
Data S1: Text file of the alignment corresponding to the phylogenetic tree in Figure 1

>PtDIR32

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RATVVHH

>PtDIR34

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PPLSFFMHDLGGSHPSNRIVTGIIARTEINGIPFSQPNNNFPLQGGTPLVNINNLNL
INPNNAPLLTGTLGTQNTFLQNTGNNNNVANGNNQPFVTAGNLPAGSALQKLMFGSITV
VDNELTEGHELGSavigkaQGFYLASSMDGTSHTMAFTVLLHGGENHGDVEDTISFFGVH
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>PtDIR33

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VPFAKPNGANLPINNGVPQNNNNNGLINNNNL PFLTGLGGTTQPVLQNNGNFNNAFNL P
QSTGGNLP SGSAFQQLMFGTITVIDDEITEGHDLGSGFIGKAQGFYVASSVDGTSQTMAF
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ETLLEFAVYVSY

>PtDIR35

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LQELEFGSVTEIGEDLFVYGS LVVGKAQGLYVASEDGTSHMMAMTVKFVKNKYKDGLRF
FGVHKTDVPESHIAVIGGTGKYHSANGYAVINAVGVGSKSTAGEENRTKGNLLFNVYLS

>PtDIR30

MARMAAFV CALIICIAIVPAAYGEYYTKSRHVPRKEKVTRLHFFLHDILSGKNPSAVKVA
GSNRTEGDKSPTPFGSVYAIDDPLKVGPEPDSKTIGNAQGLYLSSSQDYSKFTIVMCVDF
GFTEGKFKGSSFSVFSRNPVTEADREAVVGGRGKFRMARGFAKVKTSHFNATNGDAVLE
YKVTLIH

>PtDIR29

MARMVALVYALIICVAVVPSYGEYYSKGSHVPRKEKVPRLHFSLHDIVSGKSPCAVVKVA
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RMANGFAKISASFLNVTGDAILE

>PtDIR31

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VTNLQFYFHDILSGKNPTAIKVAQPSADNKSPTLFGSIMMADDPLTEGDPNSKPVGRAQ
GIYSAGQNELALIMAMNFAFTDGIYNGSCISLLGKNPAMNPVREMPIVGGTGLFRFARG
YAVAQTYWLDLTTGDAIVGYNVTVVH

>PtDIR22

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ALVGYNDTVVH

>PtDIR16

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>PtDIR13

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FNSTQLKGTINFAGADDIMKTTRDLSVVG GTGDFFMTRGIATLMTDAYEDDRYFRLRVDV
QLYECF

>PtDIR18

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EYNVTVVHFRMFLLLVSAVFPFPHFFYL VSTC

>PtDIR20

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QEEAALLMAMNFVFLQ GKYNSTISILGRNHVFSKVREMPVIGGSGLFRFARGYAQANTY
SFNAKTGD AVEYNVYVLHY

>PtDIR14

MRASCILLCFMFLAVSSAYPGKKKQYKPCKEFVLYFHDILYNGKNAANATSAIVA APEG
ANL TILAGQNHFGNIIVFDDPITLDNNLHSP PVGRAQGMYYDTKNTFTSWLGFTFALNS
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ECW

>PtDIR19

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MAMNFAFIEGKYNGSTITVLGRNEVFSTVREMPVIGGSGLFRFARGYVQARTH MVDLKTG
DATVEYNVYVFHY

>PtDIR21

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SAGQEETALLMAMNFVFLQ GKYNSTISILGRNHVFSKVREMPVIGGSGLFRFARGYAQA
STHSFDLKSGDAVEYNVYVLHY

>PtDIR15

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SRPVARAQGFYFYDKKSTYTAWFAFTLIFNSTKHKGTLNIMGADLMTEETRDFS VVG GTG
DFFMARGIATIHTDTFQGDYYFRLKMDIKLYECY

>PtDIR17

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TNGQIQ TQLGPDGLGLGFGTITVIDDTL TNSPELGSQQLGKAQGVYVASSADGSTQMMAF
TAMFEGGEFGDSLNFYGIYRIGSAMSRLSVTGGTGKFNAIGFAEVRGLIPPGQAVTDGA
ETLLRISVHLKY

>PtDIR25

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FLMALNFVFTEGKYNGSTLSILGRNSVLSGIREMPVVGSGGLFRFARGYAQAKTHDLDFK
TGDAIVEYNVYVFHY

>PtDIR40

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FRLATGFAQLKTCFLNATNGDAIV

>PtDIR39

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LMTMNFVFMGKFNSTLSVLGRNSVFSTVREMPIVVGSGGLFRFARGYAQASTHMFDRIT
GDAVVEYNVYVFHY

>PtDIR37

QGIYASASQSELSFLMALNFVFTEGKYNGSTLSILGRNNVGLFRLARGYAQAKTREIDFK
TGNATVEYNVYVFHY

>PtDIR38

MAKISTNATSSVFVLFNIIILFSLTLVTVKSDSFSGHLSPKKLGLKREKLSHLHFYFHDI
VGGRNPTAVPVVRAAITKKSFSFGLVTMMDDPLTVKPEIGSKLVGRAQGIYASASQSEL
SFLMALNFVFTEGKYNGSTLSILGRNNVFSGIREMPIVVGSGGLFRFARGYAQANTHEIDF
KTGNAIVEYNVYVFHY

>PtDIR36

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MVLNLFTEGKYNGSTLSILGRNSIFSIREMPIVVGSGGLFRFARGYTQAKTYTVNLKTN
DAVVEYNVYVFHY

>PtDIR12

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>PtDIR23

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YVANHFHSHDRSSTVNGV

>PtDIR24

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MGSISIVGGTHNIKPADHPVVGTTGDFMFVQGYVTSSPVDLQGLTVTYKIVFHLWPSYA
NKFSLHDKHVGNDIIT

>PtDIR26

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PVAPPVTAAPLPVGPINTATRPNGPAPVAVATSDTEAKPAGPQTTTTSPPLSFFMHDI
LGGSPASNRIVTGIIARTDINGIPFSQPNNNIFPLQDGTPLVNINNINPNTAPLLTGLT

GAQNTNTLLQNTGNNNNVVNSNNQPFVTAGNFPAGSALQKLMFGSITVVDELTEGHELGS
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>PtDIR28

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TVIHY

>PtDIR27

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>PtDIR1

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VFHY

>PtDIR9

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>PtDIR4

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VSHY

>PtDIR5

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QTQLGPDGLGLGFGTITVIDDILTNSPELGSQQLGKAQGVYVASSADGTTQMMAFTAMFE
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ITVHLKY

>PtDIR6

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>PtDIR8

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ECW

>PtDIR11

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>PtDIR7

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Y

>PtDIR2

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>PtDIR3

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>PtDIR10

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>OsDIR27

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>OsDIR31

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>OsDIR28

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>OsDIR30

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AYVTTSPi*

>OsDIR29

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>OsDIR25

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FHTPEAVI*

>OsDIR23

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FHTPKAVV*

>OsDIR9

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FITTPSERSIVGGTGKLRFARGYMTSKLLSSTDAIVVVFDMYFTLDH*

>OsDIR15

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DLFVLLHKP*

>OsDIR21

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>OsDIR17

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FLMSRGVATLRTDAIEGFKYFRVQMDIKLYECYV*

>OsDIR18

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DAFEGFTYFRLQMDIKLYECYV*

>OsDIR19

MAAWSMASLMIVAIFLLSLTSASVVHGRSSRRRFVRSYDEPCMEMRLYLHDILYDYSNS
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KKDDFAWFAFSIVFNSTARRGTLNLMGADPNAATRDIVVGGTGDFLMSRGVATLRTDA
IEGFKYFRVQMDIKLYECYV*

