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Comparative and evolutionary analyses of cyclophilins in *Cucumis sativus*, *Phaseolus vulgaris*, and *Vitis vinifera*

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SUPPLEMENTARY MATERIAL

Supplementary File S1: Amino acid sequences of *C. sativus, P. vulgaris* and *V. vinifera.*

Cucumis sativus

>Cuc1

MHILRLLPILAFLLFFAFFTITSAQDSHLGSARVVFQTNYGDIEFGFFPKVAPRTVDHIFKL
VRLGCYNTNHFFRVDKGFVAQVADVVGGRLAPMNEEQRTEAEKTVVGEFSDVKHVRGI
LSMGRYDDPDSAQSSFSMLLGDAPHLDGTYAIFGKVTKGDDTLKKLEELPTRREGIFVM
PTERITILSSYYYDTNLDSCEEDRSTLKRRLAASFVEIERQRMKCFP*

>Cuc2

MEEPLNGNGNVDSASAKAETEEDPAIGPGPAPRSRPKRPLQFEQAYLDTIPSANMYEKSY
MHRDVVTHVAVSSADFFITGSDDGHLKFWKKKPIGIEFAKHFRSHLGPIEGIAVSVDGLLC
CTISNDHSVKIYDVVNYDMMVMIRLPFIPGAAEWVYKQGDVKARLAISDRNSSFVHIYD
ARSGSNEPIASREVHLGPVKVMKYNHVFDSVISADARGLIEYWTPDTLQFPENNVNFKL
KSDTNLFEIVKCKTTVSAIEVSPDGKQFSITSPDRRIRVFWYRTGKLRRVYDESLEVAQDL
QRSDAPLYRLEAIDFGRRMAVEKEIEKAESAPQPNAVFDESSNFLIYTSLLGIKVVNLHTN

KVARILGKVENNDRFLRIALYQGDKSSKKVRKIPSAAANANESKEPLTDPTLLCCAFKKH
RIYLFSRREPEEPEDATKGRDVFNEKPPADELLAVSDIGKSVTTSLPDNVILHTTMGDIHM
RLYPEECPKTVENFTTHCRNGYYDNLIFHRVIKGFMIQTGDPLGDGTGGQSIWGREFEDE
FHKSLRHDRPFTVSMANAGPNTNGSQFFITTVATPWLDNKHTVFGRVIKGMDVVQTIEK
VKTDKADKPYQDVKILNVSVPKP*

>Cuc3

MGRIRCFLDISIGGDLEGRIVVELYDDVVPKTAENFRALCTGEKGIGPHTGVPLHFKGSCF
HRVIKGFMVQGGDISAGDGTGGESIYGEKFDDENFEVKHERKGMLSMANSGPNSNGSQ
FFITTTRTPHLDGKHVVFGKVLKGMGVVRSIEHVTTGENACPIAEVIISDCGEIPEGADDG
ISNFFNDGDTFPDWPTDLEQSSDDLEWWVKAVDSVKVFGNEHYKKQDYKMALRKYRK
ALRYLDICWEKEGIDEEKSSYLRKTKSQIFTNSSACKLKLGDLKGALLDTDFAMRDGDD
NVKALFRQGQAHMALNDIDSAVESFKKASDLEPNDAAIKKELAAARKKIADRRNQERK
AYSKMFQ*

>Cuc4

MPRGFSLLYQPRCLLLFIVFLIFLVFVLFTHNQREEKQEEELEITHRVFLDVDIEEQRLGRI
VIGLYGQVVPKTVENFRALCTGENGKTTSGKALHYKGTLFHRIVSGFVIQGGDILYGDG
KGYESIYGGTFADENFRIKHSHAGVVSMVNSGPDSNGSQFFITTIKSSWLDGEHVVFGKV
IQGMDYVYAIEGGAGTYSGKPRKKVTIADSGEIPKSKWDEEA*

>Cuc5

MSVLIVTSLGDIVIDLHTDICPLTSKNFLKLCKIKYYNGCLFHTIQKDFTAQTGDPTGTGT
GGDSIYKFLYGDQARFFSDEIRLDLKHSKTGTVAMASAGENLNASQFYFTLRDDLEYLD
GKHTVFGEVAEGLDTLTRINEAYADEKGRPYKNIRIKHTYILDDPFDDPPQLAELIPDSSP
DGKPKDEVVDEVRLEDDWVPLDEQLGAEELEEVFRAKEAHSRAVVLETIGDIPDAEIKP
PDNVLFVCKLNPVTEDEDLHTIFSRFGTVLSAEIIRDYKTGDSLCYAFIEFETKEACEQAY
FKMDNALIDDRRIHVDFSQSVAKLWSQYRRKDYTTDKGGGCFKCGALDHMARDCTGG
STKFILKDDNVQHGGDESRYDFVFDEDNGNNNRKERRRRDHDHDRHVERPNARKPSPA
GRERYGEKKGASDRNESNDRNRFREREMHRENKDRQSRGDRDDFEDRRDHERQRKRQ
NDRDAHKKKELDYRKRSSNDHDAYGDRDYEANRNRSGREYSDRSEKRKDGEFYGRRH
ADKSSHEEKRHDIREYRKDERGYGKRSFDSEKAEMKDGPHYKKRYTDDDGYKDRREE
REPRRRSREEYTER*

>Cuc6

MWASAEGGPPEVTLETSMGSFTVELYFKHAPRTCRNFIELSRRGYYDNVKFHRIIKDFIV
QGGDPTGTGRGGESIYGKKFEDEIKPELKHTGAGILSMANAGPDTNGSQFFITLAPCPSL
DGKHSIFGRVCRGMEIIKRLGSVQTDNNDRPIHDVKILRASVKD*

>Cuc7

MIQGGDPTGTGKGGTSIWGKKFNDEIKESLKHNARGILSMANSGANTNGSQFFITYAKQ

PHLNGLYTIFGRVIHGFEVLDIMEKTQTGPGDRPLAEIRLNRVTIHANPLAG*

>Cuc8

MTNPKVFLDILIGRVKAGRIVMELFADTTPKTAENFRALCTGEKGIGRSGKPLHYKGSKF
HRIIPDFMCQGGDFTKSNGTGGESIYGLKFADENFKLKHTGPGMVSMANAGPNTNGSQF
FISTSGPLSWLDGKHVVFGKVVDGYDVVEKMNEKGTESGDPKVPVVIEDCGQITES*

>Cuc9

MSTVYVLEPPTRGKVVLNTTCGPLDIELWPKEAPKAVRNFVQLCLEGYYDNTIFHRIIKD
FIVQGGDPTGSGTGGESIYGGVFPDEFHSRLRFKHRGLVACANAGSPHSNGSQFFITLSRC
DDLDKKHTIFGKVTGDSIYNLTNLGELETEKDDRPVDPPKIKSIEVLWNPFDDIVPRAPAK
LVVTSTLDSENKDTKKKAVKKLNLLSFGEEAEEDEKELAAVKKKIKSSHDVLDDPRLLK
SEIPSSELDSKRTREMQLSVRETLASKKPESRRDSEAENSNLPQYSDSDDDETNFDARMR
QQILRKRTELGDAPSHQKSKNGTSNSKKHEGSTRSRPDTEKTKREEPKVEKLSLKKKGIG
SEARAERMANADSDLQLLGDAERGRQLQKLKKRRLQGREDEVICIMRNFVLHFSISIYL
FVLGKKEPSNAESGGANDDLSDWKSVRLKFTAEPGKDRMSRSDDPNDYVVHDPLLEKG
KEKFNKMQAKQKRREREWAGKSLT*

>Cuc10

MAASLPTTPLVAFASGSDTKASGPSNSVKLHRLQFPSSSSFLSGSLHFPSLTTSLNPLSSRIV
VRSSVRASAEVPPLQAKVTNKVYFDVSIGNPVGKLAGRIVIGLFGDDVPKTAENFRALCT
GEKGFGFKGSVFHRVIEDFMIQGGDFEKGNGTGGKSIYGRTFKDENFNLSHTGPGIVSMA
NAGPNTNGSQFFICTVKTQWLDLRHVVFGQVLEGFEIVKLIESQETDRADRPLKKVVISD
CGELPVA*

>Cuc11

MTSLRRLFSAVCLWILFLIATLFLILNHLEDHGVSSQLKVAEENPATVTHKVYFDIEIGGKP
SGRVVIGLFGETVPKTAENFRALCTGEKGIGRSGKSLHYKGSKFHRIIPSFMIQGGDFTRG
DGRGGESIYGEKFADENFLLKHDGPGFVSMANSGEDTNGSQFFITTIKTSWLDGHHVVF
GKVLSGMDVVFKIEAEGNQGDGKPKTEVSISQSGELPV*

>Cuc12

MASTVSMSVFSTLPSPSQGKCRLPSLSSRSISLQVQTTNSPVTTLTWGSQRLSFPILREASP
VKNRRLICANSATKNVELQAEVSTKCFFDVEIGGESAGRIVIGLFGDVVPRTVENFRALC
TGEKGYGYKGCSFHRVIKDFMIQGGDFTNGDGTGGISIYGPSFRDENFSLKHVGPGVLS
MANAGPDTNGSQFFICTVKTPWLDNRHVVFGHVIEGMDVVKRIESQETSNLDIPRMPCR
IVNCGELEVKVD*

>Cuc13

MPNPKVFFDMTIGGTPAGRIIMELYADVTPRTAENFRALCTGEKGVGKGGKPLHYKGSSF
HRVIPNFMCQGGDFTAGNGTGGESIYGAKFADENFIKKHTGPGILSMANAGPGTNGSQFF

ICTAKTDWLDGKHVVFGQVVEGMNVVKDVEKVGSSSGRTSKPVVIADCGQLS*

>Cuc14

MSKKKNPLVFLDVSIGGEPVQRIIIELFANVVPKTADNFRALCTGEKGIGKTTEKPLHYKG
TFFHRIIKGFMAQGGDFSRGNGTGGESVYGGKFSDENFKLKHDGPGILSMANSGPNTNG
SQFFITFKPQPHLDGKHVVFGKVVMGMDVVKKIEQIGTADGKPGEPVKIVNCGEPSEIKD
EAVVKKEKEKKKKLNKIKSSESSSDDQGRGRQKKSSKDRRKKRKRYSSSDSYSSDTESD
SYSSDSDSSLSDSSSSSDGKYRKRRSKRTAKPQHGRKRKGRKREKRGRLGKRSKRKAK
WSSGSSTDTGSESTSDSSSSSDGERVDHRATTRRKIKNSKHSETKSKGITDEKESLNPVTE
TTVEKQKSQDLNLLQEEGELSPKHDDIPNNNHKTETEKLERSPNQRPVSDGSNSSRSTTP
ERPRNIPRSNLTRSPVKTFGNPGMKYNEWNRPRSSRSPVRSPIRKAADSSVSNHGQTSSR
SHSPNGTPKRVRKGRGFTEQYSFVRRYRTPSPERPRNYGGRNNYGRSHNGYSSYRNKRD
WSPDRRYRSPPRGRSPSRYRRRSRSVSRSPGSYRGRYRDRSKSRSPVRSSSPLEKRTQISD
RLKSRLGPKSKFSPEKETSQSRNYNRNRSLSRSISPDKHRTAAASPSRSRSSSLSGQKGLV
SYGNGSPES*

