

Table S1. Sequences in the evolutionary tree.

Species name	Accession number	name code	sequenceYTH motif
<i>Mimulus guttatus</i>	Migut.N0 0538.1	MgDF1 A	KLSSVAPDREQYNQPEFSVTYDDARFFIIKSYSEDDVHKSIIKYNVWASTPNGNKKLDAAYQDAQQRPG GCPVFLFFSVNTSGQFVGVAEMTGPVDFNKNVEYWQQDKWVGCFPVKWHIVKDLPNSSLKHITLEN NENKPVNTSRDTQEVKLDQGLQVLKIFKDHTSKQCILDDFEFYEDRQKRIQEKKAKQQQY EKSSVTPDLEEYNRPDPETYSDAKFFIIKSYSEDDVHKSIIKYNVWASTSNGNKKLEAAYQDAQQKPGGC
	Migut.D0 2575.1	MgDF2 A	PVFLFFSVNTSGQFVGVAEMVGPVDFNKNVEYWQQDKWIGCFPLKWHIVKDLPNSSLKHITLENNEN KPVNTSRDTQEVKLEPGLAVLKIFKDHTSRQCILDDFEFYEDRQKKIQEKKARQQQF
	Migut.J00 855.1	MgDF1 B	VESTSKLHVHHLNSPDFITDYDRAKFFVIKSFSEDNIIHKSIIKYSVWASTPLGNRKLDAAAYCETKEMEGIC PVFLFFSVNASGQFCGVAEMIGPVDFENDADYWQQDRWSGQFPVKWHIHKDVPNSRFRHILLENNEN KPVTHSRDSQEVKLEQGIEMQLQIFKNHDAETSLDDFNFYDEREKTLLERKAKQRAI
	Migut.O0 0389.1	MgDF1 C	AQGNITIFKDQYNKIDFPVDYANAKFFVIKSYSEDDVHKSIIKYNVWSSTPNGNKKLTTAYQDAHRTTL GDLRGCPIFLFFSVNASGQFCGVAEMTGPVDFHRDMDFWQQDKWSGSFPVKWHIHKDLPNSNFRHIIL ENNENKPVNTSRDTQEICYEKGLEMLRIYKSHTLKTSLDDFMYYENRQRILQEERTRLLRK
	Migut.G0 0015.1	MgDF2 C	AQGNITIFKDQYNKIDFPVDYANAKFFVIKSYSEDDVHKSIIKYNVWSSTPNGNKKLTTAYQDAHRTGL GDLRGCPIFLFFSVNASGQFCGVAEMTGPVDFHRDMDFWQQDKWSGSFPVKWHIHKDLPNSNFRHIIL ENNENKPVNTSRDTQEICYKKGLEMLRIYKSHTLKTSLDDFMYYENRQRILQEERTRLLRK
	Migut.N0 0839.1	MgDF3 C	EQIGLPAKVDFKNLQDFQTVYENAKFYVIKSYSEDDIHKSIKYDVWSSTQNGNRKLDAAFNEANARTN CPVFLFFSVNASGQFVGVAEMIGHVDFSKSMDFWQLDKWNGFFPLQWHIVKDVNTLLRHILLENNND NRPVTFTRDTQEIGLKQGLEMLSIFKNHSGKSLDDYSFYEKREKELKAKRKNAARS
	Migut.H0 1337.1	MgDC1 A	SRNATPLPQGASRYFVVKSCNRENLELSVQQGVWATQRSNEAKLNEAFESVENIILFVSNKTRHFQGC AKMTSRIGGSVGGGNWKHAHGTAAHYGRNFALKWLKLCELTFDKTRHLRNPYNENLPVKISRDCQEL PSIGEQLASLLYLEPDSDLMAIAIAAELKREEEK
	Migut.M0 1886.1	MgDC2 A	SRTATPLPQGTSTRYFVVKSCNRENLELSVQQGVWATQRSNEAKLNEAFESVDNIILFVSNKTRHFQGC AKMTSRIGGSISGGNWKNAHGTAAHYGNFVSVKWLKLGELSFNKTTRHLRNPFNENLPVKISRDCQELE PSIGEQLASLLYLEPDSDLMAVALAAEAKREEEK
	Migut.A0 0893.1	MgDC1 B	SSEMKKDKLNNTRYFIIKSLNHNENIQLSVKKEIWATQVMNEPILEEAFQNSGKVLIFSVNMSGFFQGYA QMMSSVGWRRDTIWSQASGKSNPWGRSFKVWLRNLDAFQKTLHLKNPWNDFKPVKISRDCQELP GDIGRALCELLDEGGGIDLNLKRDEIARGDFSASR
	Eucgr.B03 590.1	EgDF1 A	NKVSVIPDREQYNKADFPEDYEDAKFFIIKSYSEDDVHKSIIKYSVWASTPNGNKKLDAAYREAQEKPGS SPVFLFFSVNTSGQFVGVAEMVGPVDFHKSVEYWQQDKWNGCFPVKWHIVKDVNSMLKHITLENN ENKPVNTSRDTQEVKLQGLKMIKIFKEHPVKTCLFDDFEFYENRQKAIQEKKARQQYQ
<i>Eucalyptus grandis</i>	Eucgr.B03 591.1	EgDF2 A	NRSSVVPDCTQYNKVDFPEDYNDKAFIIKSYSEDDVHKSIIKYNVWASTPNGNKKLDAAYREAQEKKA AGCPIFLFFSVNTSGQFVGVAEMVGPVDFHKNVEYWQQDKWMGCFPVKWHIVKDVPNLLKHITL NNENKPVNTSRDTQEVKLQGLKMIKIFQTHLVKTCLDDDFEYENRQRAIQEKKARQLQF
	Eucgr.J03 195.1	EgDF1 B	SASITKIPHGSYNHIDFITEYDDAKFFVIKSYSEDNVHKSIIKYGWASTPNGNRKLDAAAYREAKEKPDTC PVFLFFSVNASAHFCGVAEMVGPVDFDRSFDYWQQDRWSGQFPVKWHIVKDVPSQLRHIVLENND NKPVTNSRDTQEVKLEQGIEMLNIFKNYETDTSILDDFEFYEREKVIQEGKARQQAS
	Eucgr.H0 4096.1	EgDF1 C	AQGIHIDTDQYNKDDFCVDYEDAKFFVIKSYSEDDVHKSIIKYNVWSSTPHGNKKLQSAVEDAQKIAAE KTTNCPIFLFFSVNASGQFCGVAEMVGQVDFHKNMDFWQQDKWTGSFPVKWHIHKDQNTAFRHIIL ENNENKPVNTSRDTQEIMQKQGLEMLKIFKNNGLKTSLDDFTYEGRQKLMQEERARMYVS
	Eucgr.E02 496.1	EgDC1 A	GRGPTPLPPGVSRYFIVKSCNRENLELSVQQGVWATQRSNEAKLNEAFDSAANVILFVSNRTRHFQGC AKMTSRIGGAASGGNWKYAHGTAAHYGRNFVSVKWLKCELSFQKTRHLRNPYNENLPVKISRDCQELE PSVGEQLASLLYLEPDSSELMPISLAAESKREEEK
	Eucgr.D0 1949.1	EgDC1 B	SIANRKGWYSIRYFIIKSLNHHNLQLSIEKGIWATQVMNEPILEEAFHNSGKVLIFSVNMSGFFQGYA QMMSPIGWRRDKVWSQGNRNRPWGRSFKVWLRLYDLFPQKTLHLKNLLNDNKPVKISRDCQELP QDVGEALCELLDCCADVDGETRRDSAPLEK
<i>Glyma</i>	Glyma.08 G124600.1	GmDF1 A	DKTSTVPDRDQYNKADFPPEYTDKFFVIKSYSEDDIHKSIKYNVWASTQNGNKKLDAAYHEAQQKP GGCPVFLFFSVNTSGQFVGVAEMIGPVDFNKSVEYWQQDKWNGCFPLKWHVVKDVPNNLLRHITLD NNENKPVNTSRDTQEVMLEPGLKLIKIFKEYTSKTCILDDFGFYEARQKTILEKKAKQQFP
	Glyma.05 G166600.1	GmDF2 A	DKTSTILECDQYNKADFPPEYTDKFFVIKSYSEDDIHKSIKYNVWASTQNGNKKLDAAYQEAQQKPG GTPVFLFFSVNTSGQFVGVAEMIGPVDFNKSVEYWQQDKWNGCFPLKWHIVKDVNNLLRHITLDNN ENKPVNTSRDTQEVMLEPGLKLIKIFKEYTSKTCILDDFGFYEARQKTILEKKAKQQFP
	Glyma.19 G110800.1	GmDF3 A	KEVPPVPDKEQYNGKDAENYSDAKFFVIKSYSEDDIHKSIKYSAWASTPNGNKKLDAAYQEAKEKPG GCPIFLLFSVNTSGQFVGVAEMLGPVDFGKTVDYWWQDRWTGCFVSKWHIVKIDIPNSVLRHITLENNE NKPVTNSRDTQEVKFEKGVQIAKIFKEHSSQTCILDDFGFYEARQKTILEKKAKQQQL
	Glyma.16 G041600.1	GmDF4 A	KEVPLVPDKEQYNGKDLAENYSDAKFFVIKSYSEDDIHKSIKYSAWASTPNGNKKLDSAYQEAKEKPG GCPIFLLFSVNTSGQFVGVAEMLGPVDFGKTVDYWWQDRWTGCFVSKWHIVKIDIPNSVLRHITLENNE NKPVTNSRDTQEVKFEKGVQLVKIFKEHSSQTCILDDFGFYEDREKVTQEKKSKEQQL
	Glyma.02	GmDF5	KEVPLVPNNEQYNGKDFPENYSDAKFFVIKSYSEDDIHKSIKYVWASTFNGNKKLDAAYHESKEKPG