>OsDIR14

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>OsDIR22

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NSTANSTSAAAAKPTALATAVSPNGTFFGEVVVFDDPMTEGTRALPPSSLRETAAARAQ
GVYLYDSKEVYDAWF AFSVFNSTGRRGTLNLMGADLMSEKTRDISVVGGTGDFFMSRGV
ATLR TDAVEGLVYFRLQMDIKLYECYI*

>OsDIR16

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>OsDIR20

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LYDGKAASTLNAWLA FSVFNSTARRGTLSLMGAVLNFALGSHRLDLVGWFYLG LMDIL
DERERV*

>OsDIR2

MHNELYMHLIYNQTISGPNPNQLVVVNGSQQAPLFFGLTAISDWITLDGPGPNASVVGRA
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EHKIVQVDCTGRIYEIKIHAFYIPMNSSAILGKKYKIW*

>OsDIR1

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LGGATNAAFTSNSNNNNNGVPVFAGGSLPQGTTLQKLLFGTMTVV DDELTEAPGLGSPAV
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>OsDIR4

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WSITGGTGELALARGIAKFKA VQMSSLSNVYELTLHAYYSPMDSCGQYDFNGKSQNYMSV
RRNRKFSTLSNNRGSTGIPIEQPQFDKYMSNCVSSTG*

>OsDIR3

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VAAQGIVEHNVIQEAGGAWTYELKIHAFYTPMQSSGVGAYGCNSWKLGP*

>OsDIR5

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FKGACGFAEVRPLIATGQHVT DGAETLLRISVHLA*

>OsDIR7

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VLDGRVDFGAAGDMERAVVGGTGRFRRARGYSLMTKFGNPTPNTGVFEMDVYVTTMA*

>OsDIR6

MVDKAAVWLVVIALAAAANGAFAGRVLEEQPAAPAPAEAPVAPVDPLPAPTDPPADTVV
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KNIPFVNAGDLPAGATLQNLLFGTTTVIDDELTEGHELGAADVGRAQGFYVASSQDGTSK
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EHTTDGVETLLQFSIHLI*

>OsDIR52

MADPSKLQITPCGMLVQGNQINF TKLYLHHTPAGPEQNQSAVTSNDKKTGLGCIVVNNWS
VYDGIGSDAKLVAYAKGLHVFAGAWHNSFSLVFEDERLKGSTLQVMGLIVEEGDWAIVGG
TGQFAMATGVILKKMQEQKQYGNIELTIHGFCPLLKGSQCPVTKIGPWGSSHEGTVQDI
TESPKRLESITLYHGWSVDSISFTYLDHAGEKHKAGPWGGPGGDPIMIEFGSSEFLKEVS
GTFGPYEGSTVITSINFITNKQTYGPFGRQEGTPFSVPAQNNSSIVGFFGRSGKYINAVG
VYVQPI*

>OsDIR53

MGSLCGTMIILAMLPAITMADPYCDCDCPQQCEVKLHYLHQFRAGANHPNRNEEFVT
SGGPSGLGAGLIHDWSLTGLDPNVNIVGRAQGW HIVASQSSPANWYLSQNIVFQDSKYA
GSTLQVMGIIEGSEEKVGESVIVGGTGEFTNARGNIKYRAIKKEDVEWIRELDIQVFYTP
NTPSDVQVAKNITKGN*

>OsDIR50

MSASNNKLQFTPRSSLFQGNEINF SMLYLHHTPAGPRPDQSGLTGNNRETGLGPLVVNNW
PVYDGIGRDAKVVARAQGLHIYAGNWHNSFSLVFKDERSGSTLEV MGIVVERGEWAIVGG
TGQFAMANGVIFKKFHEQKQEGNIMELTIQGFCPVLKGSQTLRDYIVNIMVLDINVLCF
LMKHLIFDSISFIYLDQAGQKHRAGPWGGPGGDPYMIEFGSSELLKEVSGTYGLYEGWKV
IRSIKFVTNKKPYGPFGR*

>OsDIR49

MSASKLQFTPCSTPIQGNEINF SKLYLHHTPAGPRPNQSGVTSTNKETGLGSLVVNNWQV
YDGIGCDAKVVAHAQGLHVYAGNWHNSFTLVFEDERFKGSTLEV MGIVVEQGEWAIVGGT
GQFAMANGVIFKKFHEQKKEGNIMELTIKGFCPVLKGSQGLVTKIGPWGGIDGGRAQD
ITATPKRLESITIHSGWTIDSISFIYFDQAGEKHRAGPWGGPGGDPCTIEFGSSEFLKEV
SGTFGPYEGWKVIRSIKFVTNKKTYGPFGRQEGTPFSVPVQNNSTIVGFFGRSGKYLDTV
GIYVHPR*

>OsDIR43

MPLLLQLALAVAVAVAMVGTATTTTTHTRFYMHDTVTASASGGGPAATAVRVVRGVAAAA
LPGDAVNRFGLDYAIDDPLTDGADAASSAAVGRARGFYMFSSRTDSALLFSATMEFTAGV
HRGGAVSVLARDAILDEVRELPVVGGAGVLRGAAGYGLLRTHSFNATTNNAVLQIDLYLS
V*

>OsDIR46

MATIAVTQTGTAKITIIHLNGHNLSPYTQERKKSNDQDQKLCPTVVQM QSQQLQCPLLYN
QQHQCSPLLTINPFLHLPIEMAPKVFPVPLCVVVLAAALAAGPPVADAASAHLHFYMHDV
LGASAVQVVRGPRGMFGNTVVMDDVLTEGPAATSSVLGRAQQYIVASTGSMDLMVMTMNV

VLSSGPFAGSSVTVVGRDDTGAAVRELTVVGGTGQFRMARGYVLWRTIRPDLELDVYVN
P*

>OsDIR47

MASSSKLSSAFALAVVLLLAGGVMPAAEAASAHLHFFMHDTLTGAAPTAVQVVNGPRSH
FGDTIVIDDVLTAAASRSSAAVGRAKGQYVWASSGNPELLVTMEVVLTSQPFAGSSVTVV
GRDDIAAPVRELSVVGGTGEFRMASGYVLWKTVSLDHPNAILELDVYVNP*

>OsDIR48

MAAMLISRRSIQLVLVVAAVVAIAGAVHAAAGETTATTTTHIKVYWHDVVSGPSPTAVQVA
RAATTNSSASFFGAVVVIDDPLTSGPDLNASSPVGRAQGTYSAGKDTVALLMNMNFVFQ
SGRYNGSTVAIMGRNEVFAAVREMAVVGGTGVFRWARGYAQARTHTLDMKTGDATVEYNL
YINH*

>OsDIR51

MASYEITSRGALIKGREFNFSNLYLYHIYNSSEPNNQQIIDNVSSSTAMGGLTVNNWTVY
DGVASDATLVARGQGLHTYAGNWHCSFTLVFEDERFNGSTLEVKGIFEETHDWAIVGGTG
EFAMASGVIKKTVEYERTPEGTHIELTIRGFCPDF*

>OsDIR42

MASLSSVLVGCFLLA-AAVFLHRNGASTTTTTTHLHFYMHDAYTGPAPTAMRVVSGRSLLD
GDNGNGNGNGDDGSPPRQFGDIVALNNALTEGPSAGSARVGTAQGFVVRVSEGGVLSDL
LHMVLEAGEHRGSSVTAKGRIDMDAGERESVVIGGTGRFRLARGYMTKNYDYSLATGGI
VEIDLULKH*

>OsDIR39

MASLCSLLSSSLILAVAVFLRHHIGASTTTTTTHLHFYMHDTYTGPAPTTMRVVSGRS
LLDDGDGNNDATSPSSSSPPRRQFGDIVLNSALTEGPSANKGGMVTDVSLHVLEAG
EHRGSSVTAKGRIDMDAGERESVVIGGTGRFRFARGYMTKNHYKKAHDRDRHYRCWNN*

