

Supplementary Information

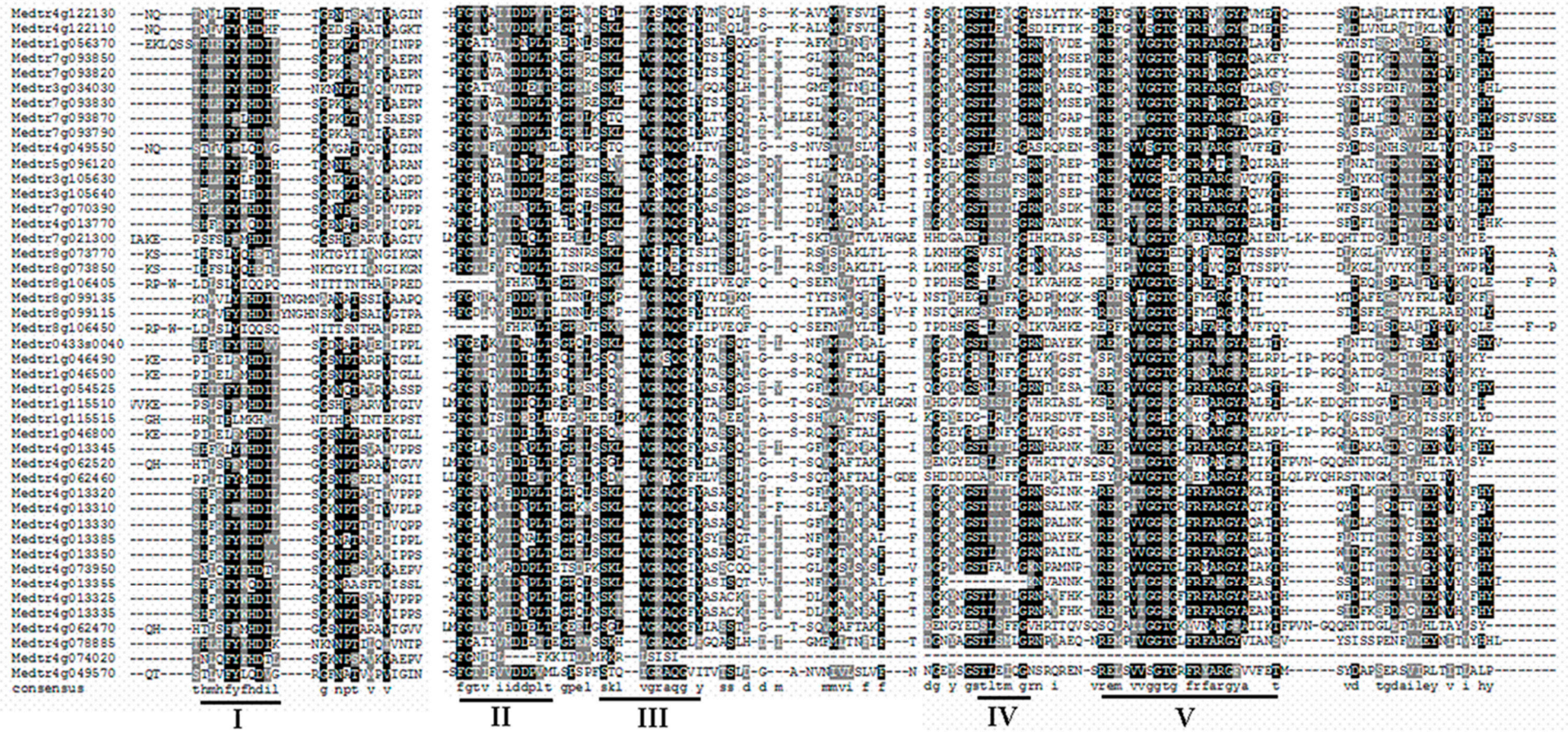


Figure S1. Partial alignment of *M. truncatula* dirigent and dirigent-like proteins showing the conserved five motifs (I–V) described in [29]. The alignment was performed with Kalign and the conserved residues were shaded using BoxShade (see Materials and Methods section).

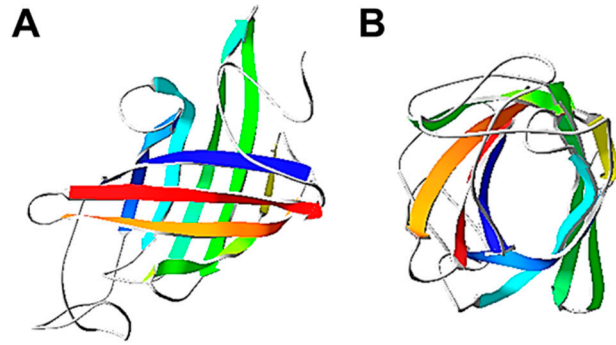


Figure S2. Putative 3D structure of the dirigent-like proteins Medtr1g054525.1 from *M. truncatula*. (A) lateral view showing the β -barrel; (B) the same structure viewed from the top to show the hydrophobic core (*i.e.*, the cavity where the substrate binds).

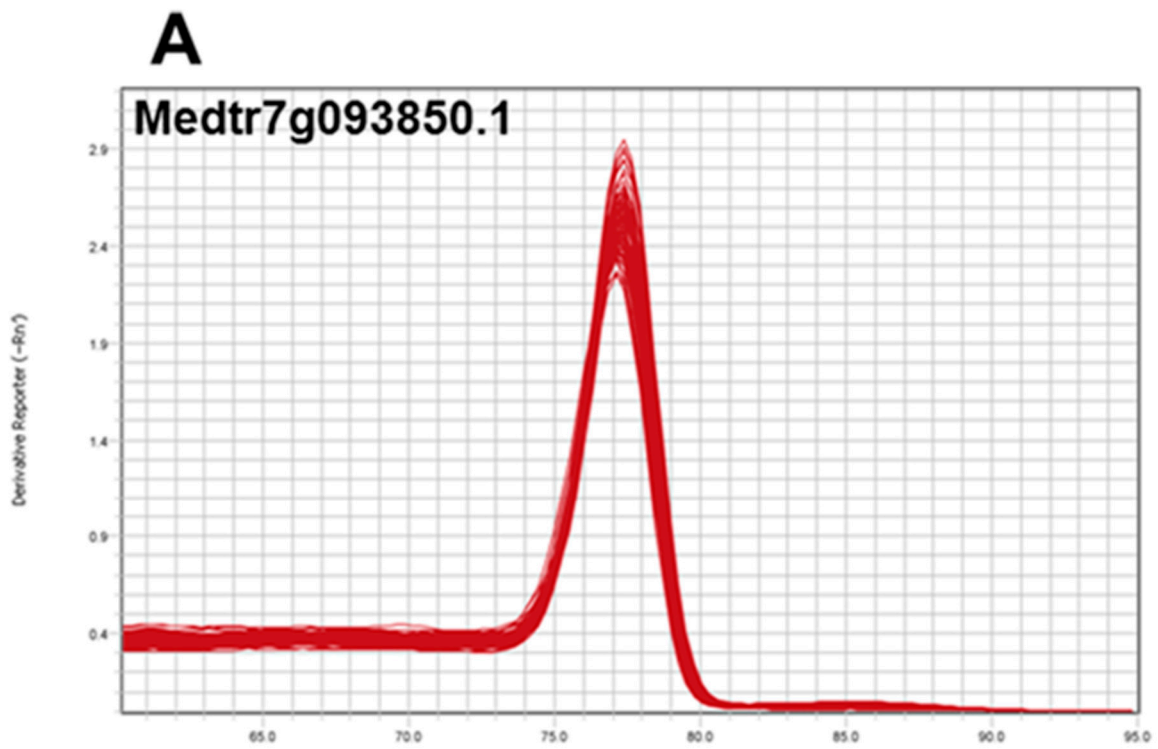


Figure S3. *Cont.*

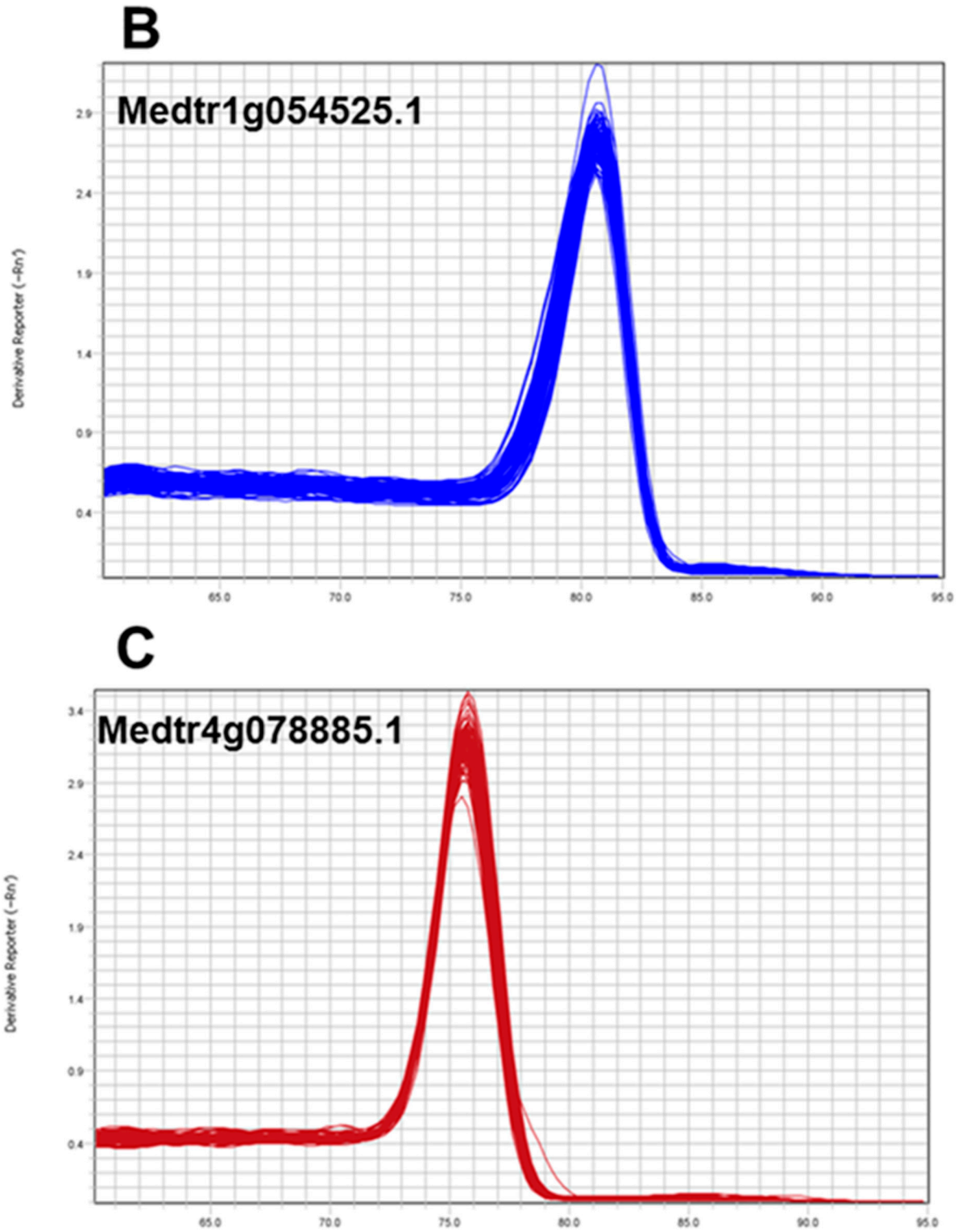


Figure S3. Melt curve analysis of the three genes coding for the dirigent-like proteins Medtr7g093850.1 (A), Medtr1g054525.1 (B) and Medtr4g078885.1 (C) in roots, stems and leaves of alfalfa.