<i>Glycine max</i>	G072000.1	A	DCPVFLFSVNTSGQFVGLAEMVSPLDFGRTVEYWQQDRWSGCFSVKWHIIKDIPNSVLRPITLNNEN KPVNTSRDTQEVKFEKGIQILKIFKQHSSKTCILDDFGFYETREKMIQERKSMEQQL
	Glyma.08	GmDF1	SASTAKFQNESLNRSDFATDYKDAKFFVIKSYSEDNVHHSIKYGVWASTPNGNRKLDDAYRQAMEKQ
	G226100.1	B	DACPIFLFFSVNASAQFCGVAEMVGPVNFDSVDFWQQDKWWSGQFPVKWHIIKDVPNSSQFRHIILENN DNKPVNTSRDTQEVKLGQGVEMLTIFKNYETDVSILDDDFDYEDRQKAMQERKARQQSS
	Glyma.07	GmDF2	SGSTAKFQNESLNRSDFATDYKDAKFFVIKSYSEDNVHHSIKYGVWASTPNGNRKLDDAYRQAMEKQ
	G000900.1	B	DACPIFLFFSVNASAQFCGVAEMVGPVNFDSVDFWQQDKWWSGQFPVKWHIIKDVPNSSQFRHIILENN NDNKPVTNSRDTQEVKLTQGVEMLTIFKNYETDVSILDDDFDYEDRQKAMQERKARQQSS
	Glyma.17	GmDF1	TQENIIISTDQYNREDFPVNYENAKFFVIKSYSEDDVHHSIKYNVWSSTPHGNKKLQSTHEDAKRIASGN
	G038400.1	C	FGSCPIFLFFSVNASGQFCGVAEMIGPVDNFNDMDFWQQDKWWSGFPVKWHIIKDVPNANFRHIILENN NENKPVNTSRDTQEIMYSKGLEMLKIFKNHNLKTSLLDDFMYENRQKIMQEEKAKLLIR
	Glyma.07	GmDF2	TQENIIISTDQYNREDFPVNYENAKFFVIKSYSEDDVHHSIKYNVWSSTPHGNKKLQSAHEDAKRIASGK
	G233400.1	C	FGSCPIFLFFSVNASGQFCGVAEMIGPVDNFNDMDFWQQDKWWSGFPVKWYIIKDVSNANFRHIILENN NENKPVNTSRDTQEIMYSKGLEMLKIFKNHHLKTSLLDDFIYYENRQKIMLEEKTKLLIR
	Glyma.15	GmDF3	EQGNIVYIPDQYNMEDFPLGYENAKFFVIKSYSEDDVHHSIKYNVWSSTPHGNKKLENAYEDAKKIAA
	G136400.1	C	EKSEVCPILLFSVNASGQFCGVAEMVGTVDFSKNMDFWQQDKWWSGFPVKWHIIKDVNPNNFRHIIL ENNENKPVNTSRDAQEIMYLKGLEMLKIFKNHTLKTSLDDFMYENRQKIMQDEKAKFLVK
	Glyma.09	GmDF4	EQGNIVYIPDQYNKEDFSLDYENAKFFVIKSYSEDDVHHSIKYNVWSSTPHGNKLENAYEDAKKIAAAEK
	G031200.1	C	SEVCPILLFFSVNASGQFCGVAEMVGTVDNFKNMDFWQQDKWWSGFPVKWHIIKDVNPNNFRHITLEN NENKPVNTSRDTQEIMYWKGLEMLKIFKNNTLKTSLDDFMYENRQKIMQDEKA
	Glyma.15	GmDF5	GNVTNKIRADQYNLPDFPTKYDHALFFVIKSYSEDDIHSIKYNVWASTPNGNKRLDGAFAQKRM
<i>Prunus persica</i>	G265400.1	C	EEKGCKCPVFLFFSVNASGQFCGVAEMTGRVDFNKSMDFWQQDKWNGYFPVKWHIIKDVNPQLRH IILENNDHKPVTSRDTQEVSPQGVEMLNIFKNYVARTSILDDFEFYESRQKVMQEKTRQSM
	Glyma.08	GmDF6	GNVTNKIRTDQYNLPDFPTKYDHALFFVIKSYSEDDIHSIKYNVWASTPNGNKRLDGAFAQKRM
	G162200.1	C	EKGCKCPVFLFFSVNASGQFCGVAEMTGRVDFNKSMDFWQQDKWNGYFVSVKWHIIKDVNPQLRHII LENNDHKPVNTSRDTQEVSPQGVEMLNIFKNYVARTSILDDFEFYESRQKVLQEKTRQSM
	Glyma.15	GmDC	NRTATPLPQGISRYFIVKSCNRENLELSVQQGVWATQRSNESKLEAFDSVENVILVFSVNRTRHFQGC
	G128500.1	1A	AKMTSRIGGSVAGGNWKYAHGTAHYGRNFSVKWLKLCESLHFKTRHLRNPYNENLPVKISRDCQELE PSIGQLASLLYLEPDSELMAISVAAESKREEEK
	Glyma.09	GmDC	NRTATPLPQGISRYFIVKSCNRENLELSVQQGVWATQRSNESKLEAFDSVENVILVFSVNRTRHFQGC
	G022200.1	2A	KMTSKIGGSVAGGNWKYAHGTAHYGRNFSVKWLKLCESLHFKTRHLRNPYNENLPVKISRDCQELEP SIGQLASLLYLEPDSELMAISVAAESKREEEK
	Glyma.01	GmDC	PTGIGVEKWHNIKYFIIKSLNHQNIHLSIEKGIWATQIMNEPILEEAFHNSGSVILIFSVNMSGSFQGYAQ
	G214100.1	1B	MMSSIGRGRDNVWSEGTGKSNPWGRSFKVKWMCLNDLPFHKTLLHLKNPLNDYKPKISRDCQELSP DIGLALCELLDGKNYTDCLPTSLSRDEFSLKG
	Glyma.11	GmDC	PAGIGVEKCHNTKYFVIKSLNHQNIHLSIEKGIWATQIMNEPILEEAFHNSGSVILIFSVNMSGSFQGYA
	G027800.1	2B	QMMTSIGRGRDNAWSEGTGKSNPWGRSFKVKWLCLNDLPFHKTLLHLKNPLNDYKPKISRDCQELSP DIGLALCKLLDGKNDTDGLLTSLSRDEFSLKG
	Prupe.6G	PpDF1	KDKTSVPDREQYNKADFPEDYTDKFFIIKSYSEDDVHHSIKYNVWASTPNGNKKLHAAAYQEAQEKSG
	002200.1	A	GCPVFLFSVNTSGQFVGLAEMLGPVDNFKNLEYWQQDKWNGCFPVKWHIVKDVPNSSLKHITLEN NENKPVNTSRDTQEVKLEPGLKMIKIFKEHLSKTCILDDFGFYESRQKTIQEKKAKQQQF
	Prupe.3G	PpDF1	NTTATKVHDESYNKPDPVTEYNDAKFFIIKSYSEDNVHHSIKYGVWASTPNGNRKLDDAYREVKEKHD
	027100.1	B	GCPILFFSVNASAQFCGVAEMVGPVDFDKSLDYWQQDKWWSGQFPVKWHMIKDVPNSSQFRHIILENN DNKPVNTSRDTQEVKLEHGIEMLNIFKNYETDMSILDDDFDYEDRQKAMQERKARQQAS
<i>Prunus persica</i>	Prupe.1G	PpDF2	GLSASGINLDSFNRLDFVTDYEDAKFFIIKSFSEDNVHHSIKYSVWASTPHGNKKLDAAYHEAQRIKGC
	002400.1	B	PVFLFFSVNASGQFCGVAEMVGSVDFEKDADYWQQDRWSGQFPVQWHIIKDVPNIRFRHILLENNDN KPVTHSRDCQEVNLKQGIELLKIFGDYDARTSIIDDFEFYDEREKSLEKRVKQAC
	Prupe.1G	PpDF1	AQGNIIIRTDQYNKDELVPDYVDAKFFVIKSYSEDDVHHSIKYNVWSSTPHGNKKLNSAYEDALRIAAG
	109700.1	C	KPRGCPILFFSVNASGQFCGVAEMGPPVDNFNDMDFWQQDKWWSGFPVKWHIIKDVNPNTSFRHIVLE NNENKPVNTSRDTQEIMYKKGLEMLKIFKNHTLKTSLDDFMYEERQKFMQEERSRLVR
	Prupe.4G	PpDF2	DSIASAIRKDQYNLPDFPTKYEQALFFVIKSYSEDDIHSIKYNVWASTPNGNKRLDSAYQDAEEKVAQ
	124900.1	C	KSCKCPVFLFFSVNASGQFCGVAEMIGRVDNFNKSMDFWQQDKWNGYFPVKWHIIKDVNPQLRHII ENNENKPVNTSRDTQEVKFLQGIEMLNIFKNHLSKTSILDDDFEFYESRQKVMQEKRIQSTP
	Prupe.1G	PpDF3	EELSFTVHRDQYNLPDFQTDYEKAKFYVIKSYSEDDVHHSIKYDVWASTPNGNKKLDASFRDAESKSRE
<i>Prunus persica</i>	579100.1	C	TGTQCPILFFSVNGSGQFIGLAEMAGQVDNFNDMDFWQVDKWSGFPVKWHVIKDPNTQLRHII NNDNRPVTFTRDTQEIGLKQGLEMLNIFKSYTAKTSLDDFIFEDREKSLKAKRSSKPAT
	Prupe.4G	PpDC1	ANRSAPLPQGISRYFIVKSCNRENLELSVQQGVWATQRSNESKLEAFDSAENVILIFSVNRTRHFQGC
	089500.1	A	AKMMSRIGGSVSGGNWKYAHGSAHYGRNFSVKWLKLCESLHFKTRHLRNPYNENLPVKISRDCQELE PSIGQLASLLYLEPDSELMAVSIAAESKREEEK
<i>Prunus persica</i>	Prupe.5G	PpDC1	TTGRKKGTLYDTRYFIIKSLNHQNIQLSIEKGIWATQVMNEPILEEAFHNSGKVLIFSVNMSGSFQGYA
	086300.1	B	QMMSSVGWRRDNVWSQSSRNPWGRSFKVKWLQNLNDLPFQKTLHLKNPLNEYKPKISRDCQELSP DVGEALCELLDGTNDVNGLSVAMEDFPSKR

