDGGGNGTAISKVAEAFPHIKCYNYDLPQAVQDAPPYPGVEHIAGDMFETVPHADAVFMKLLQDWGDEECMQILKNCGKAIPEDGKLIIVDAVLTEAGKKRSDLEEIALILDMVMLAHQRKERTEQQWGDLLRASGFDRYNIIPLPSQISIIEAFPALAH\*

>evm.model.chr6.247

MAARASSTEPPSSVDAHYKLYEMILCFAKPMALKAAVLLNIPDIIASEGHGDSLSLQQIAHISPPPQNMEYLLRILRFLASYDVFTESMQVVGEEKQWRFGLTAISELLVQRGNQQSLPFLLLIEDKFFCESYHHLNESVLEGCYAFNKAYSKSPWEYLSEHHKHNKTFNDAMVSDTAFMPLALKIYDGFKDVKTVVDVGGGVGTAISIIVKHHAHLKGINFDLPHVIDTAPAITGEHVGGNMFEQIPPADAVFMKSILHDWTDEHCVRILNKCREAIPENGKVIIMDVIVERNESLRRLGLLWDMTMMAFTSGEKERTEEEFKVLFEKAGFKSYTVLKLPAVQSIIELSKG\*

>evm.model.chr10.1253

MGDVNGSKMEEMDQVRLDGSTQTHEDMQGFVDLRKRMFGFMDSLGLRWAVEMGIPDIIAFGSQTVQDIASRLPSQSPQIEFISRTLNFLAMRGVFTKKICDDKKVRYGLTPISKWLVTNAKFCVNPVVLMNTHEAMVTSWYRFGECGLRDGVPFQVAHGKPLFSFAKDNPEFGKLFRGIATLSAPRMKPIILAYGEGFKRLKSLVDVGGGDGDAVATIQQSFPHIKCYNYDLPEVIDAPAYPGVEHIGGDMFVSVPRADALLLKLVLHNWGDKECINILRNCRHAIPEDGKLLIVGVVDKNSDGSDIAVTMDMYMLAYFGGKERTEEQWRELLHASGFDRYRFIPLSNPQFFIIAFF\*

>evm.model.chr4.2088

MGSMEKGLVIANEEKWVLGMELGNFSCLPMAMKAAVELDVLQIIANAGHGAQISPREIVHIPTTNPDAAITLARIFRVLASHSVLSSSVTTDENGKTERVYGLTPLYKYLEQNKDGVSAPLLLMSQDKVFMESWYYLKDAVLDGSQSFTKAHGVNAFEYPAKDPRFNDVINRAMAEHTMLMQKILDTYPGFNDVQEIVDVGGGIGSTLNLIVSKYPHIKGVNFDMPHVVAEAPQSPLRHVGGDMFDSVPSGYEVSNGILQWILHDWSDEHCLRLLKNCHKALPEGGKSRGKERTEEFRDLAKATGFAGGIKPVCRINGMWVMEFHKQA\*

>evm.model.chr1.876

MDATRSQQIDPKAQAQAWDFIFSFVPALVLKSALLLEIPDIIARAGPDAHLSFQQIAAQPTQNPSLDYLSRILRYLAVKGIFTHSTATDTSEVRYGLTDMAKLFVVSESNPLSLVPLLLVNHEVFMAPWHHFHDCVLEGGDAFEKDHAKDLWAYGRSDPQVNDIFNSAMASFTKVSMQIVGSYQGFNDVKTVVDVGGGVGMALAEIIGVYPHIHGINFDLPHVVANAPDLPGIQHVGNMFESVPSGDAIFMKSVLHDWDDKRCLKILENCHKALPENGKIMLAESVLPEHLNLNQ>evm.model.chr1.87MDASRSQQIDPKAQAQAWDFIFSFVPALVLKSALLLKIPDIIARAGPDAHLSLQQIAAQPTQNPSLDYLSRILRYLAVKGIFTHSTATDTSEVRYGLTDMAKLFFVSESNPLSLVPMLMQNHEVFMAPWHHFHECVLEGGDAFEKAHGKDLWAYGRSDPQDVKTVVDVGGGVGMALAIIGVYPHIHGINFDLPHVVANAPDLPGIQHVGGNMFESVPSGDAIFMKSVLHDWDDERCEILENCHKALPENGKIMLAETVLPEQSDPNQGIEILSDLVMIAHANGGRERSEGQWRGLEKAGFSGIKIVGRAEVFSTIVEAVKFTYDVKE\*