MtPrx01 29 -LTPHFYDNV-CPQALPTIKSVVLHAILREKRIGASLLRLHFHDCFV-NGCDGSVLLDDT-PNF-T-GEKTALPNIN---
 MtPrx02 25 -LTPNYDRI-CPKALPIINSIVKQAIIREPRMGASLLRLHFHDCFV-NGCDGSVLLDDT-FIF-I-GEKTAFPNIN---
 MtPrx03 27 -LTPDFYNDV-CPQALSIINTIVROKLDKFKPRMGASLLRLHFHDCFV-NGCDGSVLLDDT-PNF-I-GEKTAKGNID---
 MtPrx04 25 -LRKNFYKKS-CPQAEIIVKNITLOHVSSRPELEAKLIRLHFHDCFV-FGCDASVLLDST-AGN-T-AEKDAPNL----
 MtPrx05 50 -LELGFYTKS-CPKAEQIVANFVHEHIRNAPSLAALIRMHFHDCEV-FGCDASVLLNST-N-Q-Q-AEKNAFPNL----
 MtPrx06 27 -TRVGFYSST-CSQAESIVKSTVASHVNSDSSLAPGLLRMHFHDCEV-OGCDASVLLVAGS-G-----TEKTAFPNL----
 MtPrx07 26 -LEVGFYTYT-CGMAEFIVKDEVRKSFNKNPGIAAGLIRMHFHDCEV-FGCDASVLLDST-LSN-I-AEKDSPANP---
 MtPrx08 23 -LSLNYYEKS-CHDLEYIVLKTVTIATARDKIVFAALLRMHFHDCEV-FGCDASVLLNSK-GKN-K-AEKDGFPNL----
 MtPrx09 28 -LTTDFYKSS-CPNLTKIVRKEVVKALKNEMRMGASLLRLHFHDCFV-NGCDGSILLDGG-DDF---EKSAPFNIN---
 MtPrx10 29 -LDPSFYRDT-CPKVHSIIREVIRNVSKTDRMLASLIRLHFHDCFV-IGCDASVLLNKT-DII-V-SEQEAFPNIN---
 MtPrx100 50 -LSFSYYRKS-CPQFESILHSHVKEWIKKDYTLAASLLRLHFHDCSV-FGCDGSILLNHE-G-----SERKSQVSK---
 MtPrx107 25 -LAFDFYAAS-CPTAEFIRNAVSTSSSNDPSIFGKLLRMVFHDCFV-FGCDASIMLQGN-N-----TEQSDPGNR---
 MtPrx11 29 -LDPSFYRNT-CPNVSSIIVREVIRSVSKKDRMLGSLIRLHFHDCFV-OGCDASVLLNKT-DIV-V-SEQDAFPNRN---
 MtPrx110 25 -LSSTFYDST-CPNALSTIRTSIRTAISKERRMAASLIRLHFHDCFV-OGCDASILLDST-STI-E-SEKSARPNVN---
 MtPrx111 24 -LSPSFYSQT-CPFLYPIVFRVIFFEASLTDRIGASLIRLHFHDCFV-OGCDGSVLLNNT-NII-V-SEQDALPNIN---
 MtPrx114 25 -LAFDFYAAS-CPTAEFIRNAVSTSSSNDPSIFGKLLRMVFHDCFV-FGCDASIMLQGN-N-----TEQSDPGNR---
 MtPrx116 16 -LQLGLYAFS-CQKAELIVPQVQKFRNRDKSVIAALIRMHFHDCEV-FGCDASILLDST-NNT-T-AEKDSGTNE----
 MtPrx12 40 -LNPSFYSKT-CPNVSSIIVREVIRNVSKTDRMLASLIRLHFHDCFV-OGCDASVLLNNT-ATII-V-SEQDAFPNRN---
 MtPrx13 26 -ELHAHYDQT-CPQLDKIITSETVLTASIHDPKVFARLIRLHFHDCFT-FGCDASVLLDST-ATN-Q-AEKDGFPNL----
 MtPrx14 24 -LTRGFYNNV-CPNVEQLVRSAVNQKFOQTFVITAPATLRLRFHDCFV-FGCDASILLATP-----K-AEREHPDDIS---
 MtPrx15 29 -LDNSFYRDT-CPNVHSIIVREVIRNVSKTDRMLASLIRLHFHDCFV-OGCDASILLNNT-STI-T-SEQTAFGNM---
 MtPrx16 29 -LSPDFYAKT-CPQLQSIVFOILEKVSKTDSRMEASLIRLHFHDCFV-OGCDASVLLNKT-STI-A-SEQDAGPNIN---
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 MtPrx18 41 -LSIGHYHST-CPDAEGTISQKVFAMVKKDPTLAESEIRLHFHDCIV-FGCDGSILLNHV-G-----SERTAFASK----
 MtPrx19 38 -LNMNYLMS-CPFVEPVVKNIVNRALDNDPTLAAALIRMHFHDCEV-OGCDGSILLDST-KDN-T-AEKDSPANL----
 MtPrx20 28 -LSPTFYSKT-CPTVSSIIVSNVLTNVSKTDQRMLASLIRLHFHDCFV-IGCDASVLLNNT-ATII-V-SEQQAFPNM---
 MtPrx21 24 -LHVGFYSNT-CPQVESTVHDVVREAVLFDRTKAAVLLRLHFHDCFV-FGCDGSILLNNTIQN-----BEKTAFPHA----
 MtPrx22 31 -LSKDYYSYSS-CPKLFETIVKCEVQSAISKETRMGASLLRLHFHDCFV-NGCDGSILLDDT-SSF-T-GEKTANPNKN---
 MtPrx23 69 -LTSTFYNT-CPNVSSIIVRNVVQCALONDRMLASLIRLHFHDCFV-NGCDASILLDQG-GNITL-SERNAVPNM---
 MtPrx24 46 -LSSTFYGTR-CPRALYIIRREIIAAVSRDRRLGASLLRLHFHDCFV-OGCDASVLLKDT-FIF-Q-GEQNAFPNAN---
 MtPrx25 30 -LYPCFYDYS-CPQAQNVKSIILANAVAKEPRIAASLLRLHFHDCFV-FGCDASILLDMS-GSI-I-SEKGSNPNRN---
 MtPrx26 29 -LDPSFYNST-CSIIVDSIVRGVLTNVQSQDRMLGSLIRLHFHDCFV-OGCDASILLNNT-ATII-V-SEQSAPNMM---
 MtPrx27 29 -LTPYFYRTT-CPDVFTIVRREVLNATNEEIRMAASLLRLHFHDCFV-NGCDASILLDGD-EDI---EKTATPNIN---
 MtPrx28 25 -LVNNFYGTT-CPSLQITIVRREMTKAINNEARIGASLIRLHFHDCFV-NGCDGSILLDDT-STF-T-GEKNAGPNKN---
 MtPrx29 30 -LSENFYAKK-CPNVFKAVNSVHSAVAREPRMGGSLLRLHFHDCFV-NGCDGSVLLDDT-FSN-K-GEKTALPNKD---
 MtPrx30 25 -LSPSFYSQT-CPFLYPIVFRVIYEASHTDRIGASLIRLHFHDCFV-OGCDGSVLLNNT-DII-V-SEQDAFPNRN---

MtPrx32 45 -LRPSFYLLHGCPPLAVQTI RTAITTTAVLKDPRLGASLLRLHFHDCFV-OGCDASVLLKDT-PTF-K-GEKNAAPNAN---
 MtPrx33 24 -LSSNFYFRT-CPLVLSTIKKEVISALINERRMGASLLRLHFHDCFV-OGCDASVLLDDT-SSF-R-GEKTAGPNAN---
 MtPrx34 26 -LSKDFYCSS-CPELLSIVNQGVINAIKKETRIGASLLRLHFHDCFV-NGCDASVLLDDT-SSF-I-GEKTAAPNAN---
 MtPrx35 30 -LDPNFYKDT-CPNVTSIVQSI LANVSQTDPRILASFIRLHFHDCFV-OGCDASVLLNDS-DII-V-SEQALPNAN---
 MtPrx36 20 -LSTDFYSTI-CSDVLSTIKREIDSAVGNARMGASLLRLHFHDCFV-OGCDASVLLDDT-SSF-T-GEKTAGANAN---
 MtPrx37 26 -LCTDFYCNS-CPELLSIVNQGVNNAIKKETRIGASLLRLHFHDCFV-NGCDASVLLDDT-SSF-I-GEKTAAPNAN---
 MtPrx38 27 -LSPNHYANI-CPNVQSI VRSVAVQKKFQOTFVTPATLRLHFHDCFV-OGCDASVIVASS-GNN-K-AEKDHPENLS---
 MtPrx39 27 -LSENFYGKT-CPKAVRTIRKAVQDAVMNERRMGASLLRLHFHDCFV-OGCDASVLLDDT-SNF-T-GEKNAAPNAN---
 MtPrx40 33 -LTLDFYAST-CPTVFDIVRKQMECSVLSEPRNAASVRLHFHDCFV-OGCDGSVLLDDT-YIL-K-GEKKAATNIH---
 MtPrx41 25 -LVENFYVSS-CPNVELVVAQAVTNKFTQTITITGQATLRLHFHDCFV-EGCDASVMTASP--NG-D-AEKDAKENLS---
 MtPrx42 27 -LSRHHYKNS-CPNVENIVREAVKKKFHQTFTVTPATLRLHFHDCFV-OGCDGSVIVSST-PHN-R-AEKDHPENLS---
 MtPrx43 25 -LFPNFYGRY-CPSLQTI VVRREMTKAINNEARIGASLLRLHFHDCFV-NGCDGSVLLDDT-STF-T-GEKNAAPNAN---
 MtPrx44 26 -LSPNFYAKT-CSNLQTI VVRNEMIKVIQKEARMGASLLRLHFHDCFV-NGCDASVLLDDK-GTF-V-GEKNSGPNQG---
 MtPrx45 45 -GLSPQFYQFS-CPQANDIVMSVLEKAI AKDIRIAASLLRLHFHDCFV-OGCDASVLLDSS-ATI-V-SEKNAAPNAN---
 MtPrx46 30 -LYPQFYDES-CPKVEEIVRSVAVAKAVTKEPRMAASLLRLHFHDCFV-EGCDASVLLDSS-GTI-I-SEKRSNPNAN---
 MtPrx47 32 -LVMNYYKEA-CPQAEELIKQVKKLLYKRHNIAFSMLRNIFHDCFV-KSCDASVLLTST-RRS-L-SEQ-EHDRSF---
 MtPrx48 42 -LSYGFYFAQT-CPNLENIVRKHLTKVFKSDNGQAPGLLRHFHDCFV-OGCDGSVLLDGGK-----P-GERDQPNQGG---
 MtPrx49 27 -LTTNYYDYT-CPNALSTIKSVKAAVQRENRMGASLLRLHFHDCFV-NGCDGSVLLDST-FSM-D-SEKNAAPNAN---
 MtPrx50 29 -LOVGFYSYS-CPSAEALVRSVAVKAVSLNPGIAGLIRMHFDCFV-EGCDASVLLAST-PGN-PIAEKDNFINNP---
 MtPrx52 27 -LYYNFYNRT-CPNINKIVKDNILSATANLSRIAASLLRLHFHDCFV-NGCDGSVLLDDT-DIL-K-GEKNAAPNAN---
 MtPrx53 27 -LQPGFYAKS-CPKAEQIVLKYVHDHPIPNAPSLAALIRLHFHDCFV-EGCDASVLLNST-CTN-Q-AEKDAIPNL----
 MtPrx54 28 -LSTNFYSKT-CPKLSIVQRQVQSATSKEARIGASLLRLHFHDCFV-NGCDGSVLLDDT-SNF-T-GEKNAAPNAN---
 MtPrx55 24 -LSVNYYEHT-CPQVESTIVAGAVHKATMNDKTPSALLRHFHDCFV-EGCDGSVLLKTK-GKN-K-AEKDGEPMI----
 MtPrx56 27 -LQVNYYSKS-CPKAEELIKQVQVNELYNKHGNTAISWVRNLFHDCFV-KSCDASVLLLETV-HGV-V-SEQ-TAERSF---
 MtPrx57 25 -LVNMFYGTI-CPSLQTI VVRNKMTSAIKTEPRIGASLLRLHFHDCFV-NGCDGSVLLDDT-PTF-T-GEKNAAPNAN---
 MtPrx58 27 -LYYNFYIRT-CPNLRIVRNNILSATANLSRIAASLLRLHFHDCFV-NGCDGSVLLDDT-DIL-K-GEKNAAPNAN---
 MtPrx60 36 -LQWHYYHNT-CDRAEVYVRHQVKIHWDDKSI IAKLLRLHFHDCFV-NGCDASVLLDEGPN-----FEKRAPQNR---
 MtPrx61 31 -TNEMYYDNT-CPNALVAIQQAVQNAVLGARI GASLLRLHFHDCFV-OGCDGSVLLDDT-SSF-K-GEKNSIQNAN---
 MtPrx63 25 -LIDNFYDQT-CPCLQTI VVRNTMTSAIKKEARIGASLLRLHFHDCFV-NGCDGSVLLDDT-PTF-I-GEKNAAPNAN---
 MtPrx64 77 -LEYDFYRDS-CPHAEHIVRSTLHLLYKTNPAIVPALIRLHFHDCFV-OGCDASVLLDND-EYI-D-SEKDSPXND----
 MtPrx65 30 -LKYGFYKTI-CSSVEAIVRRAVNKAVSLNPGIAGLIRMHFDCFV-EGCDGSVLLDSI-PGI-Q-SEKDHPPNPN---
 MtPrx66 21 -LKTGFYSNS-CPTAESIVRSTVVSYFNKPTIAPGLLRHFHDCFV-OGCDGSVLLTAGS-S-----SEKSAIPNL----
 MtPrx67 24 -LSSTFYDST-CPNALSTIRTVIRTA VSKERRMAASLLRLHFHDCFV-OGCDASVLLDDT-STI-E-SEKSAIPNIN---
 MtPrx70 25 -LTPNYYDRI-CPKALPVIKSI VQALIREPRMGASLLRLHFHDCFV-NGCDGSVLLDDT-PTF-I-GEKTAGPNAN---
 MtPrx71 29 -LDPAFYSKT-CPNLSIVREIVRNFTKIEPRMAALIRLHFHDCFV-OGCDASVLLANT-ATI-V-SEKALPNAN---
 MtPrx74 42 -LRVDYYAKS-CPQVEQLVGSVTSQOFKQSPVSGPATLRLHFHDCFV-EGCDASVLLTASK-PGS-KELAEKDAEDNK---