>Cuc15

MAKMKPQALLQQSKKKKGPSRISLTTILTCSLIVALFVFFLHTSYRHWSHRSKLQLENGF
SGSETEASLMDTKKSDLPGYAVFSTS

KGTIVVELYKESAPEVVDEFIDLCQKNRFSGMLFHHVIKHYSIQVGNSQDLGVAEDWILG
GKHHSQPDASLKHDAFLVGTPRGKPKNKGFEIFITTAPIP

DLSEKLIIFGQVIKGEHVVQEIEEVDTDEHYRPKSTIKINNITLRMKI*

>Cuc16

MPMPRCFLDITIGGELEGRIIIELYNHLVPKTAENFRALCTGEKGISPNTALPLHFKGVCFH
RVIKGFMIQGGDISAGDGTGGESIYGLKFEDENFELKHERKGMLSMANSGPNTNGSQFFI
TTTRAPHLDGNHVVFGKVVKGMGVVRSIEHVITGENDRPTLDVVIADCGEIPEGAHDGV
SNLFKDGDTFPDWPADLDQSPFELSWWMSAVDSIKAFGNVHFKKQDYKMALRKYRKA
LRYLDICWEREGIDEEKSTCLRKTKSQIFTNSSACKLKLGDLKGALLDTEFAIREGVNNV
KAVFRQGQAHMALNDIDSAVESFKRALDLEPNDAGIKKELAAAKKKIADRRDQERKAY
GKMFL*

>Cuc17

MGKKQHSKDRLFITKTEWATEWGGAKSKGSQTPFKRLPFYCCALTFTPFEDPVCTADGS
VFEIMNIIPYIRKYGKNPVTGAALKQEELIPLTFHKNSEGEFQCPVLNKVFTEFTHIVAIKT
TGNVFCYEAVKELNIKTKNWKELLTDESFCREDIITIQNPTALDSKVLLDFDHVKNSLKV
DDEELQKMKSDPTYNINVSGDIKQMLQELGTEKGRETALHGGGGGKAQKERAAALAAI
LAARSRIKENSKENGKGEEKPKQAFSIVDAASASVHGRSAAAAKAAPSEKTAARIAMH
MAGDRAPVNAKMVKSRYTTGAASRSFTSTSYDPVTKNEHEYIKVEKNPKKKGYVQLH
TTHGDLNIELHCDIAPRACENFITLCENGYYNGVAFHRNIRNFMIQGGDPTGTGRGGESI
WGKPFNDELNSKLVHSGRGVVSMANSGPHTNGSQFFILYKSANHLNFKHTVFGSVVGG

LTALAAMEKVPVDDNDRPLEEIKITNVAVFVNPYSEPDEEEEKQKDEKNVEDEENDKVG
SWYSNPGTGVAEDGAAGGGVGKYLKARNAQSKPLAVDASLKQNTSTKKRTAAGEFKD
FSSW*

>Cuc18

MLRTPKFLHSPNLSSQTQTQTQTQNIPTSSKFPFIKQCCKISRRNLTIGTNSLLLLLFNSQIQ
DPFLMSSKAEVEEEELQSPKNDDFLCTGKIPTKRAFLDISIDGVPAGRIIIGLYGNDSPAGV
ARFSNLVSGAAGISYRRKDFVKITSNYVQHSGVRSYGVDFELAKRNGNELVSETLKDEW
ERANEKCSGTKNLASTVGIIVRDPLKPPPKLKLVARKGKLEVDQEQVGTEPNGTEFTISV
KDSPELDDSALVIGIVLDGMEVVEKIAQVKTVKDNTTSPYFRVAKIIGDKRAVVAERGFN
RPYSKVIVTNCGLLEE*

>Cuc19

MAFALLSTSSSAAATTVALLPPHHNHRRLRSGDITLPRRSLLLLSTSLSLSTAVNPPPSLAS
PSPDTTITDRVFIDFSICPTNFLPNRESTDDGGDSLLCSDSVLLGRLVIGLYGHLVPTTASNF
KSMCTGSCGSSYKGTLVHKIFPGQFFLAGRQGRRDKGEVRPPLQLPRNTESVKSDSFLLS
HSRGGVISLCLSENDDDDDLKLDPNYHNVEFLITTGPGPCPQLDSKNIVFGTVLEGLDVV
AAISSTPTYKPSERIRQFNDLAKFLGDERAQNARTIWNRPLQTVYISDCGELKVAKPSLSP
TLP*

>Cuc20

MANTASFILCTLLLLATLTLIQAKKSKENLKEVTHKVYFDVEIDGKAAGRIEMGLFGKAV
PKTAENFRALCTGEKGVGQSGKPLHYKGSAFHRIIPSFMIQGGDFTLGDGRGGESIYGEK
FADENFKLKHTGPGLLSMANAGSDTNGSQFFITTVTTSWLDGRHVVFGKVLSGMDVVY
KIEAEGRQNGTPKSKVVIADSGELPL*

>Cuc21

MFQLMETPGKDWFLSSFMTLLQKRRRIFVHCVQERKELALKLENHYIIRDLFFIGLLEVL
WHRVEILSNEMVQLERAFMVESFQKMQVTEPHLLFSMRFFPYIDRFPFHPNELPRLKHD
GPGLLSMAIADRDTLGSHFLITFKANNHLDRKHLVFGKLVQGFDVLKKMERVDVEDGIP
TVTVKIVNCGEFNEEKRKINKVKTGKNASDDDSQEEKRRGKPKKSRERKRRKKKYDTS
DSDSSSDSELDSDSDSDSDTDLSSSSSSSESSSSDDRSRKRKRTSKRGRYRRGRRKDKRRR
KRRRHDKKSRRKSKRDLDSLSDTESDSKSRSTSEQDGLDVQGKDLNRKGISGKSAEDVP
QASDARHRRRGEADVVENDGERSPKENGERRSNGVAAVDSKSDRSLERQPDIVDDHPG
KSRSRSISPRRTMSKSMSISPRKTHSKSHSVSPKQSMSRSRSVSQSPPQAPLRSKSISRSPV
RNGSRSVSRSPVRNGSRSPGRSISRSPGRGRKGRSISRSPLRSGHQRGISRSPVRSNPQRSP
SRSPPRRASRKSISRSPARVSRSVSRSPVRSSRQSLSRSSGRAPSRRSISRSPRAPARNRRSY
SRSHTPIRRPRSPTSDRGISASRSVSPEGSPKRIRRGRGFSERYSFARRYRTPSASPVRSYRY
SGRVERDRYSNYRRYSPRRYRSPPRGRSPLRYRNSRRSRTPSASRSPRYRSRRYSRSRSPIR
SRSPVEGSRSRLSPRVGRRRSLSRSRSPSKSRSPADSQSPRRTSRDRSRSPSASPVGKKGLV
SYGDGSPDSER*

Phaseolus vulgaris

>Phv1

MARIKPQALLQQSKRKKGPARISVTTILFYILILSLVGFFLFASYRHWNNRSSLQSENHLST
SEGDNTFADSKKSDLPGYAVLNTSKGSIIIELHKESAPEVVDEFIDLCQKGHFKGMLFHLV
IKHYVIQAGDNHGAGATEDWNLRGKQHAITSMKHEAFMLGTSKGKHNHKGFDLFITTA
PIPDLNEKLIVFGQVIKGEDVVQEIEEVDTDEHYKPKISIGILDVTLKQKV*

>Phv2

MIYMLLEWQWQLQTQSMAAAFASSTPSLRLSNFGEIKGLHLPNPNPNNLKLRRRGSGFG
GCYGVTLSVRERAVGRGLRVRASSSSSGEDAIVQAKVTQKVFFDIGIGNPVGKLVGRVVI
GLYGDDVPQTAENFRALCTGEKGFGYKGSSFHRVIKDFMIQGGDFDKGNGTGGKSIYGR
TFKDENFVLSHTGPGVVSMANAGPNTNGSQFFICTVKTPWLDQRHVVFGQVLEGMDIV
RLVESQETDRGDRPKKNVTIIDCGEIPIA*

>Phv3

MSSVYVLEPPTKGKVVLSTTRGPLDIELWPKEAPKAVRNFVQLCLENYYDDTIFHRVIKD
FLVQTGDPTASGTGGESIYGGVFADEFHSRLKFKHRGIVAMASSGSPNSNGSQFFITLDRC
DWLDRKHTIFGKVTGDTMYNLLRLGEVETDKNDRPLDPPKILSVEVLWNPFEDIVPRTL
QKSQTEARVDAESKEQKKKGVKKLNLLSFGEEAEEDEKELASVKQKIKSSHDVLNDPRL
LKEETPDGELSSSRRDLQLSVRETLNSKKEEPQKDSAPGNIARLDSSDDDEADFDSRMR
MQILKKRKELGDLPPKSKLQKGGGRSIPENHDTSAPRSNAVSADEDQPKVEKLSMKKKG
VGSEARAERMANADADLQLLNETERGRQLQKQKKRRLQGREDEVLAKLQKFKSSLAA
KETPPAGKSGDVNSELSDWKGVSLKFDPESGKDRMSRNEDPNDYVVHDPLLEKGKEKF
NRMMAKQKRREREWAGRSLT*

>Phv4

MGLEKNVRVFFDVSIDADPVERIVIQLFDSIVPKTAENFRALCTGEKGIGESTGKPLHYKG
TSFHRIIKGFMAQGGDFSRGNGTGGESIYGGKFADENFKLRHDGPGFLSMANSGPNTNG
SQFFITFKRQPHLDGKHVVFGKVVNGMDALKKIELVGTSDGKPTQTVKIIDCGEVFETK
AQHTVEKEKGKRRKSGKPLNSDDSSESSDKKSRGKRKKSSKDTKTKRRRYSTSDSDSYS
SDSESDSASDSESDSSDSDSSSYGKHQKRRNKRKHGKKRKIGRNQRKRSRHSRSRRSKH
KSRRSSEDSSDSSSTSGSSSSDEKADRRSSGRKTHADNKAERNQDTEKQSSSLPRQDQIIP
EQTTDTKIRRTVDKQSHEEGELSPENGAFVNNGHDTQAEFSKPAKQHANSDVSNDNRSA
RTGRSPTRDSGELELNQGRALLQASFGQKASEPAAPKHGHRFSKSPSPNGMPKRIKKGR
GFTERYAFARRYRTPSPERSTRTYRYGDRNIRRNFDRNTSYRSYSERSPPRRYRSPPGGRN
RPRYQSRRSLSRSISRSPVRGRFRDRDRSRSPRRSLSPEDRRPPISDRLKSRLGPRSDERLA
DRRGRSKSNSRSNGSSRSRSPDATPPKRHDKRTSVSRSRSRSSSSSGQKGLVSYGDASPDS
GVR*