>OsDIR40

MAASSLSPSLLGCSFLIAAAVLLRRHDSAAATTTTTTHLHFYMHDAYTGPAPTAMRVV
SGRSLLQSTTDIVDGSSPPRQFGDIVLNNALTEGPDAGSARVGTAQGFVVRVSEGLVT
DLSMHLVMEAGEHRGSSVAIKGRIDVGVGVRESVVVGGTGRFRLARGYMASSSYDYSLAA
GGVVEIHVYLQH*

>OsDIR45

MAHELIPAQTTSSTHKHLNLDLFLHQAYSQPNKNQQVLIKPGGNYLQPGGNYLQFGVLAV
HDWPLYDDEDQSKGKLVARARGHHMQTVQEMVDQWFTTGQIVFDGSEFVGSTLLVAGTY
TTGQKGEWAIVGGTGKFSLAQGVHKEMVRTNPGTGEVRLLQIRAKYSTVESCEQNAED
KQKNHDIRLKTLLQFARYREWIEREPSALVNFDYKASEVDAAINDTNRHLLGTGGFGT
VYKAVIRGATVAVKITNEISHRGVRAFAQEFISRANAVSPFKPILGVSLQGLIRFL*

>AtDIR6

MAFLVEKQLFKALFSFLLVLLFSDTVLSFRKTIDQKKPCKHFSFYFHDILYDGDNVANA
TSAIIVSPPGLGNFKFGKFVIFDGPITMDKNYLSKPVARAQGFYFYDMKMDFNSWFSYTL
VFNSTEHKGTNLNMGADLMMEPTRDLSVVGGTGDFFMARGIATFVTDLFQGAKYFRVKMD
IKLYECY

>AtDIR10

MAGQKILLSLVIALVVTFAAAARLLDEENAFSATTTTLGSGSGSTGIGFGAGTGSSGSGS
TGFGFGAGSGSGSGSTGSLGAGTGSIPSSGSGPGLPTASSVPGSLAGGSGSLPTTG
SATGAGAGTGSALGGGPGAGSALGGGAGAGPALGGGAGAGPALGGGAGAGSALGGGGAGA

GPALGGGVAGSGSALGGGASAGPDNTLVFFMHDILGGSNPTARAVTGVVANPALSGQLPF
AKPNGANLPVSNGVPSNNNNNGIVNNNNVPFLVGLGGTTANILQNNNNNGNNILNGFPVAS
GGQLPSGSALQMLMFGTMTVIDDELTEGHELGSLLGKAQGYVVASAIDGTSQTMAFTAM
FESGGYEDSISFFGLRTAVSESHIGVMGGTGKYVNARGFAILKTFTGSSGTQQNQPHQF
TDGLETVVECTVYLSY

>AtDIR22

MIQKAVSNSSTSFSGSITMTDNALTSQVNVSTVVGQSQGFYAGAAQRELGLMAMNFAFK
TGKYNGSTITILGRNTVFSKVREMTTVVGSGIFRLARGYVEARTKWFDPKTGDATVEYNC
YVLHY

>AtDIR9

MAKALHITIFLFISSNLLAFINSARLLDEIQPQPQLVPTGQIPTVAPTEAEEEDGTDDN
PGLATTTTTASAVTVPAGPAEATEPLLEFFMHDVLGGSHPSARVVTGIVAQTEVNGIPFS
KASNSIFPVDNGVPLVNSNNINSVINPNTAPLLTGLGGAQTSTVIQNTNGNSNDALSANS
LPFVTAGNLPPGAALQHLMFGTITVDDDELTESELGSAVIGRAQGFYLASSLDGTSQTL
SLTVLLHGEHDQHDTLDDAISFFGVHRTASHASQIAVIGGTGKFEHAKGYAIVETLHNQD
NQHITDGQDTILHFSVYLYKA

>AtDIR15

MKSTLIFFTLCLSMVMARHESYYGNTKPAKLNEEKVTRVRFYLHDTLSGQNPTAVRIA
HANLTGGSASPVGFGSLFVIDDPLTVGPEKHSKEIGNQGMYVSGCKDLSKFTIVMYADL
AFTAGKFNGSSISIFSRNPVAEEVGEREIAIVGGRGKFRMARGFVKVTKNKIDMKTGDAV
LRYDATVYHY

>AtDIR24

MAKALSLTIFLFLIASNVQSARLLDEVQTQPQLVPQVPEEEDDSPQAVTTTPTPIPLPG
PATGGPEPILEFFMHDVLGGSHPSARVVTGIVAQTEVNGIPFSKSSNNIFPVDNAVPLVN
ANSINNINPNTAPLLTGLSGSQANTVIQNSNGNSQGSLSNNLPFVTTGQLPPIAALQQ
LMFGSITVDDDELTEGHELGSIIIGRAQGFYLASSLDGTSQTLSTVLLHEDHDDHDTLD
DAISFFGVHRTASHASHIAVVGGTGRFEHAKGYAVVETLHNQEDQHVTGDGHDHDTILHFSVY
LTYKA

>AtDIR4

MGKNLGLVVSFYLCITFALGEYFSETRPITPKQLVVTNLHFFHDTLTAPNPSAILIAKP
THTRGDNDSSSPFGSLFALDDPLTVGDPKSEKIGNARGMYVSSGKHVPTLTMYVDFGF
TSGKFNGSSIAVFSRNTITEKEREVAVVGGRGRFRMARGVAQLNTYYVNLNGDAIVEYN
VTLYHY

>AtDIR2

MAKRFLLLPLLLSTILLSVSVTESEAYSTTKPCQGYKPKDFTHLHFYFHDVISGDKPTA
VKVAEARRTNSSNVNFGVIMIADDPLTEGPDPSKEVGRAQGMALTAMKNISFTMVFNL
AFTAGEFNGSTVAMYGRNEIFSKVREMPIIGGTGAFRFARGYAQAKTYKVVGGLDAVEYN
VFIWH

>AtDIR19

MGSFLSFFLISSRTLALVLISVTGETLESNFLHHKKEKLTHFRVYWHDIVTGQDSSSVSI
MNPPKKYTGATGFGLMRMIDNPLTLTPKLSSKMVGRAQGFYAGTSKEEIGLLMAMNFAIL
DGKYNGSTITVLGRNSVFDKVREMPVIGGSLFRFARGYVQASTHEFNLTGNAIVEYNC
YLLHY

>AtDIR18

MMKQSPFSLTISFLIAALFTATTALDPAPEDPIFELYMHDILGGSSPTARPITGLLGNI
YNGQVPFAKQIGFVPPQNGVAIPNANGAMPTVNGINGIPLGTGLSGTAFSGQNLNGIQTQ
LGPDGLSLGFGTTITVIDDIITSGPDLGSQPLGKAQGVYVASSADGSTQMMAFTAMLEGGE
YNDNLNFYGIYRIGSAMSHLSVTGGTGRFKNACGFAEVRPLIPAGQHFVDGAEMLLRIIV
HLKY

>AtDIR3

MSKLILILTAQILLLTATALAGKNGEDFARTINRKHLGLGKKEKLTHLRVYWHDIVTGRN
PSSIRIQGPVAKYSSSYFGSITMIDNALTLDPINSTVVGQAQGMVVGAAQKEIGLLMA
MNLAFKTKGYNGSTITILGRNTVMSKVREMPVVGSGMFRFARGYVEARTKLFDMMKTGDA
TVESNCYILHY

>AtDIR1

MAKRFLLLLPLSSILLAVSVTAYSTTTPYQGYKPEKFTHLHFYFHDVISGDKPTAVKV
AEARPTTLNVKFGVIMIADDPLTEGPDPSKEVGRAQGMVASTAMKDIVFTMVFNVYFT
AGEFNGSTIAVYGRNDIFSKEVRELPIIGGTGAFRFARGYALPKTYKIVGLDAVVEYNVFI
WH