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MtPrx75 36 -LDYDFYRLS-CPRTERIVRKHLEDVFEKDSGQAPGILRLRFHDCFS-OGCDASILLNGV----D-GEDEKQHDANFA
MtPrx76 24 -LSSTFYDST-CPNALSTIRTSIRTAVSKECRMAASVIRLHFHDCFV-OGCDASILLDDT-SFI-E-SEKNALPNIN---
MtPrx78 21 -LRFGFYSEF-CPQVEEIVGEVVQSYQORDITAGALIRLHYHDCFV-NGCDASILLDSR-VNR-T-AEKDAKPNK----
MtPrx79 34 -LTLDYKQT-CPOFOQIIQOTVTSKQIQSPITAAATLRLFLHDCLENGCDASVLLSST-PFN-K-AERDNDINLS---
MtPrx81 27 -LTTNYYDYT-CPNALSTIRSVVEAAVEKENRMGGSLRLHFHDCFV-NGCDGSILLDST-PSM-D-SEKNANPNIN---
MtPrx82 60 -LRYNFYKDS-CPEAENIVRSAVTDIYSDHRDLAHSLLRLEFHDCFV-OGCDASILLE-D-RNI-S-YEKQAIIPNO----
MtPrx83 73 -LKQGFYSES-CPTAEKIVADALVEITKTNPAIANIIRLQFHDCFV-VGCDSSVLLDYT-FTG---DKVEKSSMLN-GQ
MtPrx84 28 -LSTNFYSKT-CPKLSSTIVKSTLQTAISKEARMGASILRLRFHDCFV-NGCDGSILLDIT-SSF-T-GEKNANPNRN---
MtPrx85 38 -LGTDIYQYS-CPEAEALIFSWVEQAVSSDPRMAASLLRLHFHDCFV-NGCDASVLLDIT-ENF-V-GEKTAAPNVN---
MtPrx86 25 -LSSNYYDEI-CPQALFIIKSVVKCAIIREFRMGASLLRLHFHDCFV-NGCDGSILLDIT-FTF-I-GEKTAIPNIN---
MtPrx87 30 -LKYGFYKTI-CPSAEAIIVRRAVNKAVSLNPGITAGLIRMHFHDCFV-RGCDGSVLLDSI-PGI-R-SERDHPANFP---
MtPrx88 22 -LKVGFYSSS-CPRAELIVRQVVERSFNQDRSMTAALLRMHFHDCFV-RGCDASILLDSK-KGN-E-SEKAAARANL----
MtPrx89 20 -LELGFYASS-CKAESIVKQVVQKRFNRDKSITAAALLRMHFHDCFV-RGCDASILLDSTI-KNN-I-SEKDTGAND----
MtPrx90 26 -LVHDEYYKEK-CPLAEDIVRHNVAVAVLKDPRLAASLLRLHFHDCFV-MGCDASVLLDSV-EGM-T-SEKQAGPNVN---
MtPrx91 23 -LIPNYYQKS-CPKFEDIVKQTVTDKQKTPSTAGAAIRLRFHDCMT-GGCDASVLVSSN-SFN-K-AERDADINLS---
MtPrx92 26 -LSYNYEKT-CPDVEFIVAKTVKAATASDKTVFAALLRMHFHDCFV-RGCDASVLLNSK-GSN-K-AEKDGPNA----
MtPrx93 29 -LSYNYKNS-CPNLESILVERELMSVFMTDIRAPSAELRIMFHDCQV-OGCDASILLDIT-YAT-Q-SSEIASSGNF---
MtPrx94 40 -LRPGFYSKT-CPKAETIVRDVMRKALIREPRSVASVMRLQFHDCFV-NGCDGSVLLDIT-FTM-L-GEKLALSNIN---
MtPrx95 28 -LRPGYYSKT-CPQAETIVRDVMRNALKKEPRSVASVMRFQFHDCFV-NGCDGSVLLDIT-FTM-L-GEKLALSNIN---
MtPrx97 25 -LVNMFYGRF-CPSLQTIIVREMANAIKTEARIGASILRLRFHDCFV-NGCDGSILLDIT-ATF-T-GEKNAAPNKN---
MtPrx98 28 -LSTSFYSSS-CPKLSSTVQSTVQSAISNEARMGASILRLRFHDCFV-NGCDGSILLDIT-SNF-T-GEKNANPNRN---
consensus 241 l fy t Cp l ivk v ai e rigasllrlhfhDCfv ngCdaSvllld t t gek a pn n

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MtPrx01 100 -SLR--GFSVVDEIKAAVIVKV--CKGPFVVCADILATAARDSV--ATLGG--EQFFNVVLGRRDARTASKAAA--N-A-N-L
MtPrx02 96 -SLR--GFEVVDQIKEMVTKA--CKRDVVSCADILATAARDSV--ATLGG--KQYWVQVVLGRRDSREASRDAA--N-T-N-L
MtPrx03 98 -SLK--GFMVLDIIEKALDKA--CKGPFVVCADILAVIARDSV--SILGG--PSYWVQVVLGRRDARNASMKDA--E-S-Y-L
MtPrx04 95 -SLA--GFDVIDEIKAELEEK--CPG--IVSCADILTLATRDAT--K--NK--PN--WEVLTGRRDGTVSRSEALI--N---I
MtPrx05 119 -TVR--GFDIHDRIKSLVEAE--CPG--VVSCADIIALSARDSI--AATGG--PY--WQVPTGRRDGVVSNLLEANC--N---I
MtPrx06 94 -GLR--GFEVIDAKTKLEAA--CPG--VVSCADIVALAARDSV--VLSGG--LS--WQVPTGRRDGRVSOASDV--N-N--L
MtPrx07 97 -SLR--GFEVIDNAKAKLEEE--CKG--IVSCADIVAAARDSV--ELAGG--LG--YDVPAGRRDCKISLASDT--R-T-E-L
MtPrx08 93 -SLH--AFYVIDEAKKALEAK--CPG--VVSCADILALAARDAV--YLSGG--PK--WNVKGRIDGRTSKASET--R-Q---L
MtPrx09 97 -SVR--GFDVVDTIKTAVEESA--CSG--VVSCADILATAARDSV--LLSGG--PS--WSVVLGRRDGTISNGSLA--N-V-V-L
MtPrx10 100 -SLR--GLDVVNQIKTAVEKA--CPN--TVSCADILALSAQISS--ILAIQ--PN--WQVPLGRRDGLTANQSLA--N-Q-N-L
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MtPrx107 92 -SVG--GFSVIEIAKRVLEMF--CPG--TVSCADIIIALAARDAV--ELAGG--PR--WQIPTGRRDGMVSIASNV--RPN---I
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MtPrx13 97 -SVR--SFYVIDEAKAKLELA--CPG--VVSCADILALLARDVV--AMSGG--PY--WQVPLGRRDGRVSKASDT--A-N---L
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MtPrx16 100 -SLR--RLDVINQIKTEVEKV--CPN--KVSCADILTLAAGVSS--VLSGG--PG--WTVPLGRRDSLTAHQSLA--N-R-N-L
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MtPrx18 108 -TLR--GFQLIDEIKAELEER--CPR--TVSCADILTLAATRDAT--ILAGG--PF--WEVPLGRRDCKISIAKEA--N-L---V
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MtPrx21 92 -GVK--GFEVIERAKAQLLEAS--CPG--VVSCADIVALAARDAT--VMANG--PA--WQVPTGRRDGFVSDKSLA--G-N---M
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MtPrx27 98 -SPR--GFEVIDRIKSSVESS--CSG--VVSCADILAVARDSV--HLSGG--PF--WVVLGRRDGLVSNKTLA--N-N-A-I
MtPrx28 96 -SPR--GFEVIDAIKTSVEAA--CSA--VVSCADILALATRDGI--ALLGG--PS--WVPLGRRDARTASQSA--N-S-Q-I
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MtPrx30 96 -SLK--RLDVVNQIKTAVEEE--CPN--TVSCADIIITIAAEVSS--ILGGG--PS--WQIPLGRRDSLTAHQTLA--N-Q-N-L