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Potri.003 G222700.1	PtDF1A	DKTTVVPDREQYNKADFPPEEYDNAKFFIIKSYSSEDDVHKCIKYNVWASTPNGNKKLDAAYQEAQKS GGCPVLLFSVNTSGQFVGLAEMTGRVDFDKSV EYWQQDKWTGYFPVKWHIVKDV PNSFLKHITLEN NENKPVTNSRDTQEVKLEQGLKLIKIFKDHSSKTCILDDFVFYEDREKMIQEKKAKQQQL
Potri.001 G002000.1	PtDF2A	DKTTEVPDREQYNKADFPVEYVDAKFFIIKSYSSEDDVHKCIKYNVWASTPNGNKKLDAAYQEAQKS GGCPVLLFSVNTSGQFVGLAEMTGRVDFDKSV EYWQQDKWTGYFPVKWHIVKDV PNSLLKHITLEN NENKPVTNSRDTQEVKLEQGLEMIKIFKEHSSKTCILDDFGFYEDREKMIQEKKAKQQQL
Potri.019 G034300.1	PtDF3A	ENLLQIPDREQYNKEDFPEEYSDAKFFVIKSFSEDDVHKS IKYSVWTSTPNGNKKLDAAYKQGKENPGD CPVLLFSVNTSGQFVGLAEMVGPVDFNKTVEYWQQDKWTGCFPLKWHI IKDVPNGCLR HITLENNE NKPVTNSRDTQEVIFEKGVQILKIFKDHKGKTSILDDFSFYAGRERIMQEKRAKHNIH
Potri.014 G001000.1	PtDF1B	SKPSAKIHDESYNQSD FVTEYKDAKFFIIKSYSSEDNVHKS IKYGVWASTPNGNRKLD TAYHEAKDKQDP CPVLLFSVNASAQFCGVAEMVGPVDFDKSV DYWQQDKWSGQFPVKWHI IKDVPNSQFRHIVLENN DNKPVTNSRDTQEVKLEQGV EMLNIFKNYETDTSILDDFDFYEDRQKAMQDRKARQQAS
Potri.007 G002800.1	PtDF2B	SKPSAKIHDESYNQPD FVIEYKDAKFFIIKSYSSEDNVHKS IKYGVWASTPNGNRKLD TTYREAKEKQDPC PVLLFSVNASAQFCGVAEMTGPVDFDKSV DYWQQDKWSGQFPVKWHI IKDVPNSQFRHIVLENN NKPVTNSRDTQEVKLEQGI EMLNIFKNYETDMSIIDD FDFYEDRQKAMQERKARQQAS
Potri.006 G079900.1	PtDF3B	NSASSGIQLDLYNQ LDFVTDYKDAKFFIIKSFSEDNVHKS IKYSVWASTPHGNKKIDAAYREAKEKEGN CPVLLFSVNASGQFCGVAEMVGPVDFE KDAEYWQQDRWNGQFPVQWHIVKDV PNSRFRHILLENN DNKPATHSRDSQEVKLEQGI EMLKIFKDHDAPTSILDDFDFYDQCERALKERKAKQQPS
Potri.018 G149800.1	PtDF4B	NSASSGVQLDLYNRP VFVTDYKNAKFFIIKSFSEDNVHKS IKYSIWASTPHGNKKIDAAYREAKEKEGN CPVLLFSVNASGQFCGVAEMVGPVDFE KDA DYWQQDRWNGQFPVQWHI IKDVPNSRFRHILLENN DHKPVTHSRDSQEVKLEQGI EMLKIFKDYDAPTSIID FGFYDQCERALKERKAIQQPS
Potri.001 G056100.1	PtDF5B	QKAVADVHSESHNQV D FADYKDAKFFVIKSYSSEDNVHKS IKYGVWASTPNGNKKLDAAYREAKEN HGTCPIFLLFSVNASAQFCGVAEMVGPVDFDK NVDFWQQDKWSGQFPVKWHI IKDVPNSQFRHIVLE NNDNKPVTNSRDTQEVELEQGA EMLGIFKNYESH SILD FQFYERQKVMQVRKSRPQAS
Potri.010 G152300.1	PtDF1C	GLGNIVIQTDQYNKDD FSTDYLD AKFFVIKSYSSEDDVHKS IKYNVWSSTPHGNKKLQ TAFEDAQKLAV GRPRGCPIFLFFSVNASGQFCGVAEMIGPV DLHRDMDFWQQDKWSGFLVKWHI IKDIPNSSFRHIILE NNENKPVTNSRDTQEIMYKQGLEMLKTFKNHPLR TSILDDFMYENRQKIMQDEKARLMFK
Potri.008 G100200.1	PtDF2C	ELGNIVIQTDQYNKDD FSTDYAD AKFFVIKSYSSEDDVHKS IKYNVWSSTPHGNKKLHSAFEYAQKLDL GRPRGCPIFLFFSVNASGQFCGVAEMVGPVDFNR DMDFWQQDKWSGFLVKWHI IKDIPNSSFRHIILE NNENKPVTNSRDTQEIMYKQGLEMLKMFKNHPLK TSILDDFVYYENRQKIMQEEKARLMFK
Potri.010 G175500.1	PtDF3C	NSITSVISRDQYNLP DFPNTYDHAFFVVIKSYSSEDDIHKSIKYNVWASTPNGNKRLNSAYLDSQQKIAQI GCSCPVLFFSVNASGQFCGVAEMTGRVDFNKNM DFWQQEKWNGYFPVKWHI IKDIPNPQLRHIILE NNENKPVTNSRDTQEVKFPQGI EILNIFKNYVSKTSILDDFDFYESRQKVMHERRPRSLIS
Potri.008 G080800.1	PtDF4C	NSIASVISRDQYNLP DFPPTYKNHAFFVVIKSYSSEDDIHKSIKYNVWASTPNGNKRLDSAYQDAQQKIAE KGNSCPVLFFSVNASGQFCGVAEMVGRVDFNKNM DFWQQDKWNGYFPVKWHI IKDVPNPQLRHII LENNENKPVINSRDTQEVKFPQGI EILNIFKNYVT KTSILDDFDFYESRQKVMQEKRPRFPFIP
Potri.004 G223800.1	PtDF5C	DMLGFAMHKEQYNLP DFEI EYSNAKFFVIKSYNEDDIHKSIKYDVWASTPNGNKKLDAAFHNAEEVSS ETGTCPIFLFFSVNGSGQFVGLAEMVGQVDFN KDMDFWQIDKWNGFFPVKWHVIK DIPNGQLRHIV LENNDGHSVTF SRDTQEIGLEKGLEMLNIFKSYS AKTSM LDDFNFYENREKSLNTKKS NKPAT
Potri.003 G008400.1	PtDF6C	DELGIAMRKEQYNLP DFE TEYANAKFFVIKSYSSEDDIHKSIKYDVWASTPNGNKKLDAAFHNAEEVSS DTGYKCPIFLFFSVNGSGQFVGFAEMVGQVDFN KDMDFWQIDKWNGFFPVKWHVVK DIPNGHLRHI VLENNDGHSVTF SRDTQEIVLKQGLEMLNIFKSYS AKTSL LDDFNFYEKREKSLNTKKG NKPAT
Potri.001 G357800.1	PtDC1 A	SSFFSCVSPSQFVYFIVKSCNRENLELSVQQGVWATQRSNEIKLNEALDSADNVILIFSVNRTRHFQGCA KMASKIGASVGGGNWKYAHGTAHYGRNFSVKWLKCELSFHKTRHLRNPFNENLPVKISRDCQELEP SIGEQLASLLYLEPDS ELMASVLA AEAKREEEK
Potri.011 G089800.1	PtDC2 A	VLYVVVFWLRVKLYFIVKSCNLENLELSVQQGVWATQRSNEPKLNEAFDSAENVILIFSVNRTRHFQGC AKMTSKIGASVGGGNWKYAHGTAHYGRNFSVKWLKCELSFHKTRHLRNPFNENLPVKISRDCQELE PSIGEQLASLLYLEPDSLMAISVAAEAKREEEK
Potri.001 G113500.1	PtDC1B	SSINKKRKLCNTRYFIIKSLNQHN IQLSIENGIWATQVRNEPILEEAFHNSGRVILIYSVNMSGFFQGYAQ MISSVGWRHDNLWSESGKSNPWGRSFKVKWLR LNDLPFQKTLHLKNPLNDYKPVKISRDCQELPED IGEALCELIDGERD TDGMVKSFP RDDLPMKR
GSVIVT0 102549400 1	VvDF1 A	DRTSVFPDRDQYNHADFPVEHTEAKFFIIKSYSSEDDVHKS IKYNVWASTPNGNKKLDAAYREAEQKSA GCPVFLFFSVNTSGQFVGLAEMVGHVDFHKNVEYWQQDKWNGCF SVKWHVVKDV PNSLLKHITL E NNENKPVTNSRDTQEVKLEQGLQMLKIFKEHCSKTCILDDFAFYESRQKTIQEKKAKQQQF
GSVIVT0 103339500 1	VvDF2 A	GNLTLVPDKEQYNSEDFPENYS DAKFFIIKSYSSEDDVHKS IKYNMWASTANGNKKLDAAYQEAQGKS GSCPIFLFFSVNASGQFVGVAEMVGSVDFNRSLEYWQQDKWTGCFPVKWHVIK DIPNSLLKHITLENN ENKPVTNSRDTQEVKF EQGIQVLKIFKNHSSKTTILDDFGFYEARQRTMQEKKAKQQLF
GSVIVT0 102946000 1	VvDF1 B	STSTAKTNDGLYNQLSFVTEYKDAKFFIIKSYSSEDNVHKS IKYGVWASTPNGNRKLD AAYREAKEKQA ACPVLLFSVNASAQFCGVAEMVGPVDFDKSV DYWQQDKWSGQFPVKWHI IKDVPNSQFRHIVLENN NDNKPVTNSRDTQEVKLEQGI EILNIFKNYETDTSILDDFDFYEDRQKAMQERKARQQAS
GSVIVT0 101049400	VvDF2 B	NGTCTGVHRESYNRLDFVTEYKDAKFFVIKSYSSEDNVHKS IKYGVWVSTPNGNKRLNSAFHEAKEKHG NCPIFLFFSVNASAQFCGVAEMVGPVDYDKSV DYWKQDKWTGQFPVKWHI IKDVPNSQFRHIILENN