>AtDIR17

MEDTGSIKQEAQSHPPGIFEIPGEPVAVINGVPDEPQTDCAKDEPISSGTVSGGEWLE
GREVRKFFLGRYYSCTVTKFDKQSGWYRVEYEDGDSEDLDWSELEEVLLPLDTKNSNTNA
QSEYGEAGQRVNVKAPYPGHKPEKLVTTTVKAPYPGHKPEKLIPLVDDILTVGPEITSEE
VGRAQGFASADQNNFGLLMAFNVFVTKGEFSGSTVSMYGRNPFSKVREMPIIGGTGAF
RFRGRYAQAKTFTFNTTSGNAVVKYNVYIWH

>AtDIR13

MANQIYIISLIFLSVLLYQSTTVLSFRQPFNLAKPCKRFVLYLHNVAYDGDNTDNATSAA
IVNPLGLGDFSGFKFVIMDNPVTMDQNMLSEQVARVQGGFFYHGKTKYDTWLSWSVFNFS
TQHGKALNIMGENAFMEPTRDLPVVGGTGDFVMTRGATFMTDLVEGSKYFRVKMDIKLY
ECYY

>AtDIR21

MASLYLLLLPLFLALILAATITESKSFSTTVKAPYPGHKPKDLTHLHFYFHDIVSGDKP
TSVQVANGPTTNSSATGFLVAVVDDKLTVGPEITSEEVGRAQGMVYASADQNKLGLLMAF
NLVFTKGKFSSTVAMYGRNPVLSKVREMPIIGGTGAFRFRGRYALAKTLVFNITSGDAV
VEYNVYIWH

>AtDIR206

MSKLILILTAQILLLTATALAGKNGEDFARTINRKHLGLGKKEKLTHLRVYWHDIVTGRN
PSSIRIQGPVAKYSSSYFGSITMIDNALTLDPINSTVVGQAQGMVVGAAQKEIGLLMA
MNLAFKTKGYNGSTITILGRNTVMSKVREMPVVGSGMFRFARGYVEARTKLFDMMKTEAT
ERNLQKMSFFKSFAGNPREAAAMAMVQSSSYRVLSGKSCSNLRRNTPLDSFLAKGRSSV
KAFSFLYVSRFSTEPNNEFGHSSKRRSRGPVMAAKKASEGEKQEDGKYKQTVDLPKTGFG
MRANSLTREPQLKWEENQVFKRVSDNNNGGSFILHDGPPYANGDLHMGHALNKILKDI
INRYKLLQNYKVQYVPGWDCHGLPIELKVLQSLDQEVKELTPLKLRAKAAKFAKATVKT
QMESFKRFGVWADWNNPYLTLDPEYEAQIEVFGQMALKGYTYRGRKPVHWSPPSRTALA
EAELEYEPGHISKSIYAIFKLVGGAKTSLDEFIPNIYLA VWTTPWTMPANA AAVAVNAK
LQYSVVEVQSFEDESTVTSNKKKIPGKVLKNQQKLFVIVATDLVPALEAKWGVKLSISK
TFLGSDLENCRYTHPIDNRDCPVVIGGDYITTESGTGLVHTAPGHGQEDYATGLKYGLPL
VSPVDDEGKFTEEAGQFRGLSVLGEGNTAVVSYLDENMSLVMEESYAHKYPYDWRTKKPT

IFRATEQWFASVEGFRTATMDAINNVKWVPHQAVNRISAMTSSRSDWCISRQRTWGVPIPI
AFYHVKTKEPLMNEETINHVKSIIISQKGSDAWWYMSVEDLLPEKYRDKAADYEKGTDTMD
VWFDSGSSWAGVLGKREGLSFPADVYLEGTDQHRGWFQSSLLTSIATQGKAPYSAVITHG
FVLDEKGMKMSKSLGNVVDPRLVIEGGKNSKDAPAYGADVMLRWVSSVDYTGDLVIGPQI
LRQMSDIYRKLRLGTLRYLLGNLHDWRVDNAVPHYQDLPIIDQHALFQLENVVKNIQECYEN
YQFFKIFQIIQRFITVDLSNFYFDIAKDRLYTGGTSSFTRRSCQTVLSTHLLSILRVIAP
IVPHLAEDVWQNLFPFEYRNEDGSAAEFVFELKWPTLNEQWLSFPAEDVLFWQRLLRLRTE
VNVKLELARNEKMIGSSLEAKVYLHTADAGMAAKLLEMSEAKNEADTLQRIFITSQVEVL
SSMEKEMISSVQHTGEYVEGENKVWIGVSRAEGSKCERCWNYSQGQVGSFSDHPTLCGRCF
SVIVANPPEPAVA AVNSLA

>AtDIR8

MTNLILIFAAQILLFYAVASVGDELGRTMNGKHLGPYKKEKLTHLRVYWHNSVNGRNPSS
VMIQQPVLNSSLGSLTMMDDPLTFDVPRNATVVGQAQGMVAAAQGEIGFLMVMNFAFT
TGKYNSTITILGRNVVMSKVREMPVVGSGIFRFARGYVEARTKSFDLKAGC

>AtDIR25

MAGCKVLFFLILALAITFVSAARLLDEEEDIGLVPLPTTSPGPLPTVGLGPFPTANSIPA
TGIASGTGSASGGLGSLGTNTGPGPLSTTGSSLLPVASSGTLPTVTPGPGPLPTSSGLLPGA
SSGNLPGSGSGLPTVSGSAAATGLGAGAGSVIGGSVPDNTLVFFMHDILGGSNPTARAV
TGVVANAALSGQIPFAKPNGANLPVSNGVPSDNNNNNGILNNNNVPLLVLGGTTSNQLQN
NGNNMLNGLPVANGGQLPSGSSLQMLMFGTLTVMDNELTEGHELGSLLGKAQGFYVASA
LDGTSQMTAFTAMFESGGYEDSISFFGVHRTAASESHLGVMGGTGKYVNARGFAIVKTFT
GSSGTQQQQPHQFTDGLTVLECTVYLSY

>AtDIR16

MMIKQSPFLLLTITLFTVAVFVAALDPAPEDPIFELYMHDLGGSSPTARPITGLLGNIY
NGQVPFAKQIGFTPPENGIAIPNANGALPTVNGINGVPLGTGLSGTAYSGQNLNGIQTQL
GPDGLSLGFGTITVIDDILTSGLDLSQPLGKAQGVYVASSADGSTQMMAFTAMLEGGEY
NDNLNFYGIYRIGSAMSHLSVTGGTGRFKNACGFAEVRPLIPSGQHEVDGAESLLRIIVH
LKY

>AtDIR23

MAKEEYVSRMLVMLIMIMPLVAQGSRLHSWANRLEETGKDKVTNLQFYFHDTLSGKNPTA
VKVAQGTDEKSPTLFGAVFMVDDALTETADPKSKLVGRAQGLYGSSCKEEVGLIMAMSF
CFEDGPYKDISTISMIGKNSAMNPIREMPIVGGTGMFRMARGYAIARTNWFDPKTGDAIVG
YNVTIMH

>AtDIR20

MAKLIFFLAVQILFLAVVSSAGDGEDFARTMDRKLGLHKKLTHFKVYWHDLSGPNP
TSIMIQQPVTNSSYFGAISMIDNALTAKVPMNSTVLGQAQGFYAGAAQKELGFLMAMNFA
FKTGKYNSTITILGRNTALSEVREMPIVGGSGLFRFARGYVEARTKWINLKNGDATVEY
SCYVLHY