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MtPrx32 117 -SIR--GYEIIIESVKAQIEELL--CPN--VVSCADILALAARDV--VALGG--FN--WLVRLGRRDSTTADFNA--N-S-D-L
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 MtPrx34 97 -SIR--GFNVDDIKANVEKA--CPG--VVSCADILTLAARDV--VHLGG--FS--WNVVLGRRDSITASRSDA--N-N-S-I
 MtPrx35 101 -SIR--GLDIVNCIKAATIELA--CPS--VVSCADILALGANVSS--VLALG--FD--WEVPLGRRDSFNANQSLA--N-S-S-L
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 MtPrx37 97 -SIR--GFNVDDIKASVEKA--CPK--VVSCADILALAARDV--VHLGG--FS--WIVVLGRRDSITASRSDA--N-N-S-I
 MtPrx38 98 -LAG-I-GFDITVIKAKAALIAVPC--CPN--KVSCADILALATRDVI--NLGG--FS--YTVELGREDGLVSRSSDV--N-G-R-L
 MtPrx39 98 -SIR--GFELIDDIKSQLEDM--CPN--TVSCADILALAARDGV--AELGG--QR--WNVLLGRRDSTTANLSEA--N-T--L
 MtPrx40 104 -SLK--GFELIDDIKSNFVESE--CPG--VVSCADILTLAARDV--ILVGG--PY--WIVPVGRKDSVTASFELA--N-T-N-L
 MtPrx41 95 -LPG-I-GFDITVIKAKQAVESV--CPG--VVSCADILALATRDVI--ALLGG--FS--FSVELGRRDGLNSKASNV--E-A-N-L
 MtPrx42 98 -LAG-I-GFDITVIQAKAAVIAVPL--CPN--KVSCADILAMATRDVI--ALGG--PY--YEVELGREDGLRSKSDV--N-G-K-L
 MtPrx43 96 -SIR--GFEVIDAIKTSVEAA--CSA--TVSCADILALATRDGI--ALLGG--FS--WIVPLGRRDARTASQSAA--N-T-Q-I
 MtPrx44 97 -SIR--GFEVIDTIKTSVETA--CKA--TVSCADILALATRDGI--ALLGG--FS--WAVPLGRRDARTASQSAA--N-S-Q-I
 MtPrx45 117 -SVR--GFEVIDEIKSKLEQA--CPR--TVSCADIVALAARGST--VLSGG--FN--WEIPLGRRDSKTASLRGS--N-K-N-I
 MtPrx46 101 -SIR--GFEVIDEIKSAVEKE--CPQ--TVSCADILTLAARDST--VLTGG--FS--WIVPLGRRDSLGAISIGS--N-N-N-I
 MtPrx47 102 -GLR--NFRYIDTIKEAVERE--CPG--VVSCADILVLSAREGI--VSLGG--PY--IPLKTGRRDGRKSRVDLL--E-A-Y-L
 MtPrx48 110 MRTE--MLKTIIDIRALVHKE--CGR--IVSCADITVLAGREAV--FLSGG--FN--FEVPLGRKDGTSTFSIKGT--S-N--L
 MtPrx49 98 -SIR--GFEVVIDEIKDAVKA--CGKPVVSCADILALTAARDV--VALGG--FS--WVVKLGRRDSKTASRADA--D-SGN-I
 MtPrx50 101 -SIH--GFEVIDEAKAQLEVV--CPQ--TVSCADILTEATRDS--ILKLSGGTIN--YIVPSGRRDGRVSI SDEV--P-K-N-I
 MtPrx52 98 -SIR--GFDVIDKIKSDLENA--CPS--TVSCADILTLAARDV--YQSKG--FF--WAVPLGRRDGTASESEA--N--N-L
 MtPrx53 97 -ILR--GYEFIDTIKSLVEKE--CPG--VVSCADILTLTARDSI--HAIGG--PY--WVVPITGRRDGIISKAADTFT--S--L
 MtPrx54 99 -SVR--GFDVIDNIKTAVENV--CPG--VVSCADILALTAARDV--ALLGG--PT--WNVVLGRRDATTASQSAA--N-T-A-I
 MtPrx55 94 -SIH--AFYVIDNAKKALEAV--CPG--VVSCADILALAARDV--TILSGG--FN--WEVEKGRKDGIIISKA TET--R-Q--L
 MtPrx56 97 -GMR--NPKYVSTIKAALBEKE--CEL--TVSCADIVALSARDGI--ARLGG--FN--FEMKSGRKDSKESYVKVV--E-Q-F-I
 MtPrx57 96 -SIR--GFEVIDTIKTSVEAS--CNA--TVSCADILALAARDGV--FLVGG--PT--WVPLGRRDARTASQSAA--N-S-Q-I
 MtPrx58 98 -SIR--GFDIIDKIKSDLEYA--CPN--VVSCADILTLAARDV--YQSRG--FF--WAVPLGRRDGTASESEA--N--N-L
 MtPrx60 104 -GLG--GFVLIDRIKIVLESR--CPG--IVSCADILHLAARDA--KMAGA--FG--YEIFETGRKDG MKSDAASV--D--L
 MtPrx61 102 -SIR--GFELIDDIKSTLETM--CPN--VVSCADILTLAARDV--VLLGG--QS--WNVPLGRRDSTTASLDAS--N-S-D-I
 MtPrx63 96 -SVR--GFEVIDNIKSNVEAS--CNA--TVSCADILALAARDGV--VLLGG--FS--WTVPLGRRDARTANQSAA--N-S-Q-I
 MtPrx64 147 -SLK--GFDVIEETIKAKLEEA--CPG--VVSCADILVLAARDV--VLGG--FF--YELNFGRRDGSNSFADIATD--E--L
 MtPrx65 101 -SIR--GFEVINEAKAQIEAA--CPK--TVSCADILALFAARDSARKVSGGRID--YSVPSGRRDGRVSI FDEV--T-Q-N-L
 MtPrx66 88 -GLR--GFEVIDNAKSQIEAI--CPG--VVSCADILALAARDV--ILSIG--FS--WEVPTGRKDGRI SLSSQA--S-N--L
 MtPrx67 95 -SVR--GFEVIDKAKANVEKV--CPG--VVSCADIVAVAARDAS--FAVGG--FS--WTVKLGRRDSTVASKSQA--N-S-D-L
 MtPrx70 96 -SIR--GFEVVDQIKAAVTKA--CKRDVVSCADILALTAARDV--ALLGG--KQYW--YQVLLGRRDSRFASRDAA--N-T-N-L
 MtPrx71 100 -SIR--GLQVNRRIKTIIVEKA--CPN--TVSCADILALARTISS--VLSKG--FG--WIVPLGRRDSL TANRTLA--N-Q-N-L
 MtPrx74 114 -DLRMEGFETIRKAKEVVEKK--CPT--VVSCADILALTAARDV--HLGG--PY--YQVKKGRMDGKISMASRV--G-S-N-I

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MtPrx75 107 LREE--ALQTIENIRAIVRKQ--CFR--VVSCADILVLAARDAV--RQFGG--PD--IDVPLGRKDSLNFVSNSP-D-N--L
MtPrx76 95 -SVR--GFEIIDKAKSEVEKI--CPG--VVSCADILAVAARDAS--FAVGG--PS--WIVKLGRRDSTTASKSLA-N-T-D-L
MtPrx78 91 -TLR--GFNLIIDIKSNLEQQ--CPQ--TVSCADILTIATRDAI--ALSNG--PT--YNVLTGRRDGLVSNQFNV---T--I
MtPrx79 106 -LPG--DSFDLIVRIKTALELS--CFN--TVSCADILATAARDL--IMLGG--PH--YNVYLGRRDGRASVSSFV-D-G-F-L
MtPrx81 98 -SFR--GFEVVEIKDAVEKA--CGKF--VVSCADILAVAARDSV--VALGG--PS--WVVKLGRRDSTASRADA-D-SGN-I
MtPrx82 129 -TLK--GFEKVDLKEEVEQA--CPG--VVSCADILALAARDSV--FLGGG--PF--YFVLTGRRDSLQSFQEAAD-Q--I
MtPrx83 145 -LLK--GTEIIDDIKAKLPEQ--CPG--IVSCDTIAFSVNEGM--FLSGL--FR--TAPLGRRDALYSLASIAED-D-N-L
MtPrx84 99 -SFR--GFDVIDNIKTAVENV--CPG--VVSCADILATAARDSV--AILGG--ET--WNVKLGRRDAKTASQSAA-N-T-A-I
MtPrx85 109 -SLR--GFDVINEIKSELEVV--CPQ--TVSCADILATAARDSV--ILSGG--ET--WEVQMGRKDSITASKAGA-N-N-N-I
MtPrx86 96 -SLR--GFEVVDQIKAAVEKA--CKRF--IVSCADILATAARDSV--AILGG--HKYWYQVLLGRRDSRFASRDAA-N-I-N-L
MtPrx87 101 -SLR--GFEVINEAKAQIDAA--CPK--TVSCADILATAARDASARKVSGGRID--YSVPSGRRDGRVSIFDEV-T-Q-N-L
MtPrx88 92 -TVR--GYNLIDEIKRILENA--CPS--TVSCADIIISLATRDSV--VLAGG--PS--YNVPTGRRDGLVSTVNDV---H--L
MtPrx89 90 -SVR--GYDLIDDVKEAEBA--CPS--TVSCADIVALATRDAV--ALSGG--PK--YNIPTGRRDGLIANRDDV---D--L
MtPrx90 97 -SLR--GFEVIDKIKYLLBKE--CPL--TVSCADILAMVARDAV--ELRGG--FR--WEVWLGRKDSLESSFSGA-N-L-F-I
MtPrx91 94 -LSG--IGFEVTRAKNMLE--CPG--VVSCADILAAARDIV--VSVGG--PF--YETLLGRRDSLESKSIDA-E-N-K-Y
MtPrx92 96 -SH--AFETIDNAKKALEBA--CPG--VVSCADILAAARDAV--FLSGG--PS--WDIPKGRKDGRIKASET-I-Q--L
MtPrx93 100 -AIR--NRETIINDIKSVLEEE--CPG--QVSCADIVLAARKVSV--SLSGG--PS--IQVPEGRKDSRTSSSKEA-D-A-K-L
MtPrx94 111 -SLR--SFEVVEVKEALEKA--CPG--VVSCADIIIMASRDV--ALTGG--ED--WEVRLGRDLSLTASQEDS-D-N-I-M
MtPrx95 99 -SLR--SFEVVEVKEALEKA--CPG--VVSCADIIIMASRDV--ALTGG--ED--WEVRLGRDLSLTASQDNS-S-N-I-M
MtPrx97 96 -SFR--GFEVIDIKTSVEAS--CNA--TVSCADILALAARDGV--FLGG--PT--WVPLGRRDARTASQSAA-N-S-Q-I
MtPrx98 99 -SFR--GFDVIDNIKTAVENV--CPG--VVSCADILATAARDSV--AILGG--ET--WNVKLGRRDAKTASQSAA-N-T-A-I
consensus 321 sir gfevid ik ve Cp vvSCaDilalaardsv l gg p w vplGRrDa a s a n l