	1		DNKPVTNSRDTQEVELEQGNEMLNIFRNYESDSSILDDDFDYEDRQKAMQEKKTQHKAS
<i>Vitis vinefera</i>	GSVIVT0	VvDF3	DASNSVVHFDSDYNQPDFVTDYENAKFFIIKSYSEDNVHRSIKYSVWASTALGNRKLDAAYQKAKEIETN
	103223600	B	CPIFLCFSVNASSQFCGVAEMVGPVNFEKDAEYWQQDRWSGLFPVKWHIIKDVPNLSLFRHILNEN
	1		KPVTHSRDTQEVNLEQGIEMLKIFKSYDAHTSILEDFFDYEQRERASKERKARQQAC
	GSVIVT0	VvDF1	AQGNIIYTDQYNKDDFPVDYDAKFFVIKSYSEDDVHKSIXYNVWSSTPNGNKKLENAYEDAQRIAL
	101764900	C	GKRRGCPILFFSVNASGQFCGVAEMIGPVDHFKDMDFWQQDKWWSGFPVKWHIIKDVNTNFRHII
	1		ENNENKPVTNSRDTQEIRFKQGLEMLKIFKNHTTKTSLDDDFMYENRQRMQDEKTRLLIK
	GSVIVT0	VvDF2	NCIASLIRRDQYNLPDFPTKYDHAFFVIKSYSEDDIHKSIXYNVWASTPNGNKRDLGAYQEAKERMGD
	103669600	C	RGSKCPVFLFFSVNASGQFCGVAEMIGRVDFNKNMDFWQQDKWNGFFPVKWHIIKDVNPQLRHII
	1		ENNDNKPVTNSRDTQEVRFQGIEMLNIFKNYVSKTSILDDDFDYESRQKVMQDKKIKPSMP
	GSVIVT0	VvDF3	EELGLMVRDRDQYNLQDFQTEYENAKFYVIKSFSEDDIHKCIKYDVWASTPNGNKKLDAAFHDAEAKA
<i>Sonalu m lycopers icum</i>	102324800	C	NETGTFPIFLFFSVNGSGQFVGVAEMVGQVDFNKMDFWQLDKWNGFFPVKWHIVKDIPNSQLRHI
	1		TLESNENRSVTTYTRDTQEIGLKQGVEMLKIFKNYSARTSMFDDFNFYENREKSLHARRSSKPPP
	XP_00228	VvDC1	NKTASPLPQGISRYFIVKSCNRENLELSVQQGVWATQRSNEAKLNEAFDSVENVILIFSVNRTRHFQGC
	1594.1	A	AKMTSKIGGFVGGGNWKYAHGTAHYGRNFSVKWLKLCESLHFKTRHLRNPYNENLPVKISRDCQELE
			PSIGEQLASLLYLEPSELMAISLAAESKREEK
	GSVIVT0	VvDC1	SSANKKGKLYSTRYFIKSLNHHNIQLSMEKGIWATQVMNEPILEEAFHNSGKVLIFSVNMSGFFQGYA
	101989500	B	QMMSSVGWRRDNVWSQSGGNNPWGRSFKVKWLRHLDPFQKTLHLKNPLNDYKPKISRDCQEL
	1		SQEIGEALCELLDGKTDVGDNLKNDVSGDDLPPRR
	Solyc01g0	SIDF1A	DKPSLMPDREQYNHPDFPVTYADAKFFIIKSYSEDDVHKSIXYNVWASTPNGNKKLDAAYQEAQQNS
	28860.2.1		GGCPVFLFFSVNTSGQFVGVAEMVGPVDFNKNVEYWQQDKWVGCFFPVKWHIVKDVPNSLLKHITLE
<i>Medicag o truncat ula</i>			NNENKPVTNSRDTQEVKVEQGLQVLKIFKDHISKQCILDDFEFYEDRQKRIQDKKAKQQLF
	Solyc05g0	SIDF1B	VELTSILQPGQYNRPEFVTDYEHAKFFVIKSFSEDDNVHKSIXYGVWASTPQGNRKLDAAYAEAKEMNA
	32850.2.1		NCPVFLFFSVNASGQFCGVAEMVGPIDFENSAEYWQQDRWSGKFPVKWHIVKDVPNSQFRHILLEHN
			DNKPVTHSRDSQEVKLPEGLEMLKIFKNYETDTSLLDDFTYDEREKSLEKSKQRPL
	Solyc12g0	SIDF1C	VQGNIVIHADENRGLMDFVNAKFFVIKSYSEDDVHKSIXYNVWSSTPNGNKKLNSAYEDAQRITP
	99090.1.1		GNPRGCPILFFSVNASGQFCGVAEMTGPVDFYKDMDFWQQDKWWSGFPVKWHFIKDVPNPFRHII
			LENNENKPVTNSRDTQEIRYKKGIEMLKVFKDYASRTSLDDDFMYENRQKLQEEKAKLLIR
	Solyc01g1	SIDF2C	DQLVPAVQREKYNKEDFKTQYDNAKFIKSYSEDDIHCKVKYDVWSSTPNGNKKLDTAFVESEAKAS
	03540.2.1		GTGSSCPVFLFFSVNGSGQFLGVAEMVGQVDFNKNMDFWQLDKWWSGFFPLKWHIVKDVPNTQFRHII