>AtDIR7

MAKLILIIVTQILLIAAVVSARKGENFAKTIDKKHFGLRKEKLTHFRVYWHDLSGSNPS
SVVINPPISNSSFFGSVTVIDNRLTTEVAVNSTLVGQAQGIYAATGQRDASALMVMNFAF
KTGKYNSSIAILGRNAVLTKVREMPVIGSGLFRFARGYVEARTMWFDQKSGDATVEYS
CYVLHY

>AtDIR12

MTNQIYKQVFSFFLSVLLQSSTVSYVPKSFDLKKPCKHFVLYLHNIAYDGDNAANATAA
TIVKPLGLGDHSFGELIINNPNVTLDQNYLSKPVARAQGFYFYNMKTNYNAWVAWTLVFN
STKHKGFTTMDANPFGLPQPARDSLIVGGTGDFLMTRGIATFKTKLTQGSKYFCVEMNIK
LYECY

>AtDIR27

MVQPHGRGGGKGALIFRRTLTEGPENNSRIVGKAEGFIIPHEDFANSDFNVIYLTLETPE
YTGSVSIRSMDTHKLKEVMEVVGGTGAFAFARGIAMFNEIDDHEEEAVTTYRVKLLRF
PHTSHVDPQ

>AtDIR14

MANQIYFLSLICLSVLLCQSYTVSSFQKSLDLAKPCKRFVLHLHDIAYDGDNAANATSAA
IVNPLGLGDFSFGKVFIMDDPVTMDQNYLSKPVARVQGFFCYHGKATYDAWIAWTVVFNS
TQHKGAFTIMGENPFMEPTRDLPIVGGTGDFIMTRGIATLTTHIDGSKYFRVKLDIKLY
ECYH

>AtDIR5

MVGQMKSFLLFVFLVLTKTVISARKPSKSQPKCKNFVLYYHDIMFGVDDVQNATSAAV
TNPPGLGNFKFGKLVIFDDPMTIDKNFQSEPVARAQGFYFDMKNDYNWFAWTLVFNST
QHKGTLMNMGADLMMVQSRDLSVVGTTGDFMSRGIVTFETDTFEGAKYFRVKMDIKLYE
CY

>AtDIR11

MLQITNMATPFLLLLLPLIFSTVLLLTITVTQSKPYSKTTPFQGNKPKLTHLHFYFHDI
ISGDKPTTIRVAEAPGTNSSATVFGAVLIVDAPVTEGPELSSKEVGRAQGLYASTDMKTF
GFTMVFNVFTEGEFNGSTAALYGRNPILLEERELPIGGTGDFRFARGYALPKTYKVVN
IDAVVEYNVFIWH

>PDIR23

MAAPQSSNLSLLAVIILLVGGTHHAVGMELKKTEIEFYMHDEVVKAMKNITTMKVTHGPHGFGMIRVIDNVLTEGL
QQNSK ELGRARGMYVQDSLGSANLLMVLTVIFQAGEHSGSTLCLQGQDDTKQREISVVGGTGHRHATGHAILET
QLSMGANSILNFNITVLH

>PDIR24

MAAPQSSNLSLLAVIILLVGGTHHAVGMELKKTEIEFYMHDEVVKAMKNITTMKVTHGPHGFGMIRVIDNVLTEGL
QQNSKELGRARGMYVQDSLGSANLLMVLTVIFQAGEHSGSTLCLQGQDDTKQREISVVGGTGHRHATGNAILET
QLSMGANSILNFNITVLH

>PDIR25

MSSRLLFPVMAVIVIVFLQAAAGESEMNIIVVYMHDLNLTGRHQTSFPVAGLNGSSSNPGKFGTLVVISDAITKRPYVN
TNPGNIVGRAQGTYYVNTNPVTGLDFFMVFTLIFQNMEYNGSTLEIQGTDRFDQPQCEYAVVGGTGKFRFARGY
AVVTVESASGPNAVLFNTTFLVPS

>PDIR26

MGSGLLFPAMATATLVIVFVQAAAGQSEMNMFLFYMTDNLTGSSETAFPVAGFNGSSSDPGKFGTLVIINDAITKRP
EITKSDTDNLVGRAQGTYYVNTNPVTGLDFLMLFTIIFQNMEYNGSTLQIQGTETFGRPQREYAVVGGTGKFRFARGH
VVCTTESSSGKNAVPRFNITFRTN

>PDIR28

MGSGFSFSAMAVIVFLLAVAGEAEINMVFIHDNLRGSNVTAIPVAGLNGSSSNAGKFGTIVTISDVITRRPQITESDS
DNIVGRAQGTYYVNTNPVTGLDFLMVMTIVFQDMEYNGSTLEIQGTDRFTQPQREFAVVGGTGKFRFARGYAIASTE
ALSSPNSIIKFNTTVQI

>PDIR30

MAKEAVWSMAFILCIAMAARSEKEINMVFYMHDDVAGSNRTAAQVGAGSSIKPGFGAMVVIDDALTRTPSPDSTL
VGRAQGMYSLSLAITSPDSLLAFTAILEWPGEYSGSTLSIQGGNRMFMDQREVSVVGGTGKFRFALGYATVHN
STALQFNVTVRVP

>PDIR35

NMVFYTHDNLSGNNVTAFSVAGLNGSSSSAGKFGTVVVMDDVTKRPKINESDADNTVGRAQGIFVNTNLVTGL
DTLLVFTVIFHDMYGGSTLEIQGTDRFAYPHREVAVVGGTGKFRFARGYAILTELLSGTDSVIKENTTLRTA

>Pdh1

MGVKVALVFFMFFVLCSPFPHLVLFHDIYNGSNAANATSAIVAAPEGANLTKLASQHFHGNIVVDDPVTLDN
NLHSNQVGRAQGSYIYDTKNTFTAWLGFTFVLNSTDHRGTITLAGADPTLKKTRDVSIVGGTGDFFMHRIATIMT
DAFEGQVYFRLRVDVKFYECW

>liDIR1

MVSQMKQFLLVFILLVLSKTVISATKPSKSQSKPCKNFVFFYHDIMFGVDDVQNATSAAVTNPPGLGNFKFGKLVIF
DDPVTLDKNYQSEPVARAQGFYFYDMKNDYNWFSYTLVFNSTQHKGTNLNIMGADLMMEKTRDLSVVGTTGDF
FMSRGIVTFETDTFEGAKYFRVKMDIKLYECY*

>liDIR2

MASLVEKQLFKSLFSFLLVLLFSDTVFSSQKTLQQRKPKHFSFYFHDILYDGDNVANATSAAIVSPPGLGNFKFGK
FVIFDDPITMDKNYLSEPVARAQGFYFYDMKNTDFNAWFCYTLVFNSTEHKGTNLNIMGADLMMEPTRDLSVVGTTG
DFFMARGIATFVTDIFQGAKYFRVKMDIKLYECY*

MAIWNGRVLNLCILWLLVSIVLLNGIDCHSRKKKLPKPCRNVLVYFHDIIYNGKNAGNATSTLVAAPQGANLTIMT
GNYHFGLAVFDDPITVDNNLHSPVVGRAQGFYFYDMKNTFSAWLGFTFVLNSTDYKGTITFGGADPILAKYRDIS
VVGTTGDF LMARGIATIDTDAYEGDVYFRLRVNITLYECY*

>TpDIR5

MKAIRVLHLCFLCLLVSAILLKSADCHSWKKKLPKPCKNVLVYFHDIIYNGKNAENATSALVAAPEGANLTIMTGN
NHFGNLAVFDDPITLDNNLHSPVVGRAQGFYFYDMKNTFSAWLGFTFVLNSTDHKGTITFNGADPILTKYRDISV
GGTGDFLMARGIATISTDSYEGEVYFRLRVNITLYECY*