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MtPrx01 169 PSETFNFSQLISNFKSQGLNVKDLVALSGGHTIGFARCTTFERNRIY---N-----E-TNIDPIFAASLRK--TC
 MtPrx02 165 PPEFFNFSQLITNFKSHGINLKDVLVLSGGHTIGFSKCTNFRDRIF---N-----D-TNIDTNFAANLQK--TC
 MtPrx03 167 PSQLFNLSQLVSNFESQGLNLKDLVALSGAHTIGMAKCTSTERERIY---N-----D-TNIDPDFATCLOD--NC
 MtPrx04 159 PAEFHNTQLRQIEANKKLLHLHDLVLSGAHTIGVGHGCHLFSNRLE---NFTGKGD---QD-PSLNPTYANFLKT--KC
 MtPrx05 185 PAEFSNETTLQTLFANQGLDMKDLVLSGAHTIGISLCTSFNSRNL---NFTGKGD---QD-PSLDSEYAKNLKTF--KC
 MtPrx06 159 PAEGDSVDEQKQKFAKGLNTQDLVILVGGHTIGTTACQFFSNRLR---NFTTNGA---AD-PSIDPSFLSQLQT--LC
 MtPrx07 163 PPETFNVNCLTQLFAKGLTQDEMVLVLSGAHTIGRSHCSAFSKRLY---NFSSTSI---QD-PSLDPSYAALLKR--CC
 MtPrx08 158 PAETFNLSQLQQSFSQRALSVEDLVALSGGHTLGFSSHCSFQNRILQ---NFNATHD---VD-PSLHQSFAAKLKS--IC
 MtPrx09 163 PSEFDFLDITVSKFTNVGLNLTQVLSLGAHTIGRARCALFSNRLE---NFSGTGS---PD-STLETGMLTDLQN--LC
 MtPrx10 166 PAEFNSLDQLKSAFAAAGLSTDLVALSGAHTIGRARCFTFITDRLY---NFSSTGK---PD-PTLNTTYLQELRK--IC
 MtPrx100 182 PMGHENITSLIEYFQSKGLNVLDLVLVLSGAHTIGRTSCGSIQYRLY---NYKGTGK---PD-PSLDTKYLNFLQR--KC
 MtPrx107 158 VDTSFMDKEMKLFSSKGLSLLDLVLVLSGAHTIGTAHCNTERGRFQ---Q-DRNGSLRLID-QTIDTNYADQLIK--CC
 MtPrx11 166 PAEFNTTDQLKAFAAAGLDTTDLVALSGAHTIGRAHCSLFFVSRLY---NFNGTGS---PD-PTINTTYLQQLRT--IC
 MtPrx110 162 PLFTDITTLISHEFSKKNLSPKEMVTLVLSGAHTIGCAQCFTFRGRIY---N-----NASDIDAGFASTRQR--GC
 MtPrx111 161 PAEFFTLDQLKAFELVQGLNNTDLVLSGAHTIGRAKCTEINRLY---NFNSTGN---PD-QTINTTYLQTLRE--IC
 MtPrx114 158 VDTSFMDKEMKLFSSKGLSLLDLVLVLSGAHTIGTAHCNTERGRFQ---Q-DRNGSLRLID-QTIDTNYADQLIK--CC
 MtPrx116 149 PPETFVVKVLSQFFMTKGIITEEMVALGAXTIGVAHCGFFSNRLS---SSGK-----PD-PTMDPTLDAKLVK--LC
 MtPrx12 177 PAEFNSLDQLKAFASQGLSTDLVALSGAHTIGRAHCSLFFVSRLY---NFSNTGS---PD-PTLNATYLOQLRN--IC
 MtPrx13 162 PAFTLVGQLIQSFAKGLGVKDMVLSGGHTLGFSSHCSFEARLH---NFSSVHD---TD-PRLNTEFALDLKN--KC
 MtPrx14 161 PGPHFNINQLNMFNLHGLSQTDMVALSGAHTIGFSHCNRFNSRRIY---GFSRPSR---ID-PSLNLOYAFQLRQ--MC
 MtPrx15 166 PSEAFNLTQLKSNFDNQGLDATDLVALSGAHTIGRGCCRFFVDRLY---NFSNTGN---PD-PTLNTTYLQTLRT--IC
 MtPrx16 166 PGFSSLDQLKSSFAAAGLNTVDLVALSGAHTIGRARCFLFILDRLY---DFDNTGK---PD-PTLDPTYLKLQK--CC
 MtPrx17 166 PGENFSLDRLKSAFAAAGLNTVDLVALSGAHTIGRARCFLFILDRLY---NFNNTGK---PD-PTLDTTYLQQLRN--CC
 MtPrx18 173 PQGHENITGLIGFQERGLDMLDLVLSGSHHTIGRSTCYVMNRIY---NFNGTGM---PD-PSINIYYLKMIRK--FC
 MtPrx19 173 PSESFNASELITQEGQHGEAQMVALSGAHTLGVARCSSEKNRIS---Q-----VD-PALDTEFARTLSR--TC
 MtPrx20 165 PAEFNTLVQLKAFETAAGLNTTDLVALSGAHTIGRAHCAQFVGRLY---NFSSTGS---PD-PTINTTYLQQLRT--IC
 MtPrx21 157 PDVNDSTIQQLKTKFELNKGLEKDLVLSAHTIGTTACFFMRKRLY---EFFPFG---SD-PTINLNFPELKA--RC
 MtPrx22 168 PAETSSLNCLISRFNALGLSTKDLVALSGGHTIGCARCTTFRAHIY---N-----D-SNIDTSFARTRQS--GC
 MtPrx23 207 PNFETSLANVTAKFAAVGLNTSDLVALSGAHTIGRGCCRFFNQRLY---NFSGTGK---PD-PTLNSTYLATLQ--NC
 MtPrx24 183 PSEFLNLSGLIAAFKKGESADEMVALSGAHTIGKAKCAVFKNRRIY---N-----E-SNINPYRSLQN--TC
 MtPrx25 167 PAFNNTFQTLITKFKLQGLDIVDLVALSGSHTIGKSRCTSFQRRLY---NOTGNGK---QD-FTLDQYYAAELRT--CC
 MtPrx26 166 PAETFNLTQLKSSFDNQNLTTDLVALSGGHTIGRGCCRFFVDRLY---NFSNTGN---PD-STLNTTYLQTLQA--IC
 MtPrx27 164 PSEFDSLDTLISKFDNVGLSVKDVVTLVLSGAHTIGRARCFFSNRLE---NFSGTQE---PD-NSLEYEMLTELQN--LC
 MtPrx28 162 PGESSILSTLITMERNKGLILNDITVLVLSGAHTIGCAEQCFERTRIY---N-----E-TNIDTNFATLRKS--NC
 MtPrx29 168 PPEFSTLNNLINREKAQGLSTKDMVALSGAHTIGRARCFTVYRRIY---N-----D-TNIDSLFAKSRQR--NC
 MtPrx30 162 PGFSTLDQLKASELVQGLNNTDLVLSGAHTIGRARCFAFINRLY---NFSGTGN---PD-PTINTTYLQTLRL--IC

MtPrx32 183 PSFFLLDGLTAAPFKKGGTAEMVALSGAHTIGKAKGLIRNRIY---N-----E-SMIDPNVAKSLQAFLEC
 MtPrx33 161 PGGSDLSGLINAFNNKGGTPKEMVALSGSHTIGEASCRFFRTRIY---N-----E-NNIDSSFANSLQS--SC
 MtPrx34 163 PAFFLNLSALKTNFANQGLSAKDLVALSGAHTIGLARCVCQFRAHIY---N-----D-SIVDSLFRKSLQN--KC
 MtPrx35 167 PGERFILDDELKTSFLNQGLDITDLVALSGAHTIGRGVCLLFNDRMY---NFNNTGV---PD-PTINTTLLQSLQA--IC
 MtPrx36 157 PGGSDLSGLITSEFNKGGTPKEMVALSGSHTIGCASCRFFRTRIY---N-----D-DNIDSSFATSLQA--NC
 MtPrx37 163 PAFFFLNLSLTKTNFANQGLSVDLVALSGAHTIGLARCVCQFRAHIY---N-----D-SIVDPLFRKSLQN--KC
 MtPrx38 167 PQESFNLNQLNTLFFANGLTQTDMIALSGAHTLGFSHCDRFSNRI-----QTP---VD-PTLNKQYAAQLQQ--MC
 MtPrx39 163 PAFFFLNDGLITAFKAKGGTAEMVTLSGAHTIGLVRCRFRFRARIY---N-----E-TNIDPAFAAKMQA--EC
 MtPrx40 170 PTFDESLSVLIIPKFQGLSVTDMVSLVGSHTIGMARCONFRSRIY---DYESTSV---K-NPISDNQFNMLKS--IC
 MtPrx41 162 PKFTFNLNQLNTIFSKHGLSEKDMIALSGAHTVGFSHCDQFTNRLY-----SSQ---VD-PTIDPTVAQQLMS--GC
 MtPrx42 167 PEGFNLNQLNTLFFKHGGLTQTEMIALSGAHTVGFSHCNKFTNRVY---NFKTTSR---VD-PTLDLKYAAQLKS--MC
 MtPrx43 162 PSPASDLSLTKMFKQKGLTLRDLTVLVALSGAHTIGCAEQCFRNRRIY---N-----E-TNIDTNFATLRKA--NC
 MtPrx44 163 PGGSSDLSLTKRMFKQKSLTLNDLTVLVALSGAHTIGQTECQFRNRRIH---N-----E-ANIDRNLATLRKR--NC
 MtPrx45 183 PBNATIEGLITFEKQGLDEVDLVALSGAHTIGVAKCATFKQRLY---NQNGNNQ---PD-SNLEKTFYFGLKS--MC
 MtPrx46 167 PBNNTFQTLITKEKLGKLNIVDLVALSGSHTIGDSRCTSFRORLY---NQTGNK---SD-FTLDQNYAAQLRT--FC
 MtPrx47 168 PDHNEISAVLDKFGAMGIDTPGVVALLGAHSVGRTHCTKLVHRLY-----PEV-----D-PANPEHIPHMLK--KC
 MtPrx48 176 PQEFNKTDVTLKVEAAQNFVDVVALSGAHTIGRAHCGTFFNRLS---P-----AD-PTLDKTLAQNLEKN--TC
 MtPrx49 166 PGPAFSLSQLIKNFQDQGLNEKDLVALSGAHTIGFSRCFLFRDRIY---K-----D-NNINAYFAKQLQN--VC
 MtPrx50 169 PSFFLNADQLIANFAQKGLSIDEMVTLSGAHSIGVSHCSSFSNRLY---SFDTIS---QD-PSMDPSFAESLKT--KC
 MtPrx52 163 PSFFFELENITAKFISKGLEKKDVAVLVALSGAHTIGFAQCFTFKPRLF---DFGGSGK---SD-PSLDSLLQNLQK--VC
 MtPrx53 163 PAFFHNLTVLITLFGNVGLDANDLVLLSGAHTIGVSHCSTISTRLY---NFTGKGD---QD-PDLIDNEYAKNLTFT--KC
 MtPrx54 165 PRPTSNINILTSMPKKNVGLSTKDLVALSGAHTIGCARCTTFRVRRIY---N-----E-TNIDTSFASTRQS--NC
 MtPrx55 159 PABTFNLSQLQOSFSQKGLSLQDLVALSGGHTLGFACSSSQNRRIH---KFSPKQA---VD-PSLNPSFASNLQS--KC
 MtPrx56 163 PNHNDISSVLISSFOAIGIDVEATVALLGAHSVGRVHGMNVLVHRLY-----PTV-----D-PTLDPTHAAYLKR--FC
 MtPrx57 162 PSFFSILSLTTFMSAKGLTASDLTVLVALSGAHTIGQGEQCFRNRRIY---N-----E-TNIDTNFATLRKS--NC
 MtPrx58 163 PSFFFELENITAKFISKGLEKKDVAVLVALSGAHTIGFAQCFTFKPRLF---DFGGSGK---SD-PSLDSLLQNLQK--VC
 MtPrx60 168 PSFESISWQESLAYFKSKGLNVLDMTILLGAHTLGGTHCSYIVDRLY---NYNGTGN---SD-PSMDATFRDILRG--IC
 MtPrx61 168 PAFSLNDGLIATFARKNFTALEMVTLVALSGAHTIGLACTSFRGRRIY---N-----E-TNIDPSFAESKRL--IC
 MtPrx63 162 PRPSFNTRLTTFMLAKGLTASDLTVLVALSGAHTIGQGEQCFRNRRIY---N-----E-TNIDTNFATLRKS--NC
 MtPrx64 213 PSFYALLTQTRASFKSRGFDEREMVTLGAHSIGVIFCKFFENCY---NFSGTNE---PD-PSLDTQFLNVLRS--KC
 MtPrx65 169 PPTFSAEQLIDNFDKGLSVDVEMVTLGAHSIGVSHCSSFSKRLY---SFNLTFP---QD-PSMDPNFARILKS--KC
 MtPrx66 153 PSLEFVSVHRQKFAAKGLNDHDLVTLGAHTIGQTIICRFFSYRLY---NFTTTGN---AD-PTINQAFLAQLKA--IC
 MtPrx67 161 PKFTDILLTTLIAHFTNKGLTLKDMVTLVALSGAHTIGCAQCFTFRDRIY---N-----NASIDAGFASTRRR--GC
 MtPrx70 165 PEEFFNLSQLITNEKSHGLNLKDLVVLVSGGHTIGFSKCTNFRNRRIY---N-----D-TNIDTNFANLQK--TC
 MtPrx71 166 PAFFFLNLSLTKSSFAAQGLNTVDLVALSGAHTIGRARCSSLFVDRLY---NFSNTGE---PD-PTLDITVLLKQLQN--EC
 MtPrx74 182 PRANSTVDELKIFENSKGLTIQDMVALSGAHTIGFAHCKNFLTRLY---NYRGKQ---PD-PDNPKLLKALRM--YC