>evm.model.chr6.1244

KQEEVESHGRLAIMELANMISVPMALNAVVTLNIADIIWQKGANNPLSALQISLQIPTGSSKADAGNLERIMRMLASYNVFKETILTQSNGVSERLYSLTEIGKTLVKDEMGLSFGSYLQHHQKSLLEAWPLLHEAVLDPKHEPFRKAHGKPAYEFYGDDDAANDLMKTAMASVSVPMRTILKSYGGFDGVHRVVDVGGSSGFCLHMIIETHNHIQGINFDLPNVVAGAPSYAGMTVGGDMFESIPSGDAIFMKWILSTWSDEKCIQILRNCYRALPDGGKVIACEPVLPKYTDDQRTRALLEGDIFIMTIYSLGGKERTEEEFSQLGLAAGFSKLVALYLDPFYTVLEFHKCRPKDYIVLFKNIEGDDTHEFFEQFQLFTISGFSLCAMNITFIATGLVEVGE\*

>evm.model.chr10.1254

MDDVNGSKMEAMDQVRLDGSTQTHEDMQGFVDLRKRMFGFMDSLGLRWAVEMGIPDIIAFGSQTVQDIASRLPSQSPQIEFISRTLNFLAMRGIFTKKICDDKKVRYGLTPISKWLVTNAKFCVNPMVLMSTHEAMVAAWYRFGECGLRDGVPFQMKPIMLAYGEGFKHLQSLVDVGGDGNAVSTIRQSFPHIKCYNYDLPEVIQDAPAYPGVEHIGGDMFVSVPRADALLLKLVLNWGDKECINILRNCRHAIPEDGKLIIVDGVVDENNDGSEIELTMDMCMLAYLGGKERTEQWSELLHASGFDRYRFIPMSNSKWSIIEAFP\*

>evm.model.chr4.869

MALRAASEEISASSALPLEFDNGDQLMSRAWKIIFSMMPPMILQSAVRLKVPDIISRAGGAALSAQDIAAQLTAATQSPCNIDSLSRILTYLSSIGIFAQKIIDHVDDAASGSTREIRALTDMTKAYFVTENNPTSLAPYLLLHTHPTTAAVWNNFAECALGQDRPSAFDKRYGQDFSYTQSHADTNDMFNASMASLTKAVMSDVLPAYDGFKNVNTLVDVSAGVGQALTEIFSAYHIHATNFDRPHVIANAPAVEGIQHVSGNIFEGIPSGDEFFMKHVLHLWDDKECHDILLNYKALPANGKLILAEAVVKVCEDELDPVGCGQVMDMIMLGSTHGGRERTEQQWKDLLGASFRITKIVGRKQSLVKVIEAVKLI\*

>evm.model.chr6.1245

MDDNNNNNYNVLEKQEEVESHGRLAIMELANMISVPMALNAVVTLNIADIIWQKGANNPSALQISLQIPTGTSSKADAGNLERIMRMLASYNVFKETILTQSNGVSERLYSLTEIGQTVKDEMGLSFGSYVLQHHQKSLLEAWPLLHEAVLDPKHEPFRKAHGKPAYQFYGDDAAANLMKTAMASVSLPFMRTILKSYGGFDGVHRVVDVGGSSGFCLHMIIETHNHIQGINFDLPVVAGAPSYAGIVFALEILTQVVLAICNVFPYGSLYTGRTCPTAKFSLMKHVLVACVRCGPIPPYDPSVTHVGGDMFESIPSGDAIFMKWILSTWSDEKCIQILQNCYKALPNGGKVIAEPLLPKYTDDSQRTRALLEGDIFIMTIYSLGGKERTEEEFSQLGLAADFSKLVALYLDPYTVLEFHNTTASTRLSTEQG\*

>evm.model.chr10.1204

MDCSGDQVREIIEEKITGHEEDMEGLIELCKRMFGFMDSLGLRWAVEMGIPDIISKSGPSVQQIASHLPSESPQREIVGKEVKEVEYGLTPISKWLLTENGSCMNSMVMMETHEALFAWYYFGECVLRGGFPFKEFMGMKTDSKTWKSLVDVGGGHGTTVSQIAHSFPHIKCYNYDLQVIHQSPHYPGVQHIAGDMFMTVPHADAVFMKLILHDWGDEECMQILRNCRQAIPADGKIIVDAVWTKDGNRRSGFEEIAVMLDMLVLANHSGKERSEEQWVELLQASGFDCYNITPLDHLSIIEAVPADRE\*

>evm.model.chr4.870

MALVAASEEISASSTLPLEFDNGELISRAWKIIFSMMPPMILQSAVRLKVPDIISRAGPAALSAQDIAAQLTAATQSPCNIDILSRILAYLSSIGIFAQKIIDHVDDTASGRTAGTRERYALTDMTKAYFVTENNPTSLSHADTNDIFNASMASLTKAVMSDVLAAYDGFKDVNTLVVAGGVGQALIEIVSAYPHIHAINFDQPHVIANAPAVEGIQHVSGNIFEGIPSGDAFFMKVLHLWDDKECHDILLNCYNALSANGKLILAEAVIKVCEDELDPVGCGQAMDMIMLGFMHGRERTEQQWKDLLGDAGFRITKIVGRKQSLVKVIEAVKLI\*