>FiDIR1

MVSKTQIVALFLCFLTSTSSATYGRKPRRRPCKELVFYFHDVLFKGNVYHNATSIVGSPQWGNKTAMAVPFNYG
DLVVFDPPITLDNNLHSPVVGRAQGMFYDQKNTYNWLGFSFLFNSTKYVGTNLNAGADPLLNTKTRDISVGGT
GDFFMARGVATLMTDAFEGDVYFRLRVDINLYECW*

>LuDIR1

MAISRSNIALFFIFFICLSSANSSAKKKQHTPCKELVLFHDIYNGHNKANATAAIVAAPEGANRTILAGEFHFHGNIA
VFDDPITLDNNLHSPVVGRAQGMFYDQKNTFTAWLGFTFSLNSTEHQGTINFMGADPLMNKTRDVSIVGGTGDF
FMHRGVATIMTDSYEGEVYFRLRVDIMKDYDCW*

>LuDIR5

MKHSSSHSSCLPFLTTTTPIFLLLLSLICPAAATWRTPTHHQHGRNPNKPKQLVLYYHDILFHGNGDQGNATSA
AAANATKLGDKYKFGMLVVFDDPVTKDGHLSKAVARAQGFYFYDMKSTYNWFAFAYTLVFNSTEHKGTINIMGA
DMMSEKTRDLSVVGTTGDFFMARGIATFRTDTFQGDNYFRLEMDIKLYDCYKY*

>LuDIR6

MKHTSSFHLLTTTTLIFLLLLSLISPGDATWRTPSHHLQHAKHPKPKQLVLYYHDILFHGNGDQGNATSA
ATKLGDKYKFGMLVVFDDPVTKDGHLSKAVARAQGFYFYDMKSTYNWFAFAYTLVFNSTDHKGTNLNIMGADMM
SEETRLDLSVVGTTGDFFMARGIATFRTDTFQGDYFRLEMDIKLYECY*

>GhDIR4

MRGTSVLSWILILCVCQAAVRSQYYSDTLPYQPRPVLVTNLHFYMHEFTGTTAVVLTQANITSNNSSVPFATLVAV
NDPLRTGPEPDSELIGNVQGISLLAGSNASSTQYIEFGFNTGKFNGSSLSVFSRGPGLAVVGGRGQFAMATGTALF
NPILINATNVIMEFNFTVIHY

>GhDIR3

MRGTSVLSWILIICLSQVAVRSQYYSDTVPYHPRPVVVTNLHFYMHEFTGTTAVVLTQANITSNNSSVPFATLVAIN
DPLRTGPEPDSELIGNVQGMSSLLAGSNASSTQYIDFEFNTGKFNGSSLSVFSRGEAGLAVVGGRGQFAMATGTALF
NPLLINATNVIMEFNFTVIHY

Table S1: List of primers for the qRT-PCR analyses

Primer Name	primer sequences(5'-3')	Primer Name	primer sequences(5'-3')
DIR1-qF	CATTAACCTTAGGGCCTGAAA	DIR22-qF	ATGGCGATGGACTTTGCATTCAC
DIR1-qR	ATCTCTCTCACCGTCGAGAACA	DIR22-qR	GTGAACTACTGTATCATTGTAGCC
DIR2-qF	TTGGCAGCACTTTTATGGTG	DIR23-qF	CTGACCTTCGAGAACCCCAA
DIR2-qR	ACAATTGGCATTTCCTGAC	DIR23-qR	TTGCAACATAGGAAGGCCAGT
DIR3-qF	GCAATTGCTCGGCCCTAAA	DIR24-qF	ATGTTTGTTCAGGGTACGTGAC
DIR3-qR	TCGAAGTTGGTCTGGCCCT	DIR24-qR	AGTAATTATATCATTTCCACATGTT
DIR4-qF	AGCCTGTTGGAAAAGCTCAA	DIR25-qF	GGCCTCAAGCGAGAGAAACT
DIR4-qR	ATCACCTTGCTCGTCAAACC	DIR25-qR	CACCGTCAAAGGGTCATCCA
DIR5-qF	AACCCAACTTGACCAGACG	DIR26-qF	CGTTACCACTACAGCGCTCA
DIR5-qR	CCCTAACTCAGGGCTGTTGG	DIR26-qR	CATCTTCAACGGTGGTGGGA
DIR6-qF	TTGACCCTGTAGCAGCAACC	DIR27-qF	GTCTCCGAGTCTCAGCTTGC
DIR6-qR	GCCATTGGCATTGGGATGG	DIR27-qR	GGTCTCAACACCATCGGTCTG
DIR7-qF	GTGCCGATTTGATGATGATG	DIR28-qF	AATGCCCAAGGGCTGTATGT
DIR7-qR	GAATCGTGGCAATCCCTCTA	DIR28-qR	ACTGAGCAAACCCTCTAGCC
DIR8-qF	AGGCGCCAACCTTAACCATCT	DIR29-qF	CCTCGCCTTCACTTCTCCCTTCATG
DIR8-qR	TACATGCCTTGTGCCCTACC	DIR29-qR	CCAGTAGTAACATTGAGAAAGCTGG C
DIR9-qF	AGGCGCCAACCTTAACCATCT	DIR30-qF	GGGTCTAATCGCACCGAAGG
DIR9-qR	TACATGCCTTGTGCCCTACC	DIR30-qR	TCTGGCTCAGGTCCCACCTTT
DIR10-qF	GATGCATTCGAGGGTGAAGT	DIR31-qF	CCTTGGTGGGAGTCATGCAA
DIR10-qR	CAAATGCTGAACTCGAAGCA	DIR31-qR	GAGTTCGGATCAGGCCCTTC
DIR11-qF	ATGGCAGCACGTTTAGTGTG	DIR32-qF	TCATTGGTCATGCAGAGGGG
DIR11-qR	ATGGCATCAAATCCAACCAT	DIR32-qR	AAGCCGAGCAAACCCTGTAG
DIR12-qF	TCACGGGTCATAGGAAAAGC	DIR33-qF	CTTGCCACAAACAAGGCCA
DIR12-qR	AAATGCGAATGACCCAGTTC	DIR33-qR	TGCAGCCCCAGTTGGATTAG
DIR13-qF	GACGAGCACAAGGGCTTTAC	DIR34-qF	ATCATCGCCCGCACTGAAAT
DIR13-qR	ATATCATCCGCCCCAGCAAA	DIR34-qR	AGTGGAGCGTTGTTGGGTT
DIR14-qF	GCTCGGCTTTACATTTGCTC	DIR35-qF	TGGCAATGACAGTAAAGTTGTG
DIR14-qR	CCCAGTGCCTCCAACCTACAG	DIR35-qR	TACTCTTAGAACCAACCAACCG
DIR15-qF	ACGGAGGAGACAAGGGATTT	DIR36-qF	ATTTATGCATCGGCATCACA
DIR15-qR	TGGTAGGACTTGGTGCACAG	DIR36-qR	CTCTTGCAAAACGGAAAAGC
DIR16-qF	ACCAGTTGGTAGGGCACAAG	DIR37-qF	TATGCATCGGCATCACAAAG
DIR16-qR	GCGGAGCCTGAAATACACAT	DIR37-qR	AGTCTTCGCCTGAGCATAGC
DIR17-qF	ACGGATTGGGACTAGGCTTT	DIR38-qF	AGGAAGAGCACAGGGGATTT