			LENNENRNPVTYSRDTQEIGLKEGLEMLNLKNYSEKTSILDDFNFYEKREKVLKAKRSSKPIV
<i>Medicag o truncat ula</i>	Solyc02g0	SIDC1A	DRTAVVLPQGTSRYFIVKSCNRENLELSVQQGVWATQRSNEAKLNEAFDSVENVILIFSVNRTRHFQGC
	21760.2.1		GKMTSRIGGAANGGNWKHEHGTAYHYGRNFSVKWLKLCESLHFKTRHLRNPYNENLPVKISRDCQEL
			EPSVGEQLASLLYLEPSELMAISLAAESKRLEEK
	Solyc02g0	SIDC2A	NQAAIPLPQGSPRYFIVKSCNRENLELSVQQGVWATQRSNEAKLNEAFDSVENVILIFSVNRTRHFQGL
	70240.2.1		AKMTSRIGGAANGGNWKHEHGTAYHYGRNFSVKWLKLCESLHFKTRHLRNPYNENLPVKISRDCQEL
			EISVGEQLASLLYVEPSELMAISLAAESKREEER
	Solyc08g0	SIDC1B	STAIEKGKLYSIRYFVIKSLNHNENIQLSVNRGIWATQAMNEAILDEAFHNSSKVLIFSVNTSGYFQGYAQ
	07730.2.1		MISSVGLRRDQVWSQGNNGRNSWGRSFEVNWRLRYDLFPQRTLHLKNPWNQNKPKISRDCQELPP
			DIGEALCELLDGQDALDVNLKMDVFAELNLSKR
	Medtr8g0	MtDF1	EKNSTTPDREQYNKADFPEEYTDKFFVIKSYSEDDIHKSIXYNVWASTQNGNKKLDAAYQEAQQKSG
<i>Medicag o truncat ula</i>	88390	A	GCPILFFSVNTSGQFVGLAEMTGPVDFNKSLEYWQQDKWMGCFPLKWHIVKDVPNNVLRHITLNN
			ENKPVTNSRDTQEIMLEPGLKLLKIFKEYSSKTCILDDFGFYEGRQKTILEKKAKQQFP
	Medtr7g0	MtDF2	EVVPLVLNKEQYNGEDLSENYSDAKFFIIKSYSEDDVHKSIXYSVWASTPNGNKKLDAAYQEAGGCPIF
	85500	A	LLFSVNTSGQFVGLAEMTGPVDFDKTVEYWQQDRWTGCFNVKWHIIKDIPNGVLRHITLNNENKPV
			TNSRDTQEVKFEKGVQIVKIFKEHASKTSILDDFGFYESREKTTQERKFKEQQL
	Medtr6g0	MtDF3	KEVHPVPDKQQYTGEDLSENYSDAKFFVIKSYSEDDIHKSMKYNVWTSTPNGNKKLDAAYLEAKEKSA
	32970	A	DCPIFLFFSVNTSGQFVGLAEMVSPVDFDRTVEYWQQDRWTGCFSVKWRIKDIPNNVLRHITLNNEN
			KPVTNSRDTQEVKFEKGVLEILKIFKEHSSKTCILDDFAFYAREKTIQEKKAKEQLS
	Medtr4g0	MtDF1	NASTAKFQDESLNRPDFAFDKDAKFFVIKSYSEDNVHKSIXYGVWASTPNGNKRKLDAAYCQAKEKQ
	05110	B	DACRIFLFFSVNASSQFCGVAEMVGPVNFDSVDFWQQDKWWSGQFPVKWHIIKDVPNNSQFRHIVLEN
<i>Medicag o truncat ula</i>			NDNKPVTNSRDTQEVKLQQGIEMLTIFKNYETDTSILDDDFDYEDRQKAMQERKARQQSS
	Medtr4g1	MtDF1	NTQENIIYTDQYNREDFPIDNEIAKFFVIKSYSEDDVHKSIXYNVWSSTPHGNKKLQSAYEDARRKATG
	23630	C	KSGGCPILFFSVNASGQFCGVAEMVGPVDFNKMDFWQQDKWWSGFPVKWHIIKDVPNNGNFRHII
			LENNENKPVTNSRDTQEIMYRKGLEMLKIFKNYTLKTSLLDDFIYENRQKVMQEEKTKFLMK
	Medtr2g0	MtDF2	VNGNTKIRTDQYNLPDFPTKYDHALFFVIKSYSEDDVHKSIXYDVWASTPNGNKRDLNADFQDAQNRM
	63460	C	EEKGSKCPVFLFFSVNASGQFCGVAEMIGRVDFNKSMDFWQQDKWNGFYFPVKWHIIKDIPNPQLRHII
<i>Medicag o truncat ula</i>			LENNNDHKPVTNSRDTQEIHFPQGIEMLNIFKNYVSRTSILDDDFDYESRQKVMQEKKIRQPM
	Medtr2g0	MtDF3	EQDSIIYTDQYNKEDFPLDYDNAKFFVIKSYSEDDVHKSIXYNVWSSTVHGNRKLGNAYEDTKKVS
	32660	C	AEKSGVCPILFFSVNASGQFCGVAEMIGSVDFNKMDFWQQDKWWSGFPVKWHIIKDVPNPNFRHII
			LDNNENKPVTNSRDTQEIMYSKGLEMLKIFKNHTLKTSLDDDFMYENRQKIMHDDQAKALLIR