>evm.model.chr6.862

MAASPSSTEPQSQDAQHKLYEMILSFAKPMALKAAVLLNIPDIIAREGHGDSLSLQQIAHISPPPQSMEYLLRILRFLASFDVFTESLQIVGEDEKLWKFGLTTISELLVQNGNQQSLPFLLLIADKFFCESYHHLNESVLEGCYAFNKVYSKSLWEYVSEHPNYNKTFNDGVVSHTNLMASALKIYDGFKNVKTVVDVGGGVGTAISIIVKHHTHLKRINFDLPHVIATAPAMPGEHVEGNMFEQIPPADAVFLKSILHDWDDEHCVRILKKCREAISGNGENGGRIQSAVREAFKSYTLLKVSAVEAIIELSKA\*

>evm.model.chr6.861

MAANDSPTEPPSSVDAQHKLYEMILSFAKPMALKAAVLLNIPDIIAREGHGDSLSLQQIAHISPPPQSMEYLLRILRFLASFDVFTESLQIVGEDEKQWKFGLTTISELLVQNGNQQSAPFLLLIADKFFCESYHHLNESVLEGCYAFNKVYSKSLWEYVSEHPNYNKTFNDGVVSHRNLMASALKIYDGFKNVKTVVDVGGGVGTAISIIVKHHTHLKRINFDLPHVIATAPAMPVEHVEGICSNRYLQQTQYFSRILKKCREAISGNGKVIIVDTLVERDEGTTRRLGLLWDMMMAFTTGGKERTEEEFKVLFEKAGFKSYTLLKVSAVEAIIELSKA\*

>evm.model.chr7.385

MSGNSASALAIGHDQKNEGLQALMEMSYLCVFPMAAKAAILLQVPEILAAASGPLSAKQADKIGGNATSEAKLDRLLQALATHGLFSIHQAPPPSLKTYSLNAMSRLLVKDENGSSLAMFLLNTDPSHALPLQYLHEAILDDAAVPFEKAYGQPLFKFVAQSPQMGEAFYTAMSNLSIVTRSILQSYDGFKDVKVLVDVGGGPGLNSSLIKAAHPHISVINFDMPFVVAKASPLPGEHRGGNMLESVPSGGDAILLKVLCSRLVASFDLAMMSVFRGGKERSSKQFEGLVHSARFNFKVVLFGDMLSVMEAFKSEDA\*

>evm.model.chr2.691

MAASASSTEPFSSVDAQHKLCEMILCFAKPMALKAAVLLNIPDIIASEGHGDSLSLQEVAHISPPPRSMEYLLRILRFLASYDVFTESLQVVGEEKHWRFGLTAISELLGCYAFNKVYKSPWEYVSEHPKYNEILNDGMVSHTRALMDSALRLQGFRMLRQCGRWRRCWPHFHDRQTPSERHQFRSTHVIDTGCHNGVEHVGGNMFVQIPPADAVFIKCREAIQENGKVIIVDVVVNNARRLRRLELLWDMTMMAFTTGGKERTEEEFKVLFEKAGFKSYTLLKLPAVQSIIELPA\*

>evm.model.ctg25063.1

MDNKGGCRGNDQRKEEEIVDAHHQEDMEGFIELWKRMFGFMDSLGLRWAVEMGIPDIISSGPQSAQQIASHLPSESPQVAFISRILRFLAMRGVFTEAVGEEDQKEIRYGLTPISKWLTDNTENGSMNLMVLMETHEALVAPCKDNPGFNKLFNDAMASYSGMLMKHILAAYSDSGFGLKSIVDVGGGNGTAISKVAEAFPHIKCYNYDLPQAVQDAPPYP>evm.model.chr1.87MDASRSQQIDPKAQAQAWDFIFSFVPALVLKSALLLKIPDIIARAGPDAHLSLQQIAAQPTQNPSLDYLSRILRYLAVKGIFTHSTATDTSEVRYGLTDMAKLFFVSESNPLSLVPLLMQNHEVFMAPWHHFHECVLEGGEAFEKAHGKDVWAYGRSDPQVNEIFNSAMAWYPTQSAGILLPGSFWRWNTAPPENGKIMLAETVLPEHSDPNQGIEILSDLVMIAHANGGRERSEGWGGRLEKGRLLWNQNRRKS\*