DIR17-qR	GACATTGCGCTACCAATCCT	DIR38-qR	AGCCTCTTGCAAACCTGAAA
DIR18-qF	GCCCGCCTGCATTTCTACTT	DIR39-qF	TGATCCCTTGACCATGACGC
DIR18-qR	CGGCTACCTCCAACAACCAT	DIR39-qR	CACCGACAATCGGCATCTCT
DIR19-qF	TGTGCCACCATTGAACACTT	DIR40-qF	GGGAGCTCCATCAGTGTGTT
DIR19-qR	ATGGCCATTAACAAGCCAAG	DIR40-qR	AAACAATCGCATCACCGTTAG
DIR20-qF	AAGCTGCCCTATTGATGGCT	UBIC_qF	TTGCTTGAGGAACCTGAAC
DIR20-qR	AAGCCCACTACCTCCGATCA	UBIC_qR	GTGAGGACCGATTACAGT
DIR21-qF	GTCACCGGAGAAAACCAAGA	β-Actin_qF	GACCTTCAATGTGCCTGCAA
DIR21-qR	TGATGTGTTGGAAGGTGCTC	β-Actin_qR	ACCATCACCAGAATCCAGCA
Primer Name	primer sequences(5'-3')	Primer Name	primer sequences(5'-3')
β-Actin_qF	GACCTTCAATGTGCCTGCA		
β-Actin_qR	ACCATCACCAGAATCCAGC		

Table S2: Sequences of 10 predicted motifs of the PtDIR proteins

Name	E-value	Sites	Width	best possible matched sequences	annocation
Motif 1	1.5e-571	35	41	HFGNIAVFDDPITLDNNLHSPVVGRAQGMYYDTKNTFTAW	dirigent domain
Motif 2	7.4e-346	39	21	REMPVVGSGSLFRFARGYAQA	dirigent domain
Motif 3	8E-196	32	15	LHFYFHDIVSGKNPT	dirigent domain
Motif 4	3E-195	18	29	MAMNFVFLQGKYNGSTISILGRNHVFSKV	dirigent domain
Motif 5	3E-111	17	15	KTGDAIVEYNVYVFH	—
Motif 6	1.1E-92	8	21	DAYEGDVYFRLRVDIKFYECW	—
Motif 7	2.5E-77	16	21	GFSFVFNSTEHKGSINFAGAD	—
Motif 8	5.9E-56	8	21	HEFVRSLDRKLLGLKKEKLSH	—
Motif 9	1.1E-36	8	29	RATCILLCFFTLVASSAHPGKKKQYKPC	—
Motif10	2.1E-33	6	21	NATSAIVAAPEGANLTILAGQ	—

Table S3: Ka/Ks analysis of *PtDIR* gene pair duplications

Sequence	Ka	Ks	Ka/Ks	P-Value	Length	Divergence (MYA)
PtDIR8&PtDIR14	0.08205	0.507598	0.16163	6.77E-19	549	16.92
PtDIR8&PtDIR16	0.09762	0.751976	0.12982	4.13167E-28	546	25.06
PtDIR5&PtDIR17	0.06396	0.177159	0.36102	2.89E-05	735	5.9053
PtDIR8&PtDIR9	0.02188	0.103373	0.21166	1.80E-04	549	3.44
PtDIR21&PtDIR20	0.09651	0.231157	0.41752	2.00E-04	579	7.7
PtDIR25&PtDIR38	0.06549	0.193886	0.33777	1.07E-04	585	6.46
PtDIR7&PtDIR15	0.06211	0.489172	0.12696	1.06E-18	537	16.31
PtDIR9&PtDIR14	0.0731	0.475496	0.15374	1.18E-17	549	15.85
PtDIR9&PtDIR16	0.09721	0.736983	0.1319	1.24E-27	546	24.57
PtDIR10&PtDIR13	0.17468	1.0662	0.16383	3.10E-37	558	35.54
PtDIR16&PtDIR14	0.09004	0.318012	0.28314	2.15E-08	546	10.6
PtDIR25&PtDIR36	0.16179	0.456072	0.35474	3.21E-09	573	15.2
PtDIR27&PtDIR33	0.05994	0.236042	0.25394	3.77E-11	927	7.86

PtDIR36&PtDIR38	0.17797	0.480504	0.37039	7.38E-09	573	16.02
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Table S4: Transcription factors predicted for the binding promoters of the *PtDIR* genes

PtDIR40	G-box	GCCACGTGGA	cis-acting regulatory element involved in light responsiveness
PtDIR40	G-box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR40	G-Box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR40	ERE	ATTTTAAA	
PtDIR40	ERE	ATTTTAAA	
PtDIR40	ERE	ATTTTCATA	
PtDIR40	TC-rich repeats	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
PtDIR40	ABRE	CACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR40	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR36	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR36	ABRE	CGTACGTGCA	cis-acting element involved in the abscisic acid responsiveness
PtDIR36	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR36	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR36	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR36	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR36	ERE	ATTTTAAA	
PtDIR36	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR36	MBSI	TTTTTACGGTTA	MYB binding site involved in flavonoid biosynthetic genes regulation
PtDIR37	TC-rich repeats	GTTTCTTAC	cis-acting element involved in defense and stress responsiveness
PtDIR37	ERE	ATTTTCATA	
PtDIR37	ERE	ATTTTAAA	
PtDIR37	ERE	ATTTTAAA	
PtDIR37	ERE	ATTTTAAA	
PtDIR37	ERE	ATTTTAAA	
PtDIR37	ERE	ATTTTAAA	
PtDIR38	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR38	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR38	G-box	CACGAC	cis-acting regulatory element involved in light responsiveness
PtDIR38	ERE	ATTTTAAA	
PtDIR38	ERE	ATTTTAAA	
PtDIR38	ERE	ATTTTAAA	
PtDIR38	ERE	ATTTTAAA	
PtDIR38	ERE	ATTTTAAA	
PtDIR38	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR39	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR39	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR39	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR39	TC-rich repeats	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
PtDIR39	TC-rich repeats	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
PtDIR39	MRE	AACCTAA	MYB binding site involved in light responsiveness

PtDIR39	G-box	CACGAC	cis-acting regulatory element involved in light responsiveness
PtDIR39	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR39	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR32	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR32	ERE	ATTTCATA	
PtDIR32	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR32	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR33	ERE	ATTTTAAA	
PtDIR33	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR33	TATC-box	TATCCCA	cis-acting element involved in gibberellin-responsiveness
PtDIR33	TC-rich repeats	GTTTCTTAC	cis-acting element involved in defense and stress responsiveness
PtDIR34	TC-rich repeats	GTTTCTTAC	cis-acting element involved in defense and stress responsiveness
PtDIR34	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR34	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR34	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR34	G-box	CACGTC	cis-acting regulatory element involved in light responsiveness
PtDIR34	MBSI	aaaAaaC(G/C)GTTA	MYB binding site involved in flavonoid biosynthetic genes regulation
PtDIR34	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR34	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR34	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR34	ERE	ATTTCATA	
PtDIR34	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR35	WUN-motif	AAATTTCTT	
PtDIR35	WUN-motif	AAATTACT	
PtDIR35	TC-rich repeats	GTTTCTTAC	cis-acting element involved in defense and stress responsiveness
PtDIR35	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR35	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR35	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR29	TC-rich repeats	GTTTCTTAC	cis-acting element involved in defense and stress responsiveness
PtDIR29	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR29	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR29	ABRE	CACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR29	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR29	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR29	WUN-motif	AAATTTCTT	
PtDIR29	G-box	CCACGTAA	cis-acting regulatory element involved in light responsiveness
PtDIR29	G-box	TACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR29	G-box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR29	TGA-element	AACGAC	auxin-responsive element
PtDIR29	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR29	G-Box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR29	ERE	ATTTCATA	
PtDIR29	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR29	MBSI	TTTTTACGGTTA	MYB binding site involved in flavonoid biosynthetic genes regulation