<i>Citrus sinensis</i>	Medtr2g0 05840.1	MtDF4 C	DEFAFTVCRDQYNLPDFQTKYETAKFYMIKSFNEDDIHKGIKYDVWTSTPHGNKKLNAAFQNAEAKL SQTGTQCPIFLFFSVNASGQFVGVAEMLGPVDFKKDMKFWKLDKYNNGFFPIKWHIIKDVPNRQFAHIT LQINENKCVTFSRDTQEITLKEGLEMLKIFKSYPAKTSLDDDFYENREKLCSQRTEHTGW
	orange1.1 g005158m	CsiDF1 A	DKISLSPDRDEYNKADFPEEYTDAKFFVIKSYSEDDVHKSIIKYSVWASTPNGNKKLDAAYQEAQQKSRS CPVFLFFSVNTSGQFVGLAEMAGPVDNFKNVEYWQQDKWTGCFPVKWHIVKDVNPNSLLKHITLENN ENKPVTNSRDTQEIKLEQGLKLIKIFKDHPSTKILDDDFGYETRQKTIQEKKAKQQQF
	orange1.1 g010141m	CsiDF2 A	DNLPLIPDKEKYSGEDFPESYSDAKFFIIKSYSEDDVHKSIVKYNMWTSTPNGNKKLDAAYREAKEKSSD CPVFLFFSVNASGQFVGVAEMVGPVDFDKTVEYWQQDKWVGCFPLKWLIIKDVNPNSSLRHITLENNE NKPVTNSRDTQEVNFEIGIQILKIFKSHSSKRCILDDDFGYEARERIMQQKKAKQHQQL
	orange1.1 g005934m	CsiDF1 B	SKSVVKILDESYNQPDFVTDYKDAKFFIIKSYSEDDVHKSIIKYGWASTPNGNKKLDAAYCEAKEKQDP CPVFLFFSVNASAQFCGVAEMIGPVDFEKSVDYWQQDKWSGQFPVKWHIIKDVNPNSQFRHIVLENND NKPVTNSRDTQEVKLEQGIEMLNIFKNYVTDMSILDDDFYEDRQKAMQERKARQQAS
	orange1.1 g038459m	CsiDF2 B	NSSGSGINFELYNQDFPTDYENAKFFVIKSFSEDDVHKSIIKYGWASTPHGNKKLDAAYHEAKETDN RCPIFLFFSVNASGQFCGVAEMVGPVDFENSADYWQQDRWSGQFPVKWLIKDVNPNSRFRHLLLENN DNKPVTNSRDSQEVKLEQGVEMLRIFKEHDARTSILDDDFYDERERSLKERRAKQQVS
	orange1.1 g006798m	CsiDF3 B	NGTLDGILKGSYNQLDFVTNYKVAKFFIIKSYSEDDVHKSIIKYLWASTPNGNKKLDAAYREAKEKHG TCPIFLLFSVNASAQFCGVAEMVGPVDFDKSVDYWLQDKWSGQFPVKWHIIKDVNPNSQFRHIILEKND NKPVTNSRDTQEVLEQGIEMLNIFKNYESYSSILDDDFHFEYEQRQKAMQERKAGQQAN
	orange1.1 g005441m	CsiDF1 C	VEGNIICTEHYNKEDFQVDYVDAKFFVIKSYSEDDVHKSIIKYGWSSSTSHGNKKLQSAVEDAQKLAAG KPGGCPIFLFFSVNASSQFCGVAEMIGPVDYKDMDFWQQDKWSGSFPVKWHIIKDVNPNTSLRHILRN NENKPVTNSRDTQEIMHTEGLEMLKIFKNHPRDTSILDDDFMYYEKRQKFMQEERARLVFK
	orange1.1 g008255m	CsiDF2 C	EVLSPTVSRDQYNLPDFQVEYEKAKFYVIKSYSEDDIHKCIKYDVWSSTPNGNKKLDATFNEAEAKADE TGTRCPIFLFFSVNGSGQFVGLAEMMGKVDNFKNMDFWQLDKWNGFFPVKWHIVKDVNPNTLLRHITL ENNENKPVTNSRDTQEIGLKQGLEMLKIFKSYSAKTSLDDDFNFYENKERSFHGKSSKSPAT
	orange1.1 g048663m	CsiDF3 C	DSISLIWKDQYNLPDFRIKYDHALFFVIKSYSEDDIHKSIKYSVWSSTPNGNKKLDAAYEDAQSRIAEKG SKCPVFLFFSVNASGQFCGVAEMIGRVDNFKNMDFWQQDKWNGYFPVKWHIIKDVNPNSQFRHIILEN NDKKPVTNSRDTQEVKFPQGIELNIFKNYPSKTSILDDDFYESRQKVMQEKKVRLSVS
	orange1.1 g005338m	CsiDC1 A	NRNATPLPQGISRYFIVKSCNRENLELSVQQGVWATQRSNEAKLNEAFDSAENVILFSVNRTRHFQGC AKMTSKIGGSVGGGNWKYAHGTAHYGRNFSVKWLKLCESFHKTRHLRNPYNENLPVKISRDCQELE PSIGEQLAALLYLEPDSELMAISVAAEAKREEEK
<i>Arabido psis thaliana</i>	orange1.1 g015749m	CsiDC1 B	STDNNKGKLYNTRYFIIKSLNHQNIQLSIEKEIWATQVMNEPILEEAFHNSGKVLIFSVMMSGFFQGYA QMMSSVGWRRDNVWSQGNGKNNPWGRSFKVKWLRNLTLPFQKTLHLKNPLNDYKPKISRDCQEL PQDIGEALCHLLDGKDDVDGIQTSFHRDDLPAKR
	AT3G039 50	ETC1	DVSAVDLQRYNGENFPESFVKAKFFVIKSYSEDDVHNCIKYGAWSSSTPTGNKKLNAAAYEAKENSQEC PVYLLFSVNASGQFVGLAEMVGPVDNFNKTMEYWQQDKWIGCFPVKWHIIKDVNPNSLLRHITLANNEN KPVNTNSRDTQEVNLEHGTKIIKIFKEYMSKTCILDDYKFYETRQKIIRDKKIKQKKQ
	At3g1346 0	ECT2	DNTCVVPDREQYNKEDFPVDYANAMFFIIKSYSEDDVHKSIIKYNVWASTPNGNKKLAAAYQEAQQK AGGCPIFLFFSVNASGQFVGLAEMTGPVDFNTNVEYWQQDKWTGSFPLKWHIVKDVNPNSLLKHITL NNENKPVTNSRDTQEVKLEQGLKIVKIFKEHSSKTCILDDFSFYEVROKTIKAKQQTQK
	AT5G610 20	ECT3	SEDVSLDPKDYNKIDFPETYTEAKFYVIKSYSEDDIHKSIKYSVWSSTPNGNKKLDASYNEAKQKSDGC PVFLFFSVNTSGQFVGLAEMVGPVDNFNKTVEYWQQDKWIGCFPVKWHFVKDIPNSSLRHITLENNE KPVNTNSRDTQEVKLEQGIKVIKIFKDHAASKTCILDDFEFYENRQKIIQERKSKHLQI
	AT1G555 00	ECT4	TVTCVLPDREECNRDDFPVEYKDAKFFIIKSYSEDDVHKSIIKYNVWASTPNGNKKLDAAYQEAQQKSS GCPVFLFFSVNASGQFIGLAEMKGPVDNFNKNIEYWQQDKWTGSFPLKWHILKDVNPNSLLKHITLEYNE NKPVTNSRDTQEVKLEQGLKVVKIFKEHNSKTCILDDFSFYEARQKTIKAKKQQQS
	AT3G130 60	ECT5	NKGSACEHEESNADFVTDYTNALFIIKSYSEDDVHKSIIKYNVWASTPNGNKKLDAAYREAKDEKE PCPLFLFFSVNASSQFCGVAEMVGPVDFEKSVDYWQQDKWSGQFPVKWHIIKDVNPNSQFRHIILENND NKPVTNSRDTQEVKLEQGIEMLNIFKNYDADTSILDDDFGYEEREKIIQDRKARRQPS
	AT1G279 60	ECT9	SKMISYDRVDRFCQQLSQRDAKFFVIKSYSEDDVHKSIIKHCVWASTKNGNKKLDAAYREAKKDV ACPVFLFFSVNASSQFCGVAEMVGPVDNFNTSVEYWQQDRWSGHFPVQWLIVKDVNPNSLFRHIIIESND NKPVTNSRDTQEVGLEKGIEMLDIFISCEMRSSILDDFNFYERQIAIQDRKARQRAV
	AT5G581 90	ECT10	DSSTAGPNPSLYNHPEFVTDYKNAKFFIVKSFSEDDVHRSIIKYNVWASTPHGNKKLDTAYRDAEKM GKCPIFLFFSVNASGQFCGVSEMVPVDFEKDAGYWQQDRWSGQFPVKWHIVKDVNPNSRFRHILHNN NDNKPVTNSRDSQEVKLRQGIEMLRIFKEYEAHTSILDDFGYDELEGQKVGEDGTRKKA
	AT3G173 30	ECT6	AEGNIVINPDYRNKEDFSIEYSDARFFVIKSYSEDDVHKSIIKYGWSSSTLNGNKKLQSVYEDAQRATEK SRECPILFFSVNSSGLFCGVAEMTGPVSFDRDMDFWQQDKWSGSFPVKWHIIKDVNPNSYFRHILHNN ENKPVTNSRDTQEIIKQGLEVLKLFKHHAECTSLDDDFMYEDRQRLMQEERARLPFR
	AT1g4811 0	ECT7	AEGNIVINPSQYNKEDLRIDYNAKFFVIKSYSEDDVHKSIIKYNVWSSTLHGNKKLQSAVEDAQRIATE KSCECPILFFSVNASGLFCGMAEMTGPVSFDDKMDFWQQDKWSGSFPVKWHIIKDVNPNSYFRHILQ NNENKPVTNSRDTQEIMLKQGLEVLKIFKDHMERTSLLDDFVYYESRQRMQDERTLPYR
<i>Arabido psis thaliana</i>	AT1G792 70	ECT8	NGVGSVIRRDQYNLPDFQTKYEEAIFVIKSYSEDDIHKSIKYNVWSSTLNGNKKLDSAYQESQKKAADK SGKCPVFLFFSVNASGQFCGVAEMIGRVDYEKSMEFWQQDKWTGYFPVKWHIIKDVNPNSQFRHIILEN