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MtPrx75 173 EVEFARTIDELLTVEGSKKFDATDVVALSGAHTFGCAHCPTMFNRVI--D-----SD-EPTEPNFKKQLEA--TC
MtPrx76 161 ELFTDDLTTLISHFNKKNLTPRDMVTLGSAHTIGCAQCFTFRGRIY---N-----NASDI DAGFANTRQR--GC
MtPrx78 155 PGFFSNVSOALNFFTSKGLTLEDMVTLGSAHTIGFAKCIFFQSRIS---SFNGN----ID-PTMDPNLDAFIVE--KC
MtPrx79 173 PKPSMTMTQIVSIFTKRGETVEEMVALSGAHTVGFSSHCEISSDIY---N--NSSG---SG-SGYNPRFVEGLKK--AC
MtPrx81 166 PGPAFSLSQLIKNFDNKGINEKDLVALSGAHTIGFSRCLLFRDRIY---N-----D-KNIDANFAKQLQD--IC
MtPrx82 195 BRDDNITRTLHLFNLRGFKARETVSLLGEHNIGKIGCDFIQORLY---DFQGTGQ---PD-PSIPLIFLSQMRQ--NC
MtPrx83 212 EPMNWPMEKMDLFTKKGFTEEMVILLGAHSIGVAHCDVFMERTY---NYADTRK---PD-PLPFPPIVNEIQQ--IC
MtPrx84 165 EAPTSLNLTLSMFSAVGLSSKDLVTLGSAHTIGCARCTNFRARIY---N-----E-TNINAFASTRQS--NC
MtPrx85 175 PGENSTVDMLVAKFENVGLTLQDMVALSGAHTIGKARCSTFSSRLR---SNSVS---DG-PYVNAEFVSSLKR--IC
MtPrx86 165 EPAFFNFSQLIANFQSQGLNLKDLVWLSGGHTIGFSRCTNFRSRIY---N-----D-TNINTNFAANLQK--TC
MtPrx87 169 EPFTFSAEQLIDNEDRKGLSVDEMVTLSGAHSIGVSHCSSEFSKRLY---SFNATFP---QD-PSMDPDPARLLRS--KC
MtPrx88 156 PGPESSTISQTLQAFKSKGMTLEEMVTLLGAHTVGFVAHCSFIGKRL-----GS---ND-SSMDPNLRKRLVQ--WC
MtPrx89 154 PGNIPIGALSQFFAAKGITTEEMVTLLGAHTVGVVAHCGFFASRLS---SVRGK----PD-PTMDPALDTKLVK--IC
MtPrx90 163 EAPNSSLETLINNFKQQGLDIEDLVVLSGSHITIGPARCLSFQRRIYETKOEYHHAYD---R-YKRYTTERRILQS--IC
MtPrx91 161 ELPTMTNSQVIDIFTSKGETVQEMVALGSAHTIGFSHCKQFSNRLE---NFSKTTE---TD-EKYNPEYAAGLKK--IC
MtPrx92 161 ESESFNISQLQKSEFSQRGLSMEDLVALSGGHTLGFSSHCSSEFRNRH---NFDATHD---VD-PSINPSFASKLKS--IC
MtPrx93 166 ESPTVTVDEEFLSIFKSKGMNIQESVAIILGAHTLGVGHCLSIVGRLY---N-QNQQI-----G-NMNLGNETSLRL--AC
MtPrx94 177 ESFRANASTLIDLQRFNLTVKDLVALSGSHSIGQGRCFSIMFRLY---NQSGSGK---PD-PALDPAFRLELDK--IC
MtPrx95 165 ESFRTNATALITLFQKYNLSVKDLVALSGSHSIGKARCFSIMFRLY---NQSGSGK---PD-PAIDHVFRAELDK--IC
MtPrx97 162 ESFFSDLSTLTKMFTDKGLTASDLTVLGAHTIGQGECCQFFRNRIY---N-----E-TNIDTNFATLRKL--NC
MtPrx98 165 EAPTSLNLTLSMFSAVGLSSKDLVTLGSAHTIGCARCTTFRARIY---N-----E-TNIDTSFASTRQS--NC
consensus 401 p p l li F hglT dlvalsgahtiG arC f rly n d psid fa l C

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MtPrx01	232	-PR-N--G--G-----DNN--ITFL-----DF-T--P-TRVENTYYRLL
MtPrx02	228	-PK-I--G--G-----DDN--LAPF-----DS-T--P-NKVDTSYYKALL
MtPrx03	230	-PL-H--G--G-----DDN--FEAL-----DFLT--P-QVFDNSYYKNLV
MtPrx04	229	-QG-L--S--D-----TTT--TVEM-----DPNS--S-TTFDNDYYPVLL
MtPrx05	256	-KN-I--N--D-----NTT--IVEL-----DPGS--R-NTFDLGYYSOVV
MtPrx06	229	-PQ----N--S-----GAT-N-RIAL-----DTGS--Q-NKFDNSYYANIR
MtPrx07	233	-PQ-G--N--T-----NQN--L-VVPM-----DPSS--P-GTADVGYNDIIL
MtPrx08	228	-PL-K--N--K-----AKN--AGTT-----MDPS--A-TNFDNTYYKLL
MtPrx09	233	-PQ-T--G--D-----GNT--TAVL-----DRNS--T-DLFDNHYYKNLL
MtPrx10	236	-PN-G--G--P-----PNN--LANF-----DPTT--P-DKFDKNYYSNLQ
MtPrx100	252	-RW-----S-----AS-E-YVDL-----DATT--P-KKFDRMYYINLE
MtPrx107	230	-PI----N--A-----QPS-V-AVNI-----DPET--S-MLFDNQYYRNLL
MtPrx11	236	-PN-G--G--P-----GTN--ITNF-----DPTT--P-DKFDKNYYSNLQ
MtPrx110	226	-PS-S--S-TTSN-----DQK--LAAL-----DLVT--P-NSFDNMYFKNLI
MtPrx111	231	-PQ-N--G--T-----GNN--ITNL-----DLTT--P-NQFDNKIFYSNLQ
MtPrx114	230	-PI----N--A-----QPS-V-AVNI-----DPET--S-MLFDNQYYRNLL
MtPrx116	217	-K-----S--N-----VDG--ATEL-----DQNT--S-FVIDQEIYKQIL
MtPrx12	247	-PN-G--G--P-----GTP--IASF-----DPTT--P-DKFDKNYYSNLQ
MtPrx13	232	-PK-P--N--N-----NQN--AGQF-----LDST--A-SVFDNDYYKQLL
MtPrx14	231	-PI----R--V-----DPR-I-AINM-----DPVS--P-QKFDNQYFKNLI
MtPrx15	236	-PN-G--G--P-----GST--ITDL-----DPAT--P-DTFDSAYYSNLR
MtPrx16	236	-PQ-N--G--P-----GNN--VVNF-----DPTT--P-DKFDKNYYSNLQ
MtPrx17	236	-PQ-N--G--T-----GNN--RVNF-----DPTT--P-DTLDKNEYYNLI
MtPrx18	243	-KK-----S-----DL-D--IVHL-----DVIT--P-RTFDITYYTNLK
MtPrx19	237	-----T--S-----GDN--AEQP-----FDAT--R-NDFDNVYFNALL
MtPrx20	235	-PN-G--G--P-----GTN--ITNF-----DPTT--P-DKFDKNYYSNLQ
MtPrx21	226	-PK----D--G-----DVN--I-RLAM-----DEGS--D-LKFDKSIKKNIR
MtPrx22	231	-PK-T--SGS-G-----DNN--LAPL-----DLAT--P-TSFDNHYYFKNLV
MtPrx23	277	-PQ-N--G--S-----GNT--LNNL-----DPSS--P-NNFDNMYFKNLL
MtPrx24	246	-PR-N--G--G-----DNN--LANL-----DSTT--P-AFFDSAYYRNLL
MtPrx25	237	-PR-S--G--G-----DQN--LFFL-----DYVT--P-TKFDNMYFKNLL
MtPrx26	236	-PN-G--G--P-----GTN--ITDL-----DPTT--P-DTFDSNYYSNLQ
MtPrx27	234	-PQ-D--G--D-----GNT--TTVL-----DPYS--F-DFDNNYYFKNLL
MtPrx28	225	-PT-S--G--G-----DIN--LAPL-----DSVS--P-VTFDNNYYNLI
MtPrx29	231	-PR-K--SGTIK-----DNN--VAVL-----DFKT--P-NHFDNLYYKNLI
MtPrx30	232	-PQ-N--S--T-----GNN--LANL-----DLTT--P-NHFDKNYYSNLQ

MtPrx32	248	-PK-S--G--G-----DNN--LASF-----DATI--P-NFFDNAYYRNLL
MtPrx33	224	-PR-T--G--G-----DLN--LSPL-----DTTS--P-NTFDNAYFKNLQ
MtPrx34	226	-PR-S--G--N-----DNV--LEPL-----DHQT--P-THFDNLYFKNLL
MtPrx35	237	-PDIG--V--L-----GTN--LTNL-----DVST--P-DTFDSNYYSNLQ
MtPrx36	220	-PT-T--G--G-----DDN--LSPL-----DTTT--P-NTFDNSYFQNLQ
MtPrx37	226	-PR-S--G--N-----DNV--LEPF-----DYQT--P-THFDNLYFKNLL
MtPrx38	232	-PR----N--V-----DPR-I-AINM-----DPTT--P-RTFDNVYYKNLQ
MtPrx39	226	-PF-E--G--G-----DDN--FSPF-----DSSKPEA-HDFDNGYYQNLV
MtPrx40	240	-PPI-G--G--G-----DNN--ITAM-----DYVT--P-NLFDNSFYQILL
MtPrx41	228	-PR----N--V-----DFN-I-VLAL-----DTQT--E-HTFDNLYYKRLV
MtPrx42	237	-PR----N--V-----DPR-V-AVDM-----DPVT--P-HAFDNVYFKNLQ
MtPrx43	225	-PL-S--G--G-----DTN--LAPL-----DSVS--P-VTFDNNYYRLLV
MtPrx44	226	-PT-S--G--G-----DTN--LAPF-----DSVT--P-TKFDNYYKILLI
MtPrx45	253	-PR-S--G--G-----DNI--ISPL-----DFGS--P-RMFDNTYYKILL
MtPrx46	237	-PR-S--G--G-----DQN--LFVL-----DFVT--P-VKFDNYYKNLL
MtPrx47	233	-PD-S--I--P-----DPKAVQYVRN-----DRGT--P-MILDNNYYRNIL
MtPrx48	240	-PN----A--N-----SGN--TANL-----DIRT--P-ATFDNKYYLILM
MtPrx49	229	-PR-E--G--G-----DSN--LAPL-----DSVT--S-AKFDVAYYSQLI
MtPrx50	239	-PP-P--P--S-----NTN-P-IVML-----DVAT--P-NRLDNLYYEGLI
MtPrx52	233	-PNQA--D--S-----DSN--LAPL-----DPVT--T-NTFDNTYYKRVL
MtPrx53	234	-KN-I--N--D-----QTT--LIEM-----DPGS--R-NTFDLGYFKQVV
MtPrx54	228	-PK-T--SGS-G-----DNN--LAPL-----DLHT--E-TSFDNCYYRNLV
MtPrx55	229	-HI-K--N--K-----VKN--SGSP-----LDST--A-TYFDNAYYKILL
MtPrx56	228	-PT-P--N--P-----DPKAVQYVRN-----DLKT--E-MIIDNNYYKNIL
MtPrx57	225	-PL-S--G--G-----DTN--LAPL-----DTLT--E-TSFDNYYKNLV
MtPrx58	233	-PNQA--D--S-----DTN--LAPL-----DPVT--S-NTFDNTYYRNVL
MtPrx60	238	-PPRTKKGQ--S-----DPL-V-YLNP-----DSGK--N-YIFRESYYKRIL
MtPrx61	231	-PF-N--G--G-----DNN--ISTL-----SNS--S-INFNTYYNILLV
MtPrx63	225	-SF-S--S--DN-----DTN--LAPL-----DTLT--E-TSFDNYYKNLV
MtPrx64	283	-NE-T--D--A-----LST--SASA-----YSSHASPSLVEEQEITTDSGE--SLSNFGTLYYRILL
MtPrx65	239	-PP-P--Q--S-----QSIN-P-TVVL-----DGST--P-NDLDNMYRRLK
MtPrx66	223	-PK----N--G-----DGL-R-RVAL-----DKDS--P-AKFDVSEFFKNVR
MtPrx67	225	-PS-L--SSTN-----NOK--LAAL-----DLVT--P-NSFDNYYFKNLI
MtPrx70	228	-PK-I--G--G-----DDN--LAPF-----DS--T--P-SRVDTKYYKILL
MtPrx71	236	-PQ-N--G--P-----GNN--RVNF-----DPTT--P-DTLDKNEYNNLQ
MtPrx74	252	-PN-F--G--G-----NTD-I-VAPF-----DATI--P-FIFDHAYYGNLQ