>Phv5

MAKKKNSLVFMDVSIDGDPVERMVFELFYDVAPKTAENFRALCTGERGVGPNTGKSLH
YKGSFFHRIVKGSIARGGDFVNRNGTGGESIYGSKFPDESPRLKHDAPGLLSMPVADRDT
LGSHFMITFKADPHLDRKHVVFGKLVLGHDILKKIEDVGDKEGLPSVTVKIINCGEHNED
EKKINKSKKGRDGSSETNSHELPKGKHRKSSGDKRKRRKYYSSESDSSSDSDTKSSESDS
DSDSDISSSSYTSSSSDDRRRKRKRSRKDKHRRGKRRDKHREKRRRKQDKRSKRRS
RRE
LPSHTDSDSESKSNNFSDSESSGAEVNDQNHEDHSQRHAEGQSSSVVGKELPPMHP
NKR
EKLDIQEEEELPKENGERRSNGTGANYRSERSEGRQPDVMDDQPDKSRSQSTSISP
RRKS
KSLSISPKRRLNRSPSGSRSPHSPLQRSLSQSPVRSTRRSPNRRSISRNPMRGRKGRSISRSS
VRSHGHRSVSTSPVRPLSRSYQKTSPRTSLRRSISRSPTISPGQRSVSASPGRSPSRSQRRSS
PSRRSISRSPVRNHHHRSVSRSSVRSHGRRRDSVSPVRSLSPSHRKSPRAKSRRSISRSPVG
TRNYKSVNKGTLRSRGNRTSSASPVRSLSRSGRRSSPRAPSQRSISRSPVKTDNRRSISRSP
LRSRGHRSVSASPVRLLSSDRRRSSPRASSRRLISRSPVRVSRRSLSRSPVRSSARSLSRSS
GRVPLRSHSRSPVRGPSRVNHRSYSRSPRGRSLSRSRSPDVSPKLIRRGRGFSERYSYARR
YRTPSRSPVRSYRYNGRNDRDRYSGYRRYSPRRNRSPPPRRRTPSRFRSRRSRTPSVSRSP
RYRGRRYSRSPVRRSPVGTYRPRVERSRSLSRSSRSLSRSRSPSGSRNSVESQSPGKKSRS
RSQSLDGKKGLVSYGDGSPDSS*

>Phv6

MREEIWCERKMWASAEGGAPEVNLETSMGSFTVELYYKHAPRTCRNFIELSRRGYYDN
VKFHRIIKDFIVQGGDPTGTGRGGESIYGAKFEDEIKRELKHTGAGILSMANAGPNSNGS
QFFITLAPCPSLDGKHTIFGRVCSGMEIIKRLGSVQTDNNDRPIHDVKILRTSVKD*

>Phv7

MASSLSAQFVHCQNSLPRLQGNCSRDVSKIQRPRVVCCGTGSQLGYGKTLASRSHYAM
RFPVRQQSEAKSIRYRSMTCVNATDNALELQAKVTTKCFFDVEAGGEALGRIVLGLFGE
DVPKTAENFRALCTGEKGYGYKGSSFHRIIKDFMIQGGDFTEGNGTGGISIYGPSFKDESF
SLKHTGPGILSMANAGPNTNGSQFFICTVKTPWLDNRHVVFGHVIDGMDVVRTLESQET
SRLDVPRKPCRIVNCGELPIDG*

>Phv8

MAKKKNCLVFMDVSIDGDPVERMVFELFYDVAPKTAENFRALCTGERGVGPSTGKSLH
YKGSFFHRIVKGSIARGGDFVNRNGTGGESIYGSKFPDESPRLKHDAPGLLSMPVADRDS
LGSHFIITFKSDPHLDRKHVIFGKLVQGHNILKKIEDVGDEEGLPSVTVKIINCGEHNEDG
KKINKSKKGRDGSTETHSPELHRGKRKKSSGDKRKRRKYYSSVSNSSSDSDTKSSESDS
DSDSDTSSSYTSSSSDDRRRKRKRSRKDKHRRGKKRDQHRDKRRRKQDKRSKRKSRRE
LTCHTESDSDNKSGNSSGGESCDAQAKDQKHKDHSLKHAEGQSSLVVEKELPAVLLSKG
EKLDMLEEEEFPKENGERRSNGNEANYRSERSEGRQPDVMDDQPGKSRSQSMSISPKRE

SRSTSISRKKRLSRSPSRSRSPRAPLRRSLSRSPNRRSISRSPARGRKGKSVSRSPMQSRGY
RSVSVSPVRSLSRSNLRTSPRAPSRRSISRSPVINHNHRSVSRSPIRSRDHRNVSVSPATSLS
RSHKSSPRARSQRSISRSPVRTHNHRSVNRSPVRSSGRRSVSASPVRPLSRSRRRNSPRAP
SRRSISRSPVKTGNASRSPVRSHGHRSVSASPVRSLSRGRWRNSPRAQSRKSISRSPVRVS
RKSLSRSPVRTSARSLSRSLSRSSGRVPLRSISRSPARVPSRGNRRSYSRSPRGRSRSLSRSV
SPDVSPKRIRRGRGFSEQYSYARRYRTPSRSPVRSYRYNGRSYRDRYSGYRRYSPRRNRS
PLPRRRTPPRFRRRRSRTPSVSRSPRYRGRRYSRSRSRSPVRSRSPVGAYRPRVEKSRSLSR
SRSLSRSRASVESQSPKKASRNSRSASPSESPDAKKGLVSYEDGSPYSN*

>Phv9

MASRGTGTLIWVCLLWLFFLCATIAFFQLHLVDNRTNQPSSRSNLIKTQQLSDTPLGQDSE
GVTHKVYFDIEIHGKLAGRIVIGLFGNTVPKTVENFRALCTGEKGKGRSGESLHYKGSTF
HRIIPSFMVQGGDFTRGDGRGGESIYGDKFADENFKLKHSGPGYLSMANSGQDTNGSQF
FITTVKTSWLDGRHVVFGKVISGMDVLYKIEAEGSESGSPKNKVVISDSGELTS*

>Phv10

MAKTTSLLFCTLLLFGTLALIQAKKSKEELKEVTNKVFFDVEIDGKAAGRIEIGLYGKAV
PKTAENFRALCTGEKGIGKSGKPLHYKGSSFHRIIPSFMIQGGDFTHGNGMGGESIYGEK
FPDENFKLKHTGPGFLSMANAGPDTNGSQFFITTVTTSWLDGKHVVFGKVISGMDVVY
KVEAEGRQSGTPKSKVVIADSGELPL*

>Phv11

MSKNPKVFFDILIGKMKAGRVVMELFADTTPKTAENFRALCTGEKGIGQSGKPLHYKGS
SFHRIIPEFMCQGGDFTRGNGTGGESIYGSKFQDENFKLKHTAPGILSMANSGPHTNGSQ
FFICTTKTPWLDGKHVVFGKVVDGYSVVKEMEKVGSGSGKTSETVVIEDCGQVVEK*

>Phv12

MGKKQHSKDRMFITKTEWATEWGGAKSKDNRTPFKRLPFYCCSLTFTPFGEPVCTPDGS
VFDVMNITPYIIKYGKHPVTGTPLKLPDLIPLTFHKNSEGEYHCPVLNKVFTEFTHIVAVK
TTGNVFCYEAVKELNIKTKNWKELLTDEPFTREDLITIQNPNALDNKVLLDFDHVKNSLK
VDDEELQKMSSDPTYNINMSGDIKQMLQELGTDKGKETAMHGGGGGKAQKERAAALA
AIIAARSRVDEDSKSNPNKEAKAPQAFSIVDAASAAVHGRSAAAAKASSGDKTAARIAM
HMSGDRAPVNAKMVKSRFTTGAASRSFTSTSFDPVTKNDFEYVKVEKNPKKKGYVQL
HTTHGDLNIELHCDITPRTCENFITLCERGFYNGVAFHRSIRNFMLQGGDPTGTGRGGESI
WGKPFKDEFNSKLVHSGRGVVSMANSGPHTNGSQFFILYKSANHLNFKHTVFGVVVGG
LTALAAMEKVPVDDNDRPLEEIKITSVTIFVNPYTEPDEGEEQDKAKEKNLEDEDNDKV
GSWYSNPGAGTSESGGTGVGGGVGKYLKARNAQATSTNLDTSTAVVVKKRKVGVASS
DFKDFSAW*

>Phv13

MWIQGFRFWIKGCILLALISAISALEPELGSTRVVFQTKYGDIEFGFFPTVAPKTVDHIFKL
VKLGGYNTNHFFRVDKGFVAQVADVANGRSAPMNEDQKREAEKTVVGEFSDVKHVRG

ILSMGRYDDPDSGSSSFSILLGESPHLDGKYAIFGKVTKGDETLAKLEQLPTRKEGIFVMP
MERITILSSYYYDKDTENCQQDRSILKLKLAASAVEVERQRMKCFP*

>Phv14

MQNFLALCASGYYDGTIFHRNIKGFMIQGGDPTGTGKGGTSIWGKKFNDEIRESLKHNA
RGILAMANSGPNTNGSQFFMTYAKQPHLNGLYTVFGRVIHGFEVLDLMEKTQTGAGDR
PLAEIRLNRVTIHANPLAG*

>Phv15

MGRGRCFLDIGIGEELEGRIVVELYDDVTPKTAENFRALCTGEKGIGPNTGVPLHFKGSC
FHRVVKGFMIQGGDISAGDGTGGESIYGHKFEDENFELKHERKGMLSMANSGPNTNGS
QFFITTTRTSHLDGKHVVFGKVVKGMGVVRSIEHVVTGEDDRPILDVKIVDSGEIPEGDD
DGISNFFKDGDTYPDWPADLDESPSELDWWMKSVDSIKTFGNDHYRKQDYKMALRKY
RKALRYLDICWEKEGIDEEISSGLRKTKSQIFTNSSASKLKLGDIKGALLDTEFAMREGDN
NAKALFRQGQAYMALHDIDAAVESFKKALTLEPNDAGIKKELAAARRKIADRHDLEKK
AYSKMFQ*