			NENKPV TNSRDTQE VRLPQGNEVLNIFKNYAAKTSILDDDFYENREKVMVQKKLRFPV
AT1G098 10	ECT11		NSFALALRREMYNLPDFQTDYEDAKFFVIKSYSEDDVHKSISKYSVWSSTINGNKKLDAAFRDAETKTLE DGKKRPIFLFFSVNASRQFVGLAEMVGVDNFNKLDFWQVDKWSGFFPVEWHVVKDIPNWELRHIL DNNE DKPVTHTRDTHEIKLKEGLQMLSIFKKYSAVTFLLDDMDFYEEREKSLRAKKEHKPAT
AT1G304 60	CPSF30		NRTSHPLPQGVNRYFVVKSNRENFE LSVQQGVWATQRSNEAKLNEAFDSVENVILIFSVNRTRHFQ CAKMTSRIGGYIGGGNWKHEHGT AQYGRNFSVKWLKLCESFHKTRNLNPNYENL PVKISRDCQEL EPSVGEQLASLLYLEPDSELMAISIAAEAKREEEK
AT4G119 70	ECT12		KANKNSKPGYRTRYFIIKSLNYDNIQVSVEKGIWATQVMNEPILEGAFHKSGRVILIFSVNMSGFFQGYA EMLSPVGWRRDQIWSQGGGKNNPWGRSFKVKWLRLSELFPQKTLHLKNPLNDYKPVKISRDCQELPE DIGEALCELLDANSCDDGLLNSSSRDDYSTKR
Cch01T00 2587.1	CchYT H1		NAKFFVIKSYSEDDVHKGIKYNVWSSTPNGNKKLQSA YEDAQRIASGEPRGCAIFLFFSVSDIPLILSFAL KYYIPQVNASGQFCGVAEMTGPVDFHKDMDFWQQDKWSGSFPVKWHIIKDVPNP NFRHIILENNEN KPV TNSRDTQEIRCRQGIEMLKIFKLYTSK
Cch02T00 2736.1	CchYT H2		NAKFFVIKSYSEDDVHKGIKYNVWSSTPNGNKKLRSAYEDAQRIAFGEPRGCPIFLFFSVRDIPLILSFAL KYYIPQVNASGQFCGVAEMTGPVDFHKDMDFWQQDKWSGSFPVKWHIIKDVPNP NFRHIILENNEN KPV TNSRDTQEMFFSTHYAGDNLTIKLRD
Cch02T00 3694.1	CchYT H3		DAKFFI KSYSEDNVHKS IYGIWASTPNGNRKLDAA YREAKEKNTCPVFLFFSVN ASAQFCGVAEMV GPVDFDKSDY WQQDKWSGQFPVKWHIIRDVPNSQFRHIVLENNDNKPV TNSRDTQEAKLEQGIEML KIFNNYES
Cch03T00 2158.1	CchYT H4		NAKFFI KSFSEDNVHKS IYSVWASTPLGNRKLDAA YHEVKDANGHCPVFLFFSVN ASGQFCGVAEM IGPVDFEHDVDY WQQDRWSGQFPVRWHI IKDVPNNQFRHILENNNDNKPV THSRDSQEVKLEQGIEL KIFKDYEA
Cch05T00 0069.1	CchYT H5	<i>Camellia</i>	NAKFFVIKSYSEDDVHKS IYNVWSSTPNGNKKLQSA YEDARRIAAGEPRGCPVFLFFSVN ASGQFCGV AEMTGPVDFYKDMDFWQQDKWSGSFPVKWHI IKDVPNP NFRHIILENNENKPV TNSRDTQEVCVFVIP DTLFTC
Cch07T00 0910.1	CchYT H6	<i>a</i>	NAKFFVIKSYSEDDIHKCIKYDVWSSTPNGNKKLDA AFHDAEAKACETGT KCPIFLFFSVN GSGQFIGV AEMIGPVDFNKDMDFWQLDKWNGFFPVKWHI IKDTPNTQLRHIILENNDNRSVTYSRDTQEIGFKQGI EMLNIFNSYSE
Cch08T00 1554.1	CchYT H7	<i>chekiang</i>	ISRYFIVKSCNRENLELSVEQGVWATQRSNEAKLNEAFDSVENVILIFSVNRTRHFQGC AKMTSKIGGSV GGGNWKYAHGSAHYGRNFSVKWLKLCESFHKTRLLRNPNYENL PVKISRDCQELEPSVGEQLASLLY LEPD
Cch09T00 4551.1	CchYT H8	<i>oleosa</i>	NAKFFVIKSYSEDDVHKGIKYNVWSSTPNGNKKLQSA YEDAQRIASGEPRGCAIFLFFSVSDIPLILSFAL KYYIPQVNASGQFCGVAEMTGPVDFHKDMDFWQQDKWSGSFPVKWHI IKDVPNP NFRHIILENNEN KPV TNSRDTQEIRCRQGIEMLKIFKLYTS
Cch12T00 1174.1	CchYT H9		DAKFFI KSYSEDDVHKS IYNVWASTPNGNKKLDA A YQEAQQKSGGCPVFLFFSVNTSGQFVGVAEM TGPVDFHKNF EYWQQDKWNGCFPVNWHIVKDVSNLLKHITLENNENKPV TNSRDTQEVKLEQGLQ LLKIFKDHSSK
Cch13T00 1809.1	CchYT H10		GTRYFIIKSLTHQNIQLSIEKGIWATQVMNEPILEEAFHNSSK VILIFSVNMSGFFQGYA QMMSSVGWRR DNVWSQSGGKNPWGRSFKVKWLRLHDLFPQKTLHLKNPLNDYKPVKISRDCQELPDIGEALCELL DGKDD