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MtPrx75 237 -PN-----E--E-----SLN--AVNL-----DVRT--P-NTFDNMYYNLL
MtPrx76 225 -PS-S---RTTSN-----DQK--LAAL-----DLVT--P-NSFDNMYFKNLI
MtPrx78 223 -GS-----R--G-----NET--SVFL-----DQKT--P-FDFDNEEYFNQIV
MtPrx79 241 -GD-Y--K--K-----NPT-L-SVFN-----DIMT--P-NKFDNVYEQNLP
MtPrx81 229 -PR-E--G--G-----DSN--LAAL-----DCVT--P-AKFDEAYYMELI
MtPrx82 265 -ED-N--N--K-----NNV--SSNGMFSTFTVSKPMNVHHSSNNKGMSYKQALSSAVSS--G-ASFDTHYQQLL
MtPrx83 282 -AN-P--G--T--PLF--RNP--VVNF-----DET--P-ALLDNLFFKNMV
MtPrx84 228 -PK-A--SGS-G--DNN--LAPL-----DLQT--P-SSFDNMYFKNLV
MtPrx85 243 -SG-Q--D--N-----SNR--IAHL-----DLVT--P-ATFDNQYYNLL
MtPrx86 228 -PR-I--G--G-----DDN--LAPF-----DS--P-SRVDTKYYKALL
MtPrx87 239 -EP-P--Q--SQSQSQIQNLD-S-TVAF-----DGST--P-NDLDNMYYKELK
MtPrx88 220 -GV----E--G--KDP--LVFL-----DQNT--S-FVFDHQFYNQIL
MtPrx89 222 -K-----S--N-----SDG--AAFL-----DQNT--S-FTVDNEEYKQIL
MtPrx90 236 -EV-T--G--R-----DDK--FAPL-----DFCT--P-KRFDNQYFNII
MtPrx91 231 -QN-Y--Q--K-----DTS-M-SAFN-----DVMT--P-SKFDNMYFKNIK
MtPrx92 231 -PI-I--N--Q-----VKN--AGTT-----LDAS--S-TTFDNTYYKILL
MtPrx93 234 -PT-V--I--P-----MTN-LTFVPN-----DM--P-TIFDNQYYRDIM
MtPrx94 247 -PL-D--V--D-----QNK--TGNL-----DST--P-VIFDNQYFRILV
MtPrx95 235 -PR-D--V--D-----QNK--TGNL-----DAT--P-VIFDNQYFRILV
MtPrx97 225 -PL-S--G--G-----DTN--LAPL-----DTLT--P-TNFDNMYYNLV
MtPrx98 228 -EN-T--SGS-G--DNN--LAPL-----DLQT--P-TSFDNMYFKNLV
consensus 481 p n 1 1 d t p fdn yyrnll

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MtPrx01 260 -YKRGVLSHSDQCLEF-K---GQ---GSESDKIVQIYSKNT-F-----AFASDFKTSLIKMGN-I-KPLTG-RQ-GEIRLNC
 MtPrx02 256 -YKRGVLSHSDQCLEF-K---GD---GSCSDRIVQIYSKNS-Y-----AFAYDFGVSMIKMGN-I-KPLTG-KK-GEIRCNC
 MtPrx03 259 -SKIGLIFHSDQCLEF-K---GD---GSESDMIVEIYSRDS-D-----AFARDFKASMIKMGN-I-KPLTG-NF-GEIRTYC
 MtPrx04 258 -QNKGLFSDAAILL-T---TK-Q---SRNIVNELVSON-----KFFTEFSQSMKRMGA-I-EVLTG-SN-GEIRKRC
 MtPrx05 285 -KRRGLFESDSALL-T---NS-V---TKALVTCQLQGSLE-----NFYAEFAKSTIEKMGQ-I-KVKTG-SQ-GVIRKHC
 MtPrx06 258 -NGRGLIQSDQALL-N---DA-S---TKTFVQPYLG-L-RGLLGLTENVEFCNSMVKMSN-I-GVKTG-VD-GEIRKIC
 MtPrx07 263 -ANRGLFSDQILL-T---NT-G---TARKVHQNARNP-Y-----LWSNKFATAMVKMGQ-V-GVLTG-NA-GEIRINC
 MtPrx08 257 -QQKGLFSDQALL-D---SP-K---TKQIVSKFASQ-K---AFFDAFAKSMIKMSS-I-N---G-GQ-EVRKIC
 MtPrx09 262 -NGKGLLSHQDILLI-S---TD-EANSTSKPLVQSINDNA-T-----LFFGDFVKSMIKMGN-I-NPKTG-SD-GEIRKSC
 MtPrx10 265 -GKKGLLSHQDILE-S---TS---GADTISIVNKFASADK-N-----AFEDSFEAMIKMGN-I-GVLTG-KK-GEIRKHC
 MtPrx100 278 -KKMGLLITDQILY-S---DP-R---TSQIVSALTT-----SS-VFHFQFAVSMKFGV-I-DVLTGDDE-GEIRINC
 MtPrx107 259 -DRKVLFEQSDSVLM-N---ND-D---TRKIVELFANDQ-E-----LFFDNWGVSEVKLIS-I-GVKTG-EE-GEIRKSC
 MtPrx11 265 -VRKGLLSHQDILE-S---TS---GSDTISIVNKFATDQ-K-----AFESFEKAMIKMGN-I-GVLTG-KQ-GEIRKOC
 MtPrx110 258 -QBKGLLSHQDILE-S-G-GS-----TNSFVSEYSNNP-T-----TEKSFATAMIKMGD-I-EHVTG-SA-GVIRKIC
 MtPrx111 260 -SHKGLLSHQDILE-S---TP---NADTIAIVNSESNNQ-A-----LFFENFRVSMIKMAN-I-SVLTG-NE-GEIRLQC
 MtPrx114 259 -DRKVLFEQSDSVLM-N---ND-D---TRKIVELFANDQ-E-----LFFDNWGVSEVKLIS-I-GVKTG-EE-GEIRKSC
 MtPrx116 244 -LKRGLIQIDQKLT-L---DK-S---TSLEFVSNFASNG-E-----KRVNMFATAMIKMGK-I-GLLIG-NE-GEVRKNC
 MtPrx12 276 -VRKGLLSHQDILE-S---TS---GADTISIVNMFATDQ-K-----AFESFEKAMIKMGN-I-GVLTG-NQ-GEIRKOC
 MtPrx13 261 -AGKGVFSDQSLV-G---DY-R---TRWVEAFARDQ-S-----LFFKFAASMIKMGN-I-R---G-SDN-GEVRLNC
 MtPrx14 260 -QGKGLFSDQVLE-T---DS-R---SKATVNLFASNP-K-----AFESAFINAITKIGR-V-GVKTG-NQ-GEIRKIC
 MtPrx15 265 -IQKGLFEQSDQVLS-S---TS---GADTIAIVNSESNNQ-T-----LFFEAFAKSMIKMSR-I-KVLTG-SQ-GEIRKOC
 MtPrx16 265 -GKKGLLSHQDILE-S---TP---GADTISIVNMFANNQ-N-----VFQNFINSMIKMGN-I-GVLTG-KK-GEIRKOC
 MtPrx17 265 -GKKGLLSHQDILE-S---TP---GADTISIVNMFANSQ-N-----VFQNFINSMIKMGN-I-DVLTG-KK-GEIRKOC
 MtPrx18 269 -RKAGLLSITDQILE-S---DK-R---TSPFVDIFAT-----QPFVFTSQFAVSMVKLGN-V-QVLTG-PNE-GEIRVNC
 MtPrx19 263 -RKNGLVLSHQDILY-S---SP-R---TRNIVNAYAMNQ-A-----MFLDFQCAMVKMGL-I-DIKQG-SN-GEVRSNC
 MtPrx20 264 -VRKGLLSHQDILE-S---TS---GADTISIVNKFESTDQ-N-----AFESFEKAMIKMGN-I-GVLTG-TK-GEIRKOC
 MtPrx21 255 -EGFAVLASDARLN-D---DF-V---TKSVIDSYFNPI-NPTFGPSEENDFVQSMVKMGQ-I-GVKTG-SV-GNIRRVIC
 MtPrx22 262 -DSKGLLSHQDILE-N-G-GS-----TDSIVHEYSLYP-S-----SFSDFVTAMIKMGD-I-SPLTG-SN-GEIRKOC
 MtPrx23 306 -KNGGLLQIDQELE-S---TN---GADTISIVNMFANSQ-T-----AFEEAFVQSMINMGN-I-SPLIG-SQ-GEIRKIC
 MtPrx24 275 -FKRGLLSHQDILE-N-G-GS-----TDYKVLAYARNP-Y-----LFRFDFAKAMIKMGN-I-SPLTG-NQ-GQIRKYC
 MtPrx25 266 -AYKGLLSDEILL-T---KN---QESAELVKLYAERN-D-----LFFEQFAKSMIKMGN-I-SPLTG-SR-GNIRKNC
 MtPrx26 265 -VGNGLFEQSDQELE-S---TN---GSDTISIVNMFANNQ-T-----LFFENFVSMIKMGN-I-GVLTG-SQ-GEIRKOC
 MtPrx27 263 -NGKGLLSHQDILE-S---SDEETTSTKQIVQYSENE-R-----IFRMBFAYAMIKMGN-I-NELTG-SE-GEIRKSC
 MtPrx28 254 -ANKGLLSHQDILE-N-GVGS-----QVSLVRYTSRNN-I-----AFKRFATAMVKMSR-I-SPLTG-TN-GEIRKNC
 MtPrx29 263 -NRKGLLSHQDILE-N-G-GS-----TDSIVKYSYNNQ-N-----AFESFATAMIKMGN-N-KPLTG-SN-GEIRKOC
 MtPrx30 261 -NLNGLLSHQDILL-S---TP---NADTIAIVNSESNNQ-S-----LFFLNFRVSMIKMAN-I-GVLTG-DE-GEIRLQC