>Phv16

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EDENTLVESKKSDLPGYAVVITSKGSIIVELYKESAPEVVDEFIDLCQKGHFKGMLFHQVI
KHYVIQAGHNKGPGATEDWNLLGKKYASMRHEAFMLGTSKGNYFNKGFDLFITTAPIP
DLSEKLIVFGRVIKGEDIVQEIEEVDTDEHYQPKISIGILDVALKEIV*

>Phv17

MLQRVVRYSTQPFNPPTRTIPPSLSPIQLIPTSPSFPILKQQCRLSRRELTIFSNSCLLLLWGT
QVVNGSSARAETAVANTNNSDQPEENVVFAEEDVANTSSSARAEENRVLAEDVANTSNS
NQQEEDLNLAEENVTNTSNSDQTEENLTSTPSCTERKTTKQVFLDISIDGEPAGRVTIGLY
GDEVPAGVDRFSKVVSGAAGISYRRKEFVKIMPNYVQHGGLRSYGVDAEFSSRTGSNLG
PNSLVQEWEREYEKCPGTKNVTGSVGIIVRNPSKPPPKMKLVAKKGKLEIDQEEVGIDPN
GTEFVIVTKDSPELDTSSLVIGRVIGGMEVVQRIGQVKTVQENTGSPYFRVAKLIGDKRAV
VAERGFNRPYSKVIVTNCGLMQ*

>Phv18

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FFITTTRTPHLDGKHVVFGRVVKGMGVVRSAEHVVTGENDRPTQTVVIEDCGEIPEGQD
DGVVNFFNDGDTYPDWPADLDVKPDELSWWTSAVDSIKALGNEQYKKQDYKMALRK
YRKALRYLDVCWEKDDIDQENSASLRKTKSQIFTNSSACKLKIGDLQGALLDSDFAMHD
GDNAKALFRKGQAYMLLNDLDSALESFKKALELEPNDGGIKKEYATARKKVADRRDRE
KQAYSKMFK*

>Phv19

MAYSLPPPPPPPSLPLPNHFTRRSLLLLSTTTTTSTTLSLPSTPPPTPTVTDRFFMDFSLCP
NNFLPDRADTLSPICSDSKLLGRVVLGLFGNLVPRTVSNFKSVCLGSNATSSSYKNTLVH
KVFPGQYLLAGRQGRPDKGEVRPPRDLPRNTETVDAKAFALIHSRPGVVSLSLSENDDD
DDVKLDPEYRNVEFLITTGPGPCPQLDNKNIVFGTVLEGLDVITAIASIPTYQPSERIRQFN
DLAEFFGDGRAQNARNIWNRPLTTVYISDCGELKVTKPSLTPSLP*

>Phv20

MPNPRVFFDMSISAKPVGRIVMELYADTVPRTAENFRALCTGEKGIGRSGMALHYKGSC
FHRVIPNFMCQGGDFTAGNGTGGESIYGSKFADENFIKKHTGPGILSMANAGPGTNGSQF
FICTVKTEWLDGKHVVFGEVVEGLDVVKEIEKIGSSSGKTQGQVMISDCGQLS*

>Phv21

MQHFIPGIEAMRRAISFLVQPRCLLFVIVLTIFLILAISGSRRFEEKEEEEPEITDRVFLDVDI
DGQRLGRIVIGLYGQVVPKTVENFRALCTGEKGKNANGVKLHYKGTPFHRIISGFMFQG
GDIVHRDGRGYESIYGGTFPDENFKIKHSHAGVVSMVNSGPDSNGSQFFITTVKTGWLD
GEHVVFGKVVQGMDTVFAIEGGAGTYNGKPRKKVVIADSGLWRDTQESVG*

>Phv22

MEEHENGANASEEEALIGPGPAPRARRKRPLQFEQAYLNALPSANMYEKSYMHRDVVT
HVAVSAADFFITGSSDGHLKFWKKKPIGIEFAKHFRSHLGPIEGLAVSIDGLLCCTISDDRS
VKIYDVVNYDMMVMIRLPYTPGAVDWVYKQGDVKATLAISDRNSSFVHIYDARAGSN
DPIISKEIHMGPIKVMKYNPVYDSVLSADAKGIIEYWSSATLQFPENEVNFKLKSNTDLFE
IAKCKTSVSTIEVSPDGKQFSITSPDRRIRVFWFRTGKLRRVYDESLEVAQDLQRSDAPLY
RLEAIDFGRRMAVEKEIEKTESAPLPNAVFDESSNFLIYATLLGIKIVNLHTNKVSRILGKV
ENNDRFLRIALYQGDRSSKRVRRIPSAAANVNESKEPLTDPTLLCCAFKKHRIYLFSRREP
EEPEDATKGRDVFNEKPPADELLAVSDIGKSVTTSLPENVILHTTMGDIHMKLYPEECPKT
VENFTTHCRNGYYDNLIFHRVIKGFMIQTGDPLGDGTGGQSIWGREFEDEFHKSLRHDR
PFTVSMANAGPNTNGSQFFITTVATPWLDNKHTVFGRVAKGMDVVQGIEKVKTDKTDK
PYQDVKILNVTVPKS*

>Phv23

MAASVVGNATTNTSAGVEWHVRPPNPKNPIVFFDVTIGNIPAGRIKMELFADIAPKTAEN
FRQFCTGEYRKAGLPVGYKGCQFHRVIKDFMIQAGDFVKGDGSGCVSIYGLKLDDENFT
AKHTGPGLLSMANSGPNTNGCQFFITCAKCDWLDNKHVVFGRVLGDGLLVVRKIENVA
TGPNNRPKLACVIAECGEM*

>Phv24

MSVLIVTSLGDLVVDLHTNKCPLTCKSFLKLCKMKYYNGCLFHTVQKDFTAQTGDPTGT
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LDGKHTVFGEVAEGFETLTRINEAYVDDKGRPYKNIRIKHTYILEDPYDDPSQLSEFIPDA

SPEGKPKDEVEDEVRLEDDWVPMDEQLNPAELEEVIRSKEAHSRAVVLESIGDIPDAEIK
PPDNVLFVCKLNPVTEDEDLNTIFSRFGTVSSAEIIRDHKTGDSLCYAFIGQYVYPLCHLC
FFNCVQVVLSPIFFPISTPVAWFFPM*

>Phv25

MPNPKVFFDMTIGGQPAGRIVFELYADVTPRTAENFRALCTGEKGVGRSGKPLHFKGSIF
HRVIPNFMCQGGDFTAGNGTGGESIYGAKFADENFVKKHTGPGILSMANAGPGTNGSQF
FICTTKTEWLDGKHVVFGQVVEGLDVVKDIEKVGSGSGKTARPVAIADCGQLS*

>Phv26

MCRTIAFLVHPRVLLLFLVLSIFLIFTYTGSTTTYDSTTPKLVVEEKIEEVHEITHRVFLDIDI
DKQRLGRIVIGLYGQVVPKTVENFIALCTGRKEKSENGVKLHYKGGTPFHRIVSGFVIQG
GDIVHHDGKGSESIYGGTFPDENFKIKHSHAGVVSMANSGPDSNGSQFFITTVKASWLD
GEHVVFGKVVEGMDIVYAIEGGAGTYSGKPRKKVVIADSGEIPKSEWDEES*

Vitis vinifera

>Gsv1

MRREISILLQPRWILPILIATILLILFLSVYPRGEETAEEVPEITHRVFLDIDIDEQHIGRIVIGL
YGNVVPKTAENFRALCTGEKGKGASGKKLHYKGTPFHRIISGFMIQGGDTVHGDGRGSE
SIYGGTFRDENFRIKHSHAGVVSMVNSGPDSNGSQFFITTVKASWLDGEHVVLGKVIQG
MDIVYTIEGGAGTYNGKPRKKVVISDSGEIPKSDWEEES*

>Gsv2

MKLVLWSLLLLGTLAISQAKKSTENLKEVTHKVYFDVEIDGKPAGRVVMGLFGKTVPKT
VENFRALCTGEKGIGSSGKPLHFKGSAFHRIIPSFMIQGGDFTLGDGRGGESIYGEKFADE
NFKLKHTGPGLLSMANAGPDTNGSQFFITTVTTSWLDGRHVVFGKVLSGMDVVYKME
AEGRQSGTPKTKVVIADSGELPL*

>Gsv3

MLVRKSLIYRKHRGTQEKMSVTLHTNLGDIKCEISCDEVSKTAENFLALCASGYYDGTIF
HRNIKGFMIQGGDPTGTGKGGTSIWGKKFNDEIRESLKHNARGILSMANSGPNTNGSQF
FITYAKQPHLNGLYTVFGRVIHGFEVLDIMEKTQTGAGDRPLAEIRLNRVTIHANPLAG*

>Gsv4

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NSAGHRRLMCVNSMANEVELQAKVTTKCFFDVDIGGEPVGRIVIGLFGEVVPKTAENFR
VLCTGEKGYGYKGCSFHRIIKDFMIQGGDFTEGDGTGGISIYGSSFEDENFALTHVGPGV
LSMANAGPNTNGSQFFICTVKTPWLDRRHVVFGHVIDGMDVVRKLESQETSRSDYPKLT
CRIINCGELPMDS*

>Gsv5
MEEPQNGDGGSAVPENDDELAIGPGPAPRSRPKRPLQFERAYLDCLPSANMYERSLPHEK
NFGIPFENTGNGKHPSLNINQIQYPVHKKKLMLLRQHADFLLFVSIFKGHLKFWKKTAIG
IEFAKHFRSHLNAIEGLAVSVDGLLCCTISNDDSVKVYDVVNYDMMVMIRLPFVPGAVE
WVSKQGDVKARLAISDRNSSFVHVYDARAGSNEPIISREIHLGPIKVMKYNHVFDSVISA
DANGIIEYWNPNTLQFPENEVNFRLKSDTNLFEIVKCKTTVSSIEVSPDGKQFSITSPDHRI
RIFWFKTGKLRRVYDESLEVAQDLQRSDAPLYRLEAIDFGRRMAVEKEIEKTESAPQPNA
IFDGSSNFLIYATLLGIKVVNLHTNKVARILGKVENNDRFLRIALYQGDRSSKKVRKIPAA
AANVNESKEPLTDPTLLCCAFKKHRIYLFSRREPEEPEDATKGRDVFNEKPPPDELLAAS
DIGKAVTTSLPDNVILHTTMGDIHMRLYPEECPKTVENFTTHCRNGYYDNLIFHRVIKGF
MIQTGDPLGDGTGGQSIWGREFEDEFHKSLRHDRPFTLSMANAGPNTNGSQFFITTVATP
WLDNKHTVFGRVVKGMDVVQGIEKVKTDKADKPYQDVKILNVTVPKA*