PtDIR29	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR29	ERE	ATTTTAAA	
PtDIR31	MBSI	TTTTTACGGTTA	MYB binding site involved in flavonoid biosynthetic genes regulation
PtDIR31	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR31	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR31	WUN-motif	CCATTTCAA	
PtDIR31	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR26	G-box	TAACACGTAG	cis-acting regulatory element involved in light responsiveness
PtDIR26	G-box	TACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR26	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR26	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR26	ERE	ATTTCATA	
PtDIR26	ERE	ATTTTAAA	
PtDIR26	ERE	ATTTTAAA	
PtDIR26	TC-rich repeats	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
PtDIR26	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR26	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR26	WUN-motif	AAATTACT	
PtDIR26	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR27	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR27	TC-rich repeats	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
PtDIR27	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR27	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR27	ERE	ATTTCATA	
PtDIR27	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR27	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR28	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR28	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR28	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR28	ERE	ATTTCATA	
PtDIR25	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR25	TC-rich repeats	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
PtDIR25	TC-rich repeats	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
PtDIR25	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR25	ABRE	GCAACGTGTC	cis-acting element involved in the abscisic acid responsiveness
PtDIR25	WUN-motif	AAATTACT	
PtDIR25	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR25	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR23	WUN-motif	AAATTACT	
PtDIR23	TC-rich repeats	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
PtDIR23	TC-rich repeats	GTTTCTTAC	cis-acting element involved in defense and stress responsiveness
PtDIR23	ERE	ATTTTAAA	
PtDIR23	TATC-box	TATCCCA	cis-acting element involved in gibberellin-responsiveness
PtDIR24	ABRE	CACGTG	cis-acting element involved in the abscisic acid responsiveness

PtDIR24	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR24	ABRE	TACGGTC	cis-acting element involved in the abscisic acid responsiveness
PtDIR24	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR24	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR24	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR24	TC-rich repeats	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
PtDIR24	ERE	ATTTTAAA	
PtDIR24	ERE	ATTTTAAA	
PtDIR24	ERE	ATTTTAAA	
PtDIR24	ERE	ATTTTAAA	
PtDIR24	G-Box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR24	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR24	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR24	G-box	ACACGTGT	cis-acting regulatory element involved in light responsiveness
PtDIR24	G-box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR24	G-box	TACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR22	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR22	WUN-motif	AAATTACT	
PtDIR22	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR22	ERE	ATTTTAAA	
PtDIR22	ERE	ATTTTAAA	
PtDIR22	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR22	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR22	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR13	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR13	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR13	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR14	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR14	ERE	ATTTTAAA	
PtDIR14	ERE	ATTTCATA	
PtDIR14	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR14	ABRE	TACGGTC	cis-acting element involved in the abscisic acid responsiveness
PtDIR14	ERE	ATTTTAAA	
PtDIR15	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR15	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR15	TATC-box	TATCCCA	cis-acting element involved in gibberellin-responsiveness
PtDIR15	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR15	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR15	TC-rich repeats	GTTTCTTAC	cis-acting element involved in defense and stress responsiveness
PtDIR16	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR16	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR16	ERE	ATTTTAAA	
PtDIR16	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR16	TATC-box	TATCCCA	cis-acting element involved in gibberellin-responsiveness

[illegible]

PtDIR20	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR20	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR20	ERE	ATTTTAAA	
PtDIR20	ERE	ATTTTAAA	
PtDIR20	TCA-element	CCATCTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR20	TGA-element	AACGAC	auxin-responsive element
PtDIR20	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR21	G-box	CACGAC	cis-acting regulatory element involved in light responsiveness
PtDIR21	G-box	TAACACGTAG	cis-acting regulatory element involved in light responsiveness
PtDIR21	G-box	TACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR21	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR21	ERE	ATTTTAAA	
PtDIR21	ERE	ATTTTAAA	
PtDIR21	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR12	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR12	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR12	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR12	TC-rich repeats	GTTTTCTTAC	cis-acting element involved in defense and stress responsiveness
PtDIR12	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR12	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR12	ERE	ATTTTAAA	
PtDIR1	G-box	CACGTC	cis-acting regulatory element involved in light responsiveness
PtDIR1	G-box	TACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR1	G-box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR1	G-Box	CACGTGAAA	cis-acting regulatory element involved in light responsiveness
PtDIR1	G-Box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR1	ERE	ATTTTAAA	
PtDIR1	ERE	ATTTTAAA	
PtDIR1	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR1	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR1	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR1	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR1	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR1	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR1	WUN-motif	AAATTACT	
PtDIR1	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness

PtDIR1	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR1	ABRE	CACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR1	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR2	WUN-motif	CCATTTCAA	
PtDIR2	WUN-motif	AAATTCCT	wound-responsive element
PtDIR2	ERE	ATTCATA	
PtDIR2	ERE	ATTCATA	
PtDIR2	TC-rich repeats	GTTTTCTTAC	cis-acting element involved in defense and stress responsiveness
PtDIR3	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR3	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR4	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR4	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR4	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR4	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR4	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR5	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR5	ERE	ATTTTAAA	
PtDIR5	ERE	ATTTTAAA	
PtDIR5	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR5	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR5	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR5	G-box	TACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR5	LTR	CCGAAA	cis-acting element involved in low-temperature responsiveness
PtDIR5	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR5	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR5	TC-rich repeats	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
PtDIR6	G-box	TAACACGTAG	cis-acting regulatory element involved in light responsiveness
PtDIR6	G-box	TACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR6	TGA-element	AACGAC	auxin-responsive element
PtDIR6	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR6	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR6	ERE	ATTTTAAA	
PtDIR6	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR6	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR6	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR7	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR7	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR7	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR7	ABRE	CACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR7	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR7	TGA-element	AACGAC	auxin-responsive element
PtDIR7	G-box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR7	TCA-element	TCAGAAGAGG	cis-acting element involved in salicylic acid responsiveness
PtDIR7	G-Box	CACGTG	cis-acting regulatory element involved in light responsiveness

PtDIR7	MBS	CAACTG	MYB binding site involved in drought-inducibility
PtDIR8	WUN-motif	TAATTACTC	
PtDIR8	ABRE	CACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR8	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR8	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR8	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR8	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR8	G-Box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR8	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR8	ERE	ATTTTAAA	
PtDIR8	ERE	ATTTTAAA	
PtDIR8	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR8	G-box	CACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR9	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR9	WUN-motif	TAATTACTC	
PtDIR9	ERE	ATTTTAAA	
PtDIR9	ERE	ATTTTAAA	
PtDIR9	G-box	TACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR10	MRE	AACCTAA	MYB binding site involved in light responsiveness
PtDIR10	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR10	ERE	ATTTTAAA	
PtDIR10	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR10	TGA-element	AACGAC	auxin-responsive element
PtDIR10	TGA-element	AACGAC	auxin-responsive element
PtDIR10	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR11	G-box	TACGTG	cis-acting regulatory element involved in light responsiveness
PtDIR11	TATC-box	TATCCCA	cis-acting element involved in gibberellin-responsiveness
PtDIR11	TCA-element	TCAGAAGAGG	cis-acting element involved in salicylic acid responsiveness
PtDIR11	TCA-element	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
PtDIR11	G-Box	CACGTT	cis-acting regulatory element involved in light responsiveness
PtDIR11	ERE	ATTTTAAA	
PtDIR11	ERE	ATTTTAAA	
PtDIR11	ERE	ATTTTAAA	
PtDIR11	ERE	ATTTTAAA	
PtDIR11	ERE	ATTTTAAA	
PtDIR11	ERE	ATTTTAAA	
PtDIR11	CGTCA-motif	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
PtDIR11	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness
PtDIR11	ABRE	ACGTG	cis-acting element involved in the abscisic acid responsiveness

Figure S1. Hormone response pattern analysis of PeDIR genes by bar chart. PeDIR expression in the 'Nanlin 895' response to exogenous hormone (ABA, SA, MeJA, and ETH) treatment for 0, 3, 6, 9, 12, and 24 h.