* All accession numbers relate to the JGI Phytozome, Metazome or MycoCosm databases
 ** In cases when a name was already attributed to a protein, this name was kept with the new name, referring to the species of origin and to the phylogenetic classification of the protein, added in parenthesis
 *** For these species, only the core YTH motif are indicated

Table S2. Conserved Motif analysis of YTH proteins in *Camellia chekiangoleosa*.

Motif	Logo	E-value	Sites	Width
1		1.3e-218	8	50
2		4.9e-215	7	50
3		1.2e-096	4	50
4		7.3e-088	4	49
5		2.3e-084	4	50
6		4.6e-084	10	21
7		1.6e-052	4	42




8		6.5e-050	5	40
9		4.1e-045	4	29
10		1.7e-043	10	15

Table S3. Primer sequences.

Primer Name	Primer Sequence (5'-3')
CchYTH1-Q-F	GGTGCTATGTTAGGAGTTG
CchYTH1-Q-R	AAGCCATTACTAGAAGTGAGA
CchYTH2-Q-F	CAAGAACGGTACAATCAGC
CchYTH2-Q-R	TACACGAAACTCACCAAAT
CchYTH3-Q-F	ATGAGTCTTACAACCTGCCCGAA
CchYTH3-Q-R	GTGTGCTGGCCCATATACCAT
CchYTH4-Q-F	AGTCTTTCTCTTGTTTCGGTCA
CchYTH4-Q-R	CTTTGATTATATGCCACCGGACA
CchYTH5-Q-F	CCCTTCTTAGATACTGGTGCAT
CchYTH5-Q-R	TACCCTAGCAAAGGAACGTGTC
CchYTH6-Q-F	GCAAGCTTCATCTCAAACCGAA
CchYTH6-Q-R	TGCTGCTTCTTCAGTTGTCGTT
CchYTH7-Q-F	CGGCTAACGACAAGAACGA
CchYTH7-Q-R	TCATCAGCTCCCGAACCAC
CchYTH8-Q-F	GACGCTGTTGTAGGTAATG
CchYTH8-Q-R	GATGTAGCTGATCGGAGAT
CchYTH9-Q-F	CGTCCTCATTCTCATCTCA
CchYTH9-Q-R	TCTAAAGGTGCTTCCATAC
CchYTH10-Q-F	TCTAAAGGTGCTTCCATAC
CchYTH10-Q-R	CGCAGCCATTTACCTTAA
Actin-F	GTGGTTGTGAATGGAGGGCA
Actin-R	AGGCCAGGAGACCCATTACA
CchYTH9-F	ATGGTTTCATCAATATCACATGGAAATAACTCCCC
CchYTH9-R	CATGGGAAAAAATGTACCCTCAACATTTGCAA
1305-CchYTH9-F	TTTGGAGAGAACACGTCTAGAATGGTTTCATCAATATCACATGGAA
1305-CchYTH9-R	CTTGCTCACCATGTAGTCGACCATGGGAAAAAATGTACCCT

Table S4. PLAAC of YTH proteins in *Camellia chekiangoleosa*.

Protein Name	LLR	PAPAp _{prop}	PAPAf _i
CchYTH1	1.709	-0.043	-0.126
CchYTH2	7.976	0.011	-0.005
CchYTH3	8.537	-0.022	-0.004
CchYTH4	5.516	0.047	-0.043

CchYTH5	10.072	0.023	-0.002
CchYTH6	10.361	0.109	-0.096
CchYTH7	23.847	0.019	-0.173
CchYTH8	6.537	-0.007	-0.005
CchYTH9	11.980	0.016	-0.168
CchYTH10	-11.558	0.053	-0.007

CchYTH7 LFGPPPPVEEVLQKIQQMTSYNYGNSNRFTQNRNSNYPQQTEKPOFPQGFNAANQVTAAKSSTTESPNMQLQQQVQQSQQQVGQTQIQNFPNGQQNQGNKSSTPLPQ 107
 CchYTH10 EPILEEAFHNSSKVLIFSVNMSGFFQGYAQMMSSVGWRRDNVWSQSGGKKNPWGRSFKVKWLRRLHDLPFQKTLHLKNPLNDYKPKVKSIRDCQELPQ 97
 CchYTH6 LPLDSRSRKSAASSNISKSIIESQPLKTLGKLGSGYQSANLMKGYHPVGNFSSFTNQQGVIMHNSSMNYRSNSRVWNGNKNFNLDRNVGFDASSELTCGPRAQNGSNPSNF 114
 CchYTH8 LPYVYHTPSYGYAQSPYNPNYPYIPGAMIGVDGPFGRGAQAVDNISHGKALSHRNQLKMAITSSNGLSNFGSSAHGGAAVEKIRSKFHYGRVLNDVNGSPDALTERNRGPRTNKSKNHLAVKAYTTRAGESDAQ 133
 CchYTH5 LPYVYHTPSYGYAQSPYNPNYPYIPGAMIGVDGPFGRGAQAVDNISHGKALSHRNQLKMAITSSNGLSNFGSSAHGGAAVEKIRSKFHYGRVLNDVNGSPDALTERNRGPRTNKSKNHLAVKAYTTRAGESDAQ 115
 CchYTH1 LPYVYHTPSYGYAQSPYNPNYPYIPGAMIGVDGPFGRGAQAVDNISHGKALSHRNQLKMAITSSNGLSNFGSSAHGGAAVEKIRSKFHYGRVLNDVNGSPDALTERNRGPRTNKSKNHLAVKAYTTRAGESDAQ 133
 CchYTH2 LPYVYHTPSYGYAQSPYNPNYPYIPGAMIGVDGPFGRGAQAVDNISHGKALSHRNQLKMAITSSNGLSNFGSSAHGGAAVEKIRSKFHYGRVLNDVNGSPDALTERNRGPRTNKSKNHLAVKAYTTRAGESDAQ 111
 CchYTH9 TPVPLAVKGQNTLNGTNDLEKDRSSVAPDREQYNYKDFPESYTDKFFHKSYSRDDVHKSIFYNVWASTPENGKKLDAAVQEAQKSGGCPVLFSSVNTSGQ 110
 CchYTH3 LPSVGQDAQLSPQQYFSGFPYVQHLYPPSMQYITPFPVSQPVLSNVVSIDQQVDGMILLGRPSYPSVTSFGRGNFSGNPGGFGPHDLQQGFDAFRTSGLWSDWSKPSDRQ 103
 CchYTH4 LPSQNDMVTSGSSGQEGLYDNVLFQPGSGYFVHFGSFGGGLSGEPLSNRSNSETGSYMSPLTSPTVYPPPIGILGPYEHNAGQVSQQQRTSHGFGFLVASSARNYPHGGSYQ 113

Figure S1. Y/P/Q-rich region in CchYTHs. The Y/P/Q amino acids are highlighted in yellow. The number at the end represents the number of amino acids.