>Gsv6

MGRPRCYLDISIGEELEGRVVVELYNDIVPRTAENFRALCTGEKGIGPNTGVPLHYKGVC
FHRVIRGFMIQGGDISAGNGTGGESIYGLKFEDENFELKHERKGMLSMANSGANTNGSQ
FFITTTRTSHLDGKHVVFGKVVKGMGVVRSIEHVTTGDNDCPTVNVLIADCGEIPEGVD
NGVSNFFKDGDTYPDWPADLDENPNDLSWWTNAVDSVKAFGNEHFKKQDYKMALRK
YRKALRYLDICWEKEGIDEEKSSCLRKTKSLIFTNSSACKLKLGDLKGALLDTDFAMRDE
ENNVKALYRQGQAYMALNDIDAAAESFKKALELEPNDGGIKRELAAAKKKIADRREQE
RKAYSRMFQ*

>Gsv7

MAATRRLIAVAVIWIMVLIGTLAIIQSQLSATVSIEQKTINTTLEKESKSKEDLDGVTHKVY
FDVEVSGKPIGRITMGLFGKTVPKTIENFRALCTGEKGRGKSGKPLHYKGSAFHRIIPSFM
IQGGDFTLGDGRGGESIYGERFADENFKLNHTSPGLVSMANAGPDSNGSQFFITTVATHW
LDGKHVVFGKVLSGMEVVYKIEELGSRNGAPTQKVVISDSGELPL*

>Gsv8

MWGSADGGAPEVTLETSMGSFTVELYYKHAPRTCRNFLELSRRGYYDNVKFHRIIKDFI
VQGGDPTGTGRGGESIYGSKFEDEIKPELKHTGAGILSMANAGPNSNGSQFFITLAPAQS
LDGKHTIFGRVCRGMEIIKRLGSVQTDNTDRPIHDVKILRTAVKDLQ*

>Gsv9

MARIKPQALLLQSKKKKGPTRISITTIIFCNLVVVLVVFSLFATYRHWSNRSRNQFQSGVS
NVEENDGFVDSKRFDLPGYAILNTSKGYITVELYKDGSPEIVDKFLDLCQKGYFKGMPFH
HVIKNYVIQGGHSQGIGAAEDWTSKGKPHGHLPLSPKHEAFMLGTSKTKQDRKKFELFI
TTAPIPDLNDKLIVFGRVIKGEDVVQEIEEVDTDEHYRPKSRIGIINVTLKREA*

>Gsv10

MSSVYVSEPPTKGKVIVTTTYGPLDIELWPKEAPKAVRNFVQLCLEGYYDNTIFHRIIKGF

LVQGGDPTGSGTGGESIYGSAFADEFHSRLRFNHRGLVACANAGSPNSNGSQFFISLDRC
DWLDRKNTIFGKVTGDSLYNLPRLGDVEIDKNDRPVDPPPKIISVEVLWNPFDDLVPRKT
LAKSLPHSTNDIDNKDLKKKAVKKLNLLSFGEEAEEEEKELEAVKQKIKSSHDVLNDPRL
LKGEIPSKELNPSEVKINKDLQLSVREALSAKKEESWKESESEFSNFLDHSDDDEANFDA
RMRQQILRKRKELDDLPTKQKLNKGNSNLKDHETSTPRSSAETFDDRPKVEKLALRKK
GIGSEARAERMAKADADLQLLGEAEQQRQLQKQKKRRLQGREDEVLAKLQRFQKKISA
KPVASETESRVEGDEDDDIYSLRGTQLKFTPEPGKDRMSRSDDPNDYVVHDPLLEKGKE
KFNKMQAKQKRREREWAGKSLT*

>Gsv11

MTKKKNPLVYLDVSIDGDPIERMVFELFSDVAPKTAENFRALCTGEKGIGPKTGKPLHYK
GSFFHRIIKGSMVQGGDFLRRDGSGGESIYGGKFPDESPRLKHDGPGLLSMSVADRDTVG
SQFIVTFSANHHLDRKYVVFGKLVQGHEVLKRIESVGDEEGIPTATVKIIYCGEIPEEKRKS
IKSKIGKDASSDANSHEVRRREKHKRSSKERRKKRRRYDTSESESLSDTDTESSESDSDS
DSESSSYISSSSEDRRKKRKRSKRDKYRRGKRRDKRRDKKRKRRDKKSKRRSKRSSDSL
TDEDSNGKSGSSSADDGTDVRGPDCNPKKPPQLIAGNGSPVVEDREAVSTRHKKGEVAD
VLEKEEGESPKENGDRRSNGIEEVKSDRSAERQPDVVDDHPGKSRSRSMSPKRTMSKSM
SISPRRSLSKSPSQKPSSS*

>Gsv12

MSNPKVFFDILVGKMKAGRIVMELFADVTPKTAENFRALCTGEKGIGMWRFHQGQWD
WRRIDPRNEICR*

>Gsv13

MELFSDIAPKTAENFRQFCTGEYRKAGLPVGYKGCQFHRVIKDFMIQAGDFVKGDGSGC
VSIYGSKFEDENFIAKHTGPGLLSMANSGPGTNGCQFFITCSKCDWLDNKHVVFGRVLG
EGLLVVRKIENVATGPNNRPKLACVIAECGEM*

>Gsv14

MGKKQHSKDRMFITKTEWATEWGGAKSKNASVPFKRLPFYCCAVTFTPFGDPVCTSDG
TVFDIMNIIPYIRKFGKHPVTGAPLKQEDLIPLTFHKNSDGEYHCPVLNKVFTEFTHIVAVK
TTGNVFCYEAIKELNLKTKNWKELLTDEPFTREDLITIQNPNALDSKALLDFDHVKNSLK
LDDEELKKMGLDPTHGINVKGDMKQMLEELGTEKARQTALHGGGGNKAQNERAAAL
AAILAARSRIKEESESDKNGEGKTGQTFSIVDAASASVHGRSAAAAKATSSDKTAARIAM
HMAGERAPVNAKMVKSRFTTGAASRSFTSTSYDPVTKNEFEYIKVEKNPTKKGYVQLH
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GKPFKDELNSKLLHSGRGVVSMANSGPHTNGSQFFILYKSANHLNFKHTVFGGVVGGL
MTLSAMEKVPVDDNDRPLEEIKITGVTVFVNPYTEPDAEEEEEKTKDGKNAEDEENDKV
GAWFSNPGTGTAEPGDVGGGVGKYLKARTGQAEHAAADTGLQAMTVAKKRKLGVPTA
EFKDFSAW*

>Gsv15

MAASLTTLSNVGSLSSPRSVAQIKALGPTCNALKLPRSPFPSNVSSSSSSSFVSGSFRLVPLT
SSLNPCSRRRTGLLSSLRASAQEAPLQSKVTQKVYFDISIGNPVGKVVGRIVIGLFGDDVP
QTAENFRALCTGEKGFGYKGSTFHRVIKDFMIQGGDFDKGNGTGGKSIYGRTFKDENFK
LAHVGPGVVSMANAGPNTNGSQFFICTVKTPWLDQRHVVFGQVLEGMDIVKLVESQET
DRGDRPRKKVVISECGELPMV*

>Gsv16

MTKKKNPLVFLDVSIDGDPVEKIVIELFADVVPKTAENFRALCTGEKGVGTSTGKPLHYK
GSFFHRIIKGFMAQGGDFSKGNGTGGESIYGGKFADENFKRAHEGPGFLSMANSGPNTN
GSQFFMTFKRQPHLDGKHVVFGKVVQGIDTLKKIEQLGTGDGKPARLVKIVDCGETSEN
KIHGAVGTEKGRKKKSGKALSSDDSSDEQARGRRRNSLKDRRKKRKRKYSSSDSYSSDT
DSDSYSSDNDSASDSDSSLSDSSSSSDGRRRKRRRPLKRDKHQRGKKRKDGRKDRKRGL
RDKKSRHKSKWSSESSSGTDSGSTSSSRSSSDDEKASHHVSAHKTSNSTHTESKHPRNLG
KKTGALEQDTITKPQKDHELKMSEDDSSHEEGEFSQKNELLNNGHGTEAKSEKTAKQHP
LSDDSGKSRSLTPSPRRRAKISPRRNPSISPKKISTMSPRYQHDSRSPARKSGKRNQGNSRS
PLGSPARKATEPPASNHGRGLSRSPSPNGAPKRIRKGRGFTDRFSFARRYRTPSPERSPRRS
YPYGGRNVNARNRDRYSSYRSYSERSPQRRYRSPPRGRSPPRYRRRRSRSRSASRSPGAY
HGRNRVRSRSPMRSPSPTDNRPPISERLRSRLGPQGDDQRPSDKGRFRSRSRSRGSSGSGS
TEATPQKPCGKAASVSPSRSRSSSPDGQKGLVSYGDASPV*

>Gsv17

MGLDPTHGINVKGDMKQMLEELGTEKARQTALHGGGGNKAQNERAAALAAILAARSR
IKEESESDKNGEGKTGQTFSIVDAASASVHGRSAAAAKATSSDKTAARIAMHMAGERAP
VNAKMVKSRFTTGAASRSFTSTSYDPVTKNEFEYIKVEKNPTKKGYVQLHTTHGDLNIE
LHCDITPRACENFITLCERGYYNGIAFHRNIRNFMIQGGDPTGTGSGGESIWGKPFKDEL
NSKLLHSGRGVVSMANSGPHTNGSQFFILYKSANHLNFKHTVFGGVVGGLMTLSAMEK
VPVDDNDRPLVSITIGFLHFRIISILKLKLLGILISSN*

>Gsv18

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KTDGLQENAPPNCTAKAPTKRAFLDISIDGEPAGRIVIGLYGDDAPAGAARFSGLVSGAA
GISYRRKEFVKIMPNYVQHGGVRSYGVDAELAKRTGSNLAAESLVTEWEKMNEKCPGT
KNLAGSVGIVVRDPTKPPPKIKLVARGGKLEIDEEDVGADPNGTEFVITSKDSPELDTSTL
VIGRVLEGMEVVEKIGQVKTVQENTGSPYFRVAKLIGDKRATVAERGFNRPYSKVLITNC
GLIQ*

>Gsv19

MANAGPGTNGSQFFICTAKTSWLDGKHVVFGKVIEGLDVVKAIEKVGSSSGSTAKAVVV
SDCGQLS*

>Gsv20

MDFSICPTSFRPEADDCRDSLPLGRLVIGLYGHLVPLTVSNFKAMCTGSSGSSYKNTLVQK
IFPGQFFVAGRQGRRDKGENDDDDEIKLNPDYRNVEFLITTGPGPCPQLDNRNIVFGSVL
EGLDVVTAIASIPTYKPAERIRQLNDLAEFLGDDRAPIARATWNKPLKTVYISDCGELKVT
KPSLSPSLP*

>Gsv21

MWSKGAWIVGLLCLALAFVVGASSQEPQLGSARVVFQTNYGDIEFGFFPGVAPKTVDHI
FKLVRLGCFNTNHFFRVDRGFVAQVADVVGGRSAPMNEEQREEAVKTVVGEFSDVKHV
RGILSMGRYADPDSASSSFSMLLGDAPHLDGQYAIFGRVTKGDETLKKLEQLPTRREGIF
VMPTERITILSSYFYDTKMETCEQEKSTLKRRLAASVVEIERQRMKCFP*

>Gsv22

MSVLIVTSLGDIVVDLYTDRCPLTSKNFLKLCKIKYYNGCLFHMVQKDFTAQTGDPTATG
TGGDSIYKFLYGDQARFFNDEVHLDLKHSKTGTVAMASAGENLNASQFYFTLRDDLDY
LDGKHTVFGEVAEGLETLTRINEAYVDDKGRPYKNIRIKHTYILDDPFGDPSQLTELIPDA
SPEGKPKDEVDDDVRLEDDWVPLDEQLDTSELEELIRSKEAHSRAVVLESIGDIPDAEIKP
PDNVLFVCKLNPVTEDEDLHTIFSRFGTVISAEIIRDFKTGDSLCYAFIEFETNEACEQAYF
KMDNALIDDRRIHVDFSQSVSKLWSQYRRRDHQTGKGTGCFKCGAVDHIAKDCTGSPT
KQQQPPKYILKDNNTQHGGDNNSRYEMVFDEDTSESPKREKRRQDHGPEDQIEKEKLN
RRGSEDWKRRDHDKKDSDDRHRQSDKGQESRASRLSGSRRDPYHHEERIDREKHRERQ
DEGKRERDERDYRKRNADSDSHRERRDGRDERHHRKRNADGDRHVDRRDVGDYRKR
DTDDDDHGDGRDGRDYRKRSADNDGRGDRRDDRDHRKTKADEDRRDKRDMRDEPSY
RKRSADGDGNGGRREERGHKRHSTESNDDRDRRHRGDRREPEEDP*

Supplementary File. 2. Tabular presentation of multi domains present in cyclophilins of *Cucumis sativus, Phaseolus vulgaris* and *Vitis vinifera*.

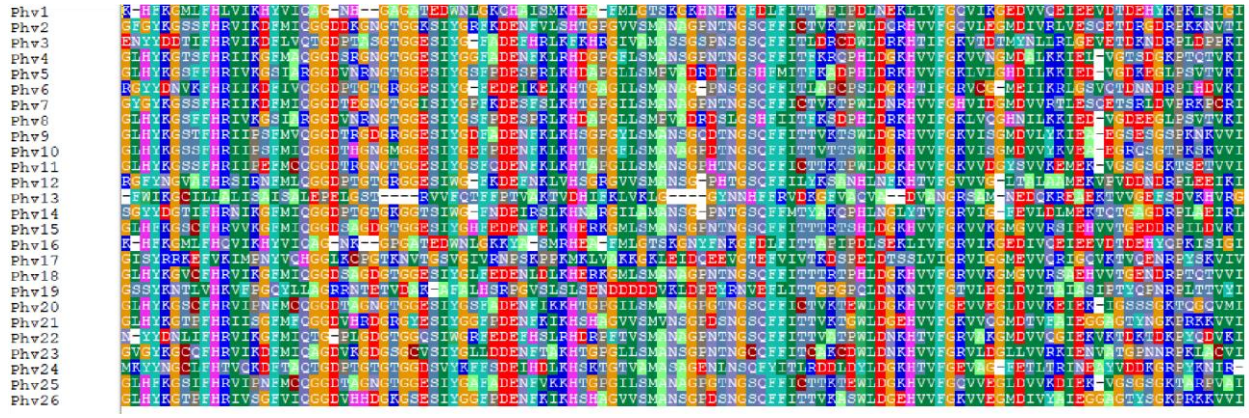
Domains	*Cucumis sativus*	*Phaseolus vulgaris*	*Vitis vinifera*
CYP	Cuc1, Cuc4, Cuc6, Cuc7, Cuc8, Cuc9, Cuc9, Cuc10, Cuc11, Cuc12, Cuc13, Cuc14, Cuc15, Cuc18, Cuc19, Cuc20	Phv1, Phv2, Phv3, Phv4, Phv6, Phv7, Phv9, Phv10, Phv11, Phv13, Phv14, Phv16, Phv17, Phv19, Phv20, Phv21, Phv23, Phv25, Phv26	Gsv1, Gsv2, Gsv3, Gsv4, Gsv7, Gsv8, Gsv9, Gsv10, Gsv12, Gsv13, Gsv15, Gsv17, Gsv18, Gsv19, Gsv20, Gsv21
WD40	Cuc2	Phv22	Gsv5
TPR-1	Cuc3, Cuc16	Phv15, Phv18	Gsv6
TPR	Cuc3, Cuc16	Phv15, Phv18	Gsv6
3a0801s09	Cuc3	Phv18	Gsv6
PEP_TPR_LIPO	Cuc3	Phv15	Gsv6
RRM_SF	Cuc5	Phv24	Gsv22
RRM	Cuc5	Phv24	Gsv22
PABP_1234	Cuc5	Phv24	Gsv22
PLN03134	Cuc5	Phv24	Gsv22
PRK12678	Cuc5	-	Gsv22
U2AF_Ig	Cuc5	-	-
Zf_CCHC	Cuc5	-	-
RING-Ubox	Cuc17	Phv12	Gsv14
SF_CC1	Cuc21	-	Gsv22
PHA03307	Cuc21	Phv5, Phv8	Gsv16
PT200449	-	Phv8	-
SOG2	-	Phv8	-
NrfG	-	Phv18	-
TypeIV_pilW	-	Phv18	-
TPR_19	-	-	Gsv6
PLN03088	-	-	Gsv6

CCSAP	-	-	Gsv11
	SD= 15	SD=19	SD= 16
	MD= 6	MD=7	MD=6
	Total=21	Total= 26	Total= 22

Supplementary.Fig. S3

[A]

[B]



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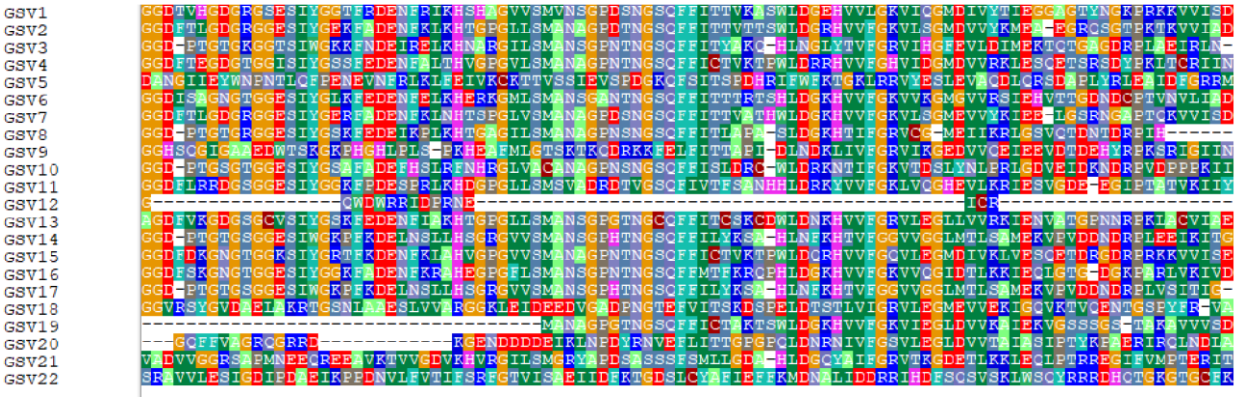
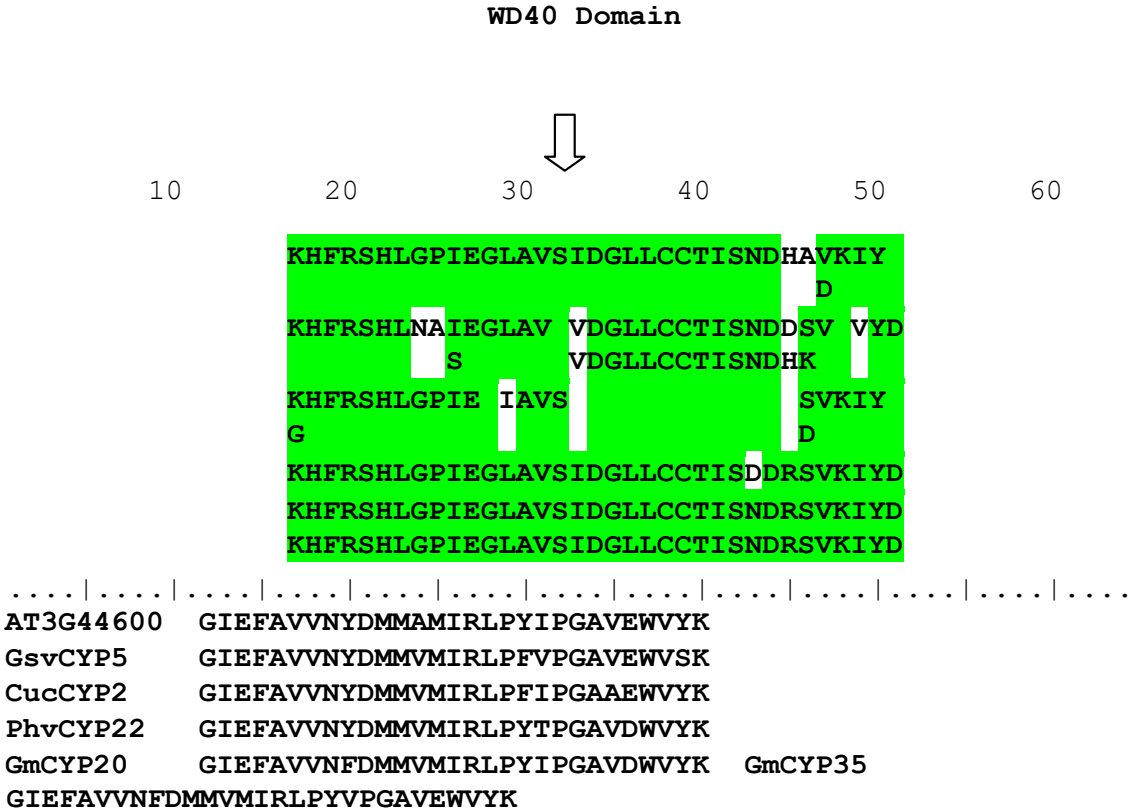
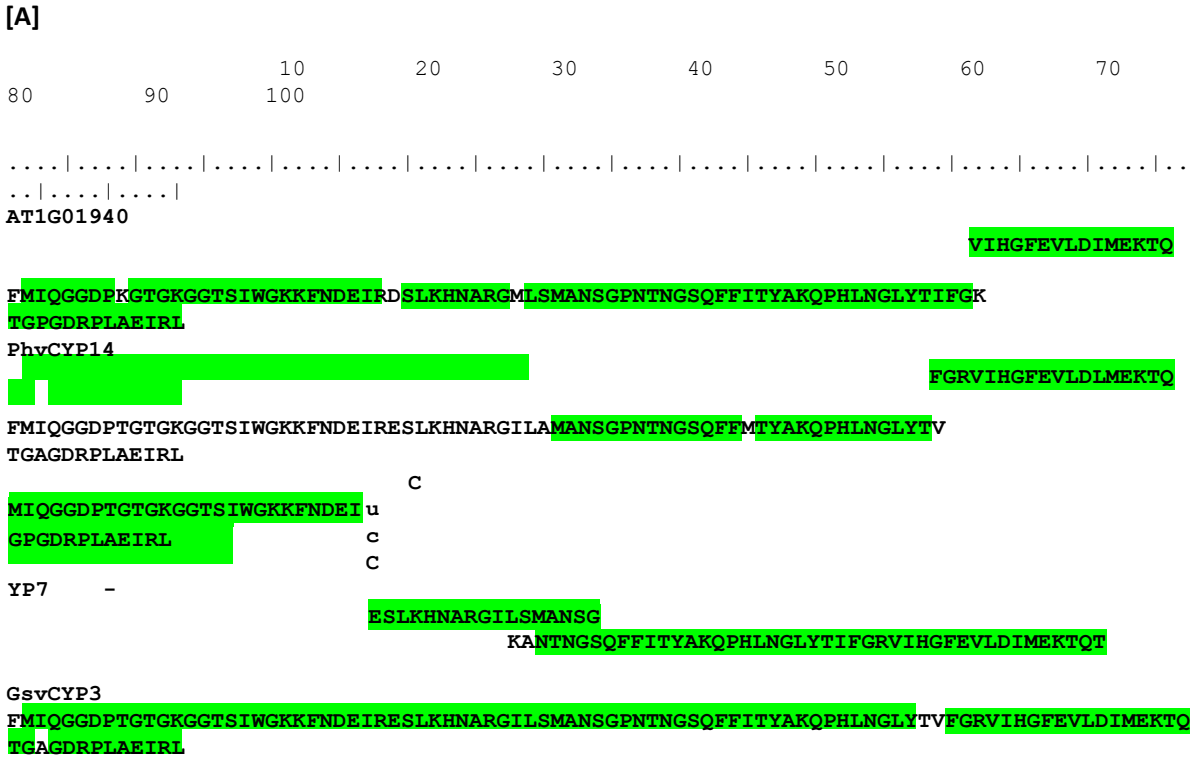
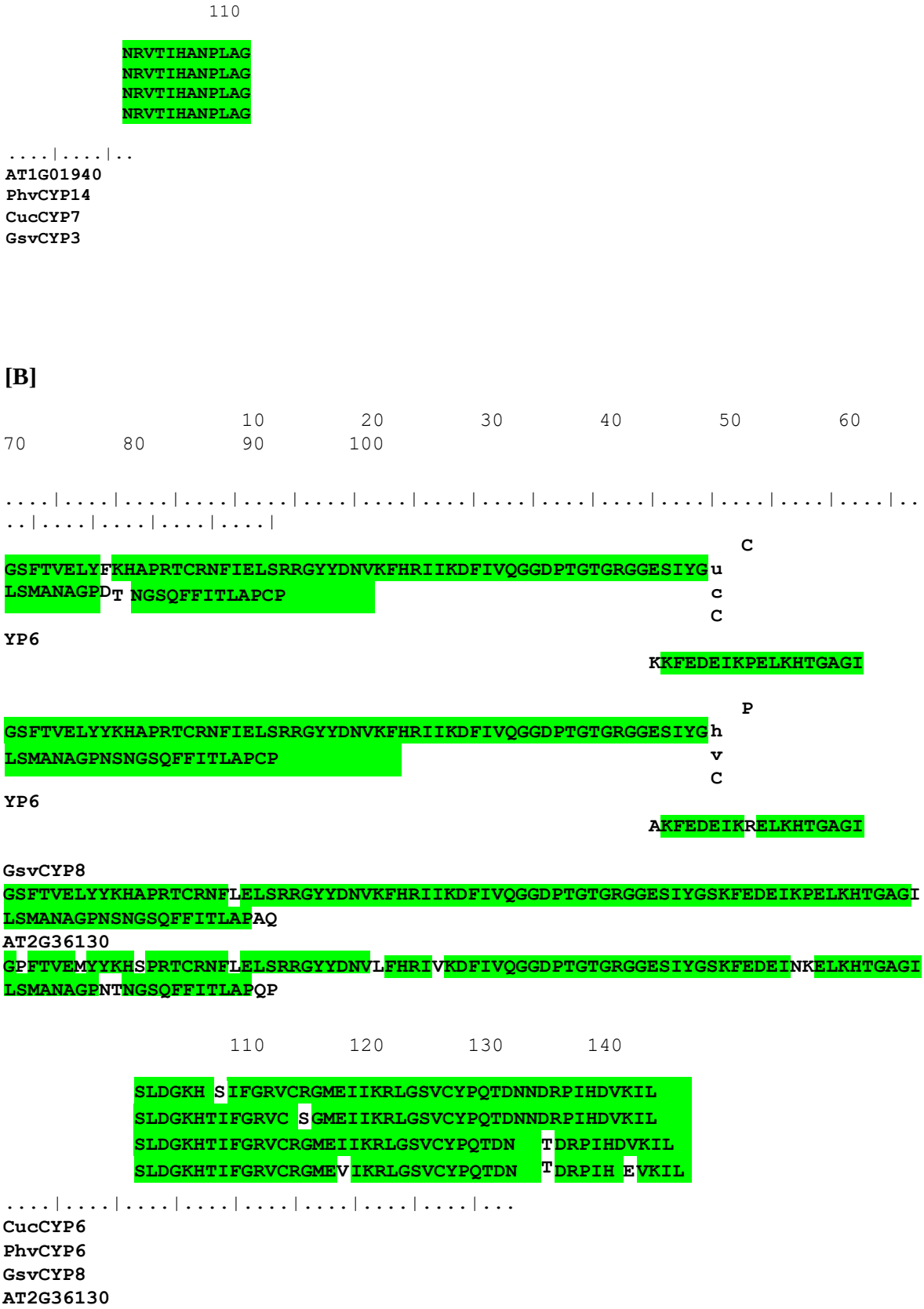


Supplementary.Fig. S4



Supplementary.Fig. S5

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NRVTIHANPLAG
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....|....|..
AT1G01940
PhvCYP14
CucCYP7
GsvCYP3
[B]
10 20 30 40 50 60
70 80 90 100
....|....|....|

Supplementary File. 6

Supple. 6.A. Identification of substitution rates for homologues CucCYP genes				
Gene Pair	**Ka Average**	**Ks average**	**Ka/Ks ratio**	**MYA**
CucCYP18-CucCYP8	0.32885	0.5661	0.580904434	129.8394495
CucCYP17- CucCYP2	0.46545	0.50565	0.920498368	115.9747706
CucCYP12-CucCYP21	0.162	0.4378	0.370031978	100.412844
CucCYP10-CucCYP14	0.12805	0.41435	0.309038253	95.03440367
CucCYP19-CucCYP7	0.31485	0.57115	0.551256237	130.9977064
CucCYP9- CucCYP6	0.1827	0.4049	0.451222524	92.86697248
CucCYP15- CucCYP5	0.2869	0.5192	0.552580894	119.0825688
CucCYP3-CucCYP16	0.041485265	0.2601	0.159497366	59.6559633
CucCYP11-CucCYP20	0.078847645	0.45355	0.173845541	104.0252294
B. Identification of substitution rates for homologues PhvCYP gene				
Gene Pair	**Ka Average**	**Ks Average**	**Ka/Ks ratio**	**MYA**
PhvCYP8- PhvCYP7	0.2163	0.4755	0.45488959	28.09287487
PhvCYP16- PhvCYP1	0.058852805	0.214	0.275013107	12.64327071
PhvCYP18- PhvCYP2	0.1311	0.552	0.2375	32.61254874
PhvCYP15- PhvCYP3	0.1287	0.41795	0.307931571	24.69278034
PhvCYP21-PhvCYP26	0.06461662	0.20865	0.309689049	12.32718894
PhvCYP10-PhvCYP9	0.075347865	0.39645	0.190056413	23.4225452
PhvCYP23- PhvCYP4	0.17415	0.54305	0.320688703	32.08377644
PhvCYP25-PhvCYP20	0.04377589	0.343	0.127626501	20.26468156
PhvCYP24-PhvCYP19	0.46535	0.56865	0.818341686	33.59624247
PhvCYP22-PhvCYP13	0.3183	0.47695	0.667365552	28.17854189
PhvCYP12-PhvCYP17	0.3293	0.41265	0.798012844	24.37965261
PhvCYP5- PhvCYP6	0.1999	0.4133	0.483668038	24.41805506
C. Identification of substitution rates for homologues GsvCYP genes				
Gene Pair	**Ka Average**	**Ks average**	**Ka/ks ratio**	**MYA**
GsvCYP17-GsvCYP14	0.023846825	0.0379292	0.628719927	7.585834
GsvCYP22- GsvCYP9	0.30325	0.6152	0.492929129	123.04
GsvCYP12-GsvCYP21	0.31409463	0.35725	0.879201204	71.45
GsvCYP16-GsvCYP15	0.1274	0.4903	0.259840914	98.06
GsvCYP5- GsvCYP10	0.205	0.43705	0.469053884	87.41
GsvCYP18-GsvCYP20	0.2945	0.4696	0.627129472	93.92

GsvCYP4- GsvCYP19	0.13	0.50405	0.257910922	100.81
GsvCYP13- GsvCYP6	0.13795	0.51925	0.265671642	103.85
GsvCYP2- GsvCYP7	0.061623895	0.2572	0.239595237	51.44
GsvCYP11- GsvCYP1	0.1594	0.4379	0.364010048	87.58

Supplementary File. 7. Tabular presentation of expression data of A*: Cucumis sativus*, B: *Phaseolus vulgaris* and C: *Vitis vinifera* derived from phytozome and cucurbit genome database (CuGenDB)

A: *Cucumis sativus*										
ID	**Root**	**Male**	**Female**	**Ovary_ unfertilized**	**Ovary**	**Ovary_ fertilized**	**Stem**	**Tendril_ base**	**Tendril**	**Leaf**
Csa1G042130	-1.64	-1.06	1.29	1.56	3.35	3.62	4.1	4.33	4.55	5.19
Csa2G009340	0.53	0.56	2.2	2.44	2.51	2.54	2.94	2.95	3.21	3.91
Csa2G234600	2.3	2.76	3.32	3.45	3.46	4.08	4.25	4.48	4.71	4.76
Csa5G128260	2.62	3.32	4.85	6.13	6.28	6.37	6.48	6.72	6.73	8.02
Csa1G153530	3.37	3.45	3.63	3.91	4.38	4.39	4.45	4.61	4.65	4.81
Csa6G495630	3.68	3.76	4.19	4.39	4.56	4.62	5.19	5.2	5.25	5.99
Csa7G237870	3.69	3.84	4.34	4.68	4.77	4.77	4.89	4.99	5.07	5.86
Csa4G646250	3.75	3.94	4.2	4.77	4.95	4.96	5.22	5.29	5.33	5.48
Csa7G378580	3.83	4.34	4.37	4.44	4.55	4.72	4.79	4.83	4.89	5.23
Csa1G690270	3.89	6.05	6.6	6.89	7.36	7.39	7.85	8.01	8.13	8.26
Csa2G100030	4.13	4.32	4.39	4.51	4.73	4.73	4.76	4.99	5.19	5.47
Csa7G074830	4.49	4.94	5.37	5.81	5.84	5.98	6.14	6.15	6.18	6.26
Csa3G125010	4.54	4.67	4.71	5.01	5.26	5.32	5.56	5.61	5.94	6.11
Csa2G380020	4.64	4.67	5.13	5.34	5.88	6.06	6.07	6.09	6.17	6.22
Csa5G202380	4.93	5.11	5.39	5.43	5.49	5.89	6.25	6.29	6.34	6.45
Csa2G270140	5.27	5.35	5.5	5.72	5.78	5.82	5.9	6.3	6.63	6.81
Csa6G093090	6.29	6.35	6.98	7.51	7.71	7.78	7.84	7.87	7.9	8.96
Csa7G407760	6.33	6.52	6.86	6.94	6.97	7.03	7.07	7.32	7.39	7.48
Csa6G185300	6.9	8.27	8.73	8.75	8.87	8.96	9.17	9.35	10.27	10.33
Csa3G777640	7.44	7.75	7.78	7.79	7.89	8.02	8.08	8.16	8.24	8.26

Csa7G009740	9.95	10.12	10.45	10.58	10.71	10.93	11.26	11.3	11.37	11.78

B: *Phaseolus vulgaris*											
ID	**Flower Buds**	**Flowers**	**Green Mature pods**	**Leaves**	**Nodules**	**Root 10th Day**	**Root 19th Day**	**Stem 10th Day**	**Stem 19th Day**	**Young Pods**	**Young Trifoliates**
Phvul.007G100400	37.3369	32.1846	22.9084	15.5893	15.125	21.587	17.9254	18.2137	23.6758	19.3723	13.2572
Phvul.007G001100	65.117	31.1173	34.8667	316.656	16.3054	13.6592	10.3738	34.3083	23.9858	68.3607	101.009
Phvul.001G045200	5.59767	5.44641	8.47114	9.11225	7.5297	8.03949	7.54622	6.24758	6.71025	8.40653	8.65381
Phvul.001G155500	5.63853	7.97657	16.6271	15.0248	19.8585	18.9385	19.0114	14.6202	14.6696	16.8517	15.9847
Phvul.001G052800	2.78777	2.95778	15.6444	12.4986	15.1211	12.5772	14.2435	9.1298	8.98049	9.49703	13.3296
Phvul.001G192400	30.3601	29.452	15.0795	15.0511	21.0024	24.429	23.2229	25.185	31.1383	31.1936	15.9656
Phvul.001G219400	62.3566	59.2811	20.3355	84.2332	30.2156	24.5226	16.7494	55.9198	38.8114	92.3158	157.695
Phvul.001G053000	8.41714	7.05429	29.8058	19.0515	20.2821	22.6194	22.5214	20.2074	18.6818	21.5311	22.447
Phvul.001G243000	23.6626	21.9041	12.7581	6.35162	9.08592	11.183	9.39069	9.42131	13.0805	10.2741	6.31578
Phvul.006G068200	309.935	177.565	138.135	110.344	117.31	170.809	129.6	189.991	209.524	256.723	108.783

Phvul.002G284200	59.5259	37.0079	19.8203	23.4894	45.9672	32.0079	29.5417	27.9945	29.4864	70.1813	17.1934
Phvul.002G010800	5.0136	5.99855	10.0207	9.08734	8.53003	9.61182	8.71859	7.78561	8.63366	7.68644	7.34335
Phvul.002G088300	47.4686	15.5857	15.2617	19.4667	17.5254	27.4296	18.3518	14.2326	18.3367	20.018	19.4186
Phvul.010G085700	18.5287	21.8367	9.03396	8.13045	12.2742	8.52847	11.6406	10.9264	14.2732	15.2669	6.68004

ID	Flower Buds	Flowers	Green Mature pods	Leaves	Nodules	Root 10th Day	Root 19th Day	Stem 10th Day	Stem 19th Day	Young Pods	Young Trifoliates
Phvul.003G294200	10.3537	8.77853	7.76653	17.8052	14.1687	20.7173	16.6147	15.4605	14.9566	17.4057	8.0383
Phvul.003G007900	0.359967	0.391633	0.0385227	0.0607452	0.520435	0.779157	1.41031	0.679891	3.41108	1.06056	0.652253
Phvul.003G178500	8.49315	16.025	4.79693	60.3432	0.349048	0.21006	0.172485	4.53188	4.19852	10.7098	33.5679
Phvul.003G246400	20.2866	15.9577	8.13448	9.7925	12.4793	22.9508	15.8373	19.7826	19.7669	28.7694	12.7908
Phvul.009G211800	12.6278	10.5347	13.9058	92.8322	3.67167	6.38607	3.2187	11.5453	8.2134	13.0703	22.1816
Phvul.009G025000	9.67761	1.49485	0.151341	0.91848	1.53796	2.65904	3.70925	2.33633	4.61052	3.88859	2.28827
Phvul.009G120200	10.2249	3.61486	4.7377	4.24027	9.29962	6.09852	6.5059	6.12278	9.00692	11.0683	4.32376
Phvul.005G126100	3.87307	5.28426	8.1905	7.89868	6.63068	7.062	7.47356	5.55744	5.93195	8.66928	8.67214

Phvul.011G203200	23.7259	21.8195	13.0606	14.4161	13.2832	15.3876	14.4828	18.6344	17.7929	16.0221	11.472
Phvul.011G177175	3.41135	4.57022	7.74417	7.88831	11.1808	9.46947	10.5469	5.58514	6.72443	8.36028	8.72268
Phvul.011G026900	1364.71	817.457	748.471	662.709	307.087	827.751	425.952	1387.49	1270.57	1436.91	600.539
Phvul.011G034400	7.61312	6.83531	10.0099	14.375	4.81224	4.04706	3.96926	7.23383	6.69988	6.96159	7.20259

C. *Vitis vinifera*			
Gene ID	**stage 1; Botrytis cinerea' vs 'control'**	**stage 2; Botrytis cinerea' vs 'control'**	**stage 3; Botrytis cinerea' vs 'control'**
VIT_203s0038g02200	-0.1	-0.1	-0.2
VIT_215s0048g01780	-0.3	0.1	0.2
VIT_207s0005g02410	-0.2	0.3	-0.5
VIT_203s0063g01030	0.4	-0.5	-0.3
VIT_213s0067g00870		0.2	0.4
VIT_208s0007g02900	-0.1	0.3	0.4
VIT_204s0008g01370	0.1	-0.1	-0.1
VIT_204s0008g05090	-0.1		
VIT_214s0081g00700	0.1	-0.2	0.4
VIT_213s0084g00620		0.2	0.5
VIT_207s0129g00040	-0.1	-0.3	-0.4
VIT_201s0146g00110	-0.2	-1.6	-1

VIT_200s0513g00020	-0.1	-0.3	-0.4
VIT_217s0000g04270	-0.1	-1.1	-0.3
VIT_218s0001g14400	-0.2	0.1	0.4
VIT_211s0118g00810	-0.5	-2	-1.6
VIT_201s0026g02070	-0.5	-0.6	-0.5

Supplementary File and figs Legends:

Supplementary. File. S1: Amino acid sequences of A. *Cucumis sativus* B. *Phaseolus vulgaris* C. *Vitis vinifera.*

Supplementary. File. S2: Tabular presentation of multi domains present in cyclophilins of *C. sativus, P. vulgaris* and *V. vinifera*.

Supplementary. File. S3: Multiple sequence alignment for cyclophilins protein family in A. *C. sativus*, B. *P. vulgaris*, and C. *V. vinifera.* Conserved regions are shown with different colors.

Supplementary. Fig. S4: Schematic representation of multiple sequence alignment showing conserved regions in *AT3G44600, GsvCYP5, CucCYP2, PhvCYP22, GmCYP20 and GmCYP35* using Clustal Omega tool (https://www.ebi.ac.uk/Tools/msa/clustalo/) further visualization was done in Mview (https://www.ebi.ac.uk/Tools/msa/mview/) and conserved region was showed different colour.

Supplementary. Fig. S5: Schematic representation of multiple sequence alignment showing conserved regions in A. *AT1G01940, GsvCYP3, CucCYP7, PhvCYP14* and B. *AT2G36130, GsvCYP8, CucCYP6* and *PhvCYP6* using Clustal Omega tool (https://www.ebi.ac.uk/Tools/msa/clustalo/) further visualization was done in Mview (https://www.ebi.ac.uk/Tools/msa/mview/) and conserved region was showed different colour.

Supplementary. File.S6: Tabular presentation of substitution rates for homologues *CucCYP, PhvCYP* and *GsvCYP*s genes.

Supplementary. File. S7: Tabular presentation of expression data of *Cucumis sativus, Phaseolus vulgaris, Vitis vinifera* derived from phytozome, cucurbit genome database (CuGenDB) and Expression atlas respectively.