MtPrx32 277 -NKGLLHSDQQLN-N-G-GS-----TDYKVSAYYNNP-L-----LFSIDFANAMIKMGN-I-SFLTG-DQ-GQIRKNC
 MtPrx33 253 -NQKGLFHSQVLE-D-E-VT-----TKSQVNSYVRNP-L-----SPKVIDFANAMEKMAN-I-GFLTG-SS-GQVRKNC
 MtPrx34 255 -ANKGLLHSDQCLE-N-G-SS-----TDNLVRKYITDN-A-----KFFKAFKAGMVKMSS-I-KFLTG-SN-GQIRKNC
 MtPrx35 267 -AGNGIFQSDQCLE-S---TP---GADTIAIVNSESSNQ-T-----LFFEFKASMIKMG-N-I-GVLTG-TQ-GEVRTHC
 MtPrx36 249 -SQKGLFSSDQALE-N-G-GS-----TDSIVDEYSSDS-S-----SEATIDFANAMVKMGN-I-NFLTG-SN-GQIRKNC
 MtPrx37 255 -AKKILLHSDHELE-NIG-SS-----TNNLVRKYATNN-A-----EFFKAFKAGMVKMSSS-I-KFLTG-SN-GQIRKNC
 MtPrx38 261 -QKGLFTSDQILE-T---DT-R---SRNTVNSFATNG-N-----VENANFITAMIKLGR-V-GVKNA-RN-GKIRKNC
 MtPrx39 257 -KSKGLIHSQCLEGN-G-TS-----TNAQVRPYSRNF-G-----RFKKIDFALAMEKMSM-L-SFLTG-TE-GEIRKNC
 MtPrx40 270 -KGEGLNSDQEMY-S---SV-F-GIEIRELVKKYADS-L-----AFFQCFSDSMVKMGN-I-TNSESFIT-GEVRKNC
 MtPrx41 257 -NGKGLSSDQVLE-T---DD-A---SRSTVVEFANDG-S-----KFFKAFVVAIKKIGR-V-GVKTG-KE-GEIRKNC
 MtPrx42 266 -KGKGLFTSDQVLE-T---DS-R---SKAAVNAFASSN-K-----IFHANFVAAMIKLGR-V-GVKNS-HN-GNIRKNC
 MtPrx43 254 -ANKGLLNSDQALE-N-GVGS-----PVSIVRAYSING-F-----AFRRDFAFAMVKMSR-I-SFLTG-TN-GEIRKNC
 MtPrx44 255 -ANKGLLHSDQVLE-N-GGGS-----QISLVRKYSRDG-A-----AFSRDFAAAMVKMSK-I-SFLTG-TN-GEIRKNC
 MtPrx45 282 -RGKGLLNSDEVLL-T---GS-V---KETRDLVKKYEQDE-S-----LFFQCFALSMIKIGN-I-RFLTG-FN-GEVRKNC
 MtPrx46 266 -ANKGLSSDEILL-T---KN---QVSADLVKKYAESN-D-----LFFEQFAKSMVKMGN-I-TFLTG-SR-GEIRKNC
 MtPrx47 265 -DNKGLLIVDHOLA-H---DK-R---TKPYVKKMAKSQ-E-----YFFKBFSPAITLLSE-N-NFLTG-TK-GEIRKNC
 MtPrx48 268 -NKQGLFTSDQDLN-I---DS-R---TKGLVNDFAVNO-G-----LFFKQFVNAEIKVSO-I-NVLVG-NQ-GEIRKNC
 MtPrx49 258 -KKKGLLHSDQELL-K---GG-----YTGALVRKYRRT-R-----TFYKIDFAKSMIKMGN-I-KFLTG-KQ-GEVRYNC
 MtPrx50 269 -NHRGLLTSQDILL-S---SQ-S---TQESVLSNANYG-S-----NWTAKFAQAMVHMGS-I-DVLSG-YD-GEIRKNC
 MtPrx52 263 -SNSGLLQSDQALL-G---DN-----TTSALVTNYSKWP-I-----LFFRDFAVSVEKMGR-I-GILAG-QQ-GQIRKNC
 MtPrx53 263 -KRRGLFQSDAALL-K---SS-T---TRSDLAQHLQSN-E-----KFFTEFGRSMEKMGR-I-NVKIG-TE-GEIRKNC
 MtPrx54 259 -QNKGLLHSDQCLE-N-G-GS-----TNSIVSGYFNNQ-N-----SFFSDFATAMIKMGD-I-KFLTG-SN-GEIRKNC
 MtPrx55 258 -QKGLLTVDEELA-T---HP-T---TKALVSKYAHSQ-M-----EFFERAFVKSMIKMSS-ITN---G-GK--QIRKNC
 MtPrx56 260 -QHKGLLTVDEELA-T---DP-R---TSPYVKKMADN-G-----YFNEQFSRAVQLLSE-N-NFLTG-DQ-GEIRKNC
 MtPrx57 254 -ASKGLFHSQALE-N-N-GS-----QDNIVRSYSTNG-A-----TFSRDFAVAMVKLSK-I-SFLTG-TN-GEIRKNC
 MtPrx58 263 -SNSGLLQSDQALL-G---DS-----TTASLVNYYSKWP-I-----LFFRDFAVSVEKMGR-I-GVLTG-QQ-GQIRKNC
 MtPrx60 272 -RNEAVLIGIDQALL-F---GD-D---TKELTEEFAGF-E-----DFRRSFAQSMKMG-N-I-KVLTG-NQ-GEIRKNC
 MtPrx61 259 -SKKGLLHSDQQLL-N-G-LS-----TSNOVIAYTIDN-E-----SEKRIDFANVMIKMGM-I-SFLTG-SD-GQIRKNC
 MtPrx63 255 -ASKGLFHSQVLE-N-N-GS-----QDNIVRSYSTNE-A-----AFSTIDFAAMVKLSK-I-SFLTG-TN-GEIRKNC
 MtPrx64 332 -QKGLIYEDQQLM-E---GE-K---TRYWVQ-YASNR-T-----LFHQDFALAMKLSD-I-RVLTG-PM-GQIRKNC
 MtPrx65 270 -NHRGLLTSQDILL-N---SG-L---TRRVVLKNARHA-A-----LWNVKFAKAMVHMGS-I-DVLTG-SE-GEIRKNC
 MtPrx66 252 -DGNGLLESQRLW-E---DS-A---TRRVVENYGGNF-RGLLGLRDFEFKAMIKLSS-V-DVKTG-ID-GEIRKNC
 MtPrx67 257 -QNKGLLQSDQVLE-G-GGGS-----TDSIVSEYSKNP-T-----TFKSIDFAAMIKMGD-I-QFLTG-SA-GIIRKNC
 MtPrx70 256 -NKQGLLHSDQCLE-K---GD---GSDRIVQILYSKNS-Y-----AFAYDFGVSMIKMGN-I-KFLTG-KK-GEIRKNC
 MtPrx71 265 -VKKGLLQSDQCLE-S---TP---NADTTSIVNPFANNO-S-----AFFESFKKAMIKMGN-I-GVLTG-KK-GEIRKNC
 MtPrx74 282 -NKMGLLASDQALA-L---DP-R---TKSLVQDFAKDK-Q-----KFFQAFASAMDKMSL-V-KVVRG-KKHGEIRKNC


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MtPrx75 265 -NHQGVFTSDQDLA-S---HP-K---TKETVNLFASNQ-K----EFFNKFANAFVKVVSQ-I-DVLTG-NQ-GEIRKSC
MtPrx76 257 -QKKGLLQSDQVLE-S-G-GS----TDSIVSEYSNNP-T----TFKSDFAAAMIKMGD-I-EPLTG-SA-GIIRSIC
MtPrx78 251 -NKRGILOIDQOLA-L---DP-I---SNVLVWVFASGN-F----NFWERFGVSWSKLAN-L-DVKVG-NQ-GEIRRNC
MtPrx79 271 -KGLGVLKSDHGLE-S---DP-S---TKPFVERFAKDQ-D----YFFKVFASSMQKLSL-I-NVQTG-RK-GEIRFEC
MtPrx81 258 -KKKGLLHSDQELL-N---GD----YTGSIVRKYRRDT-S----AFYNIFAKSMIKMGN-I-KPLTG-SQ-GEIRSNC
MtPrx82 323 -RGRGLLFADQQLM-A---EE-K---TAKLVSAYASDDGS----TFRMDFARVMMKLSN-I-DVLTG-NQ-GQVRLNC
MtPrx83 313 TKKKTLLVTD AHLF-N---DP-R---TIPIVEELAKDN-G----LFQKKFAEAMVKMGs-Y-NVITG-ND-GEVRKTC
MtPrx84 259 -QNKGLLHSDQCLE-N-G-GS----TNSIVSGYSTSP-S----SFSSDFAAAMIKMGN-I-KPLTG-SN-GEIRKNC
MtPrx85 272 -SGEGLLPSDQTLV-N---GN----DQTRQIVETIVANP-F----VFFDDFKNSMVKMGs-I-GTATQ-SI-GQIRRIC
MtPrx86 256 -HKKGLLHSDQELE-K---GD---GSQSDRLVQLYSKHS-H----AFAYDFGVSMIKMGN-I-KPLTG-KN-GEIRCNC
MtPrx87 277 -NNRGLLTSQILV-N---SG-L---TKRMVLKNARHA-A----IWNVKFAKAMVHMGN-I-DVLTG-SQ-GEIREYC
MtPrx88 248 -LGRGVLTIQNLA-L---DS-I---SKGVVTGFARNG-E----NFRERFVDVAVKLG-N-V-DVLVG-NQ-GEIRKNC
MtPrx89 249 -LKRGIHQIDQOLA-L---DK-S---TSTFVSNFASNG-D----KFVKSFAFAMIKMGK-V-GVLVG-NE-GEIRKNC
MtPrx90 265 -EGKGLLGSNDVLI-S---QD-L-DGRIRKQVWGYASNE-K----LFFDSFAKSMIKMGN-I-NVLTG-SE-GEIRRNC
MtPrx91 261 -RGMGLLATDSLME-E---DK-R---TKPFVDMYAENQ-T----KFFEDFGNAMPKLSV-I-HVKEG-KD-GEIRNEC
MtPrx92 260 -QRKGIFFSSQVLI-D---TP-Y---TKDLVSKFATSQ-D----EFYKAFVKSMVKMSS-I-N---G-GQ-EIRKIC
MtPrx93 264 -MGRGLLGIDSSIS-R---DP-R---TAPIVMRFAMDQ-S----YFFENFSSAFVKLSA-S-NVLTN-IQ-GEVRRKC
MtPrx94 275 -GGRGELNSDQTLF-T-Y-PQ-----TKGLVRFYSRDQ-S----EFFKAFVKGMKMGD-I-Q--SG-RP-GEVRRNC
MtPrx95 263 -GGRGELNSDQTLF-T-F-PQ-----TKGFVSLFSEDQ-S----EFFKAFVEGMLKLGD-I-Q--SD-KP-GEVRKNC
MtPrx97 254 -ASKGLFHSDQALE-N-N-GS----QDNLVRSYSTNG-A----TFRRFVAVAMVKLSK-I-NPLTG-TN-GEIRKNC
MtPrx98 259 -QNKGLLHSDQCLE-N-G-GS----TNSIVSGYSTNP-S----SFSSDFATAMIKMGD-I-SPLTG-SN-GEIRKNC
consensus 561  kgll sDq lf          t lv ya          ff fa amikmg i vltg  geiRrnC

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Figure S4. Alignment of *M. truncatula* class III peroxidases (partial sequences) showing in red the conserved residues described in [37]. The alignment was performed with Kalign and the conserved residues were shaded using BoxShade (see Materials and Methods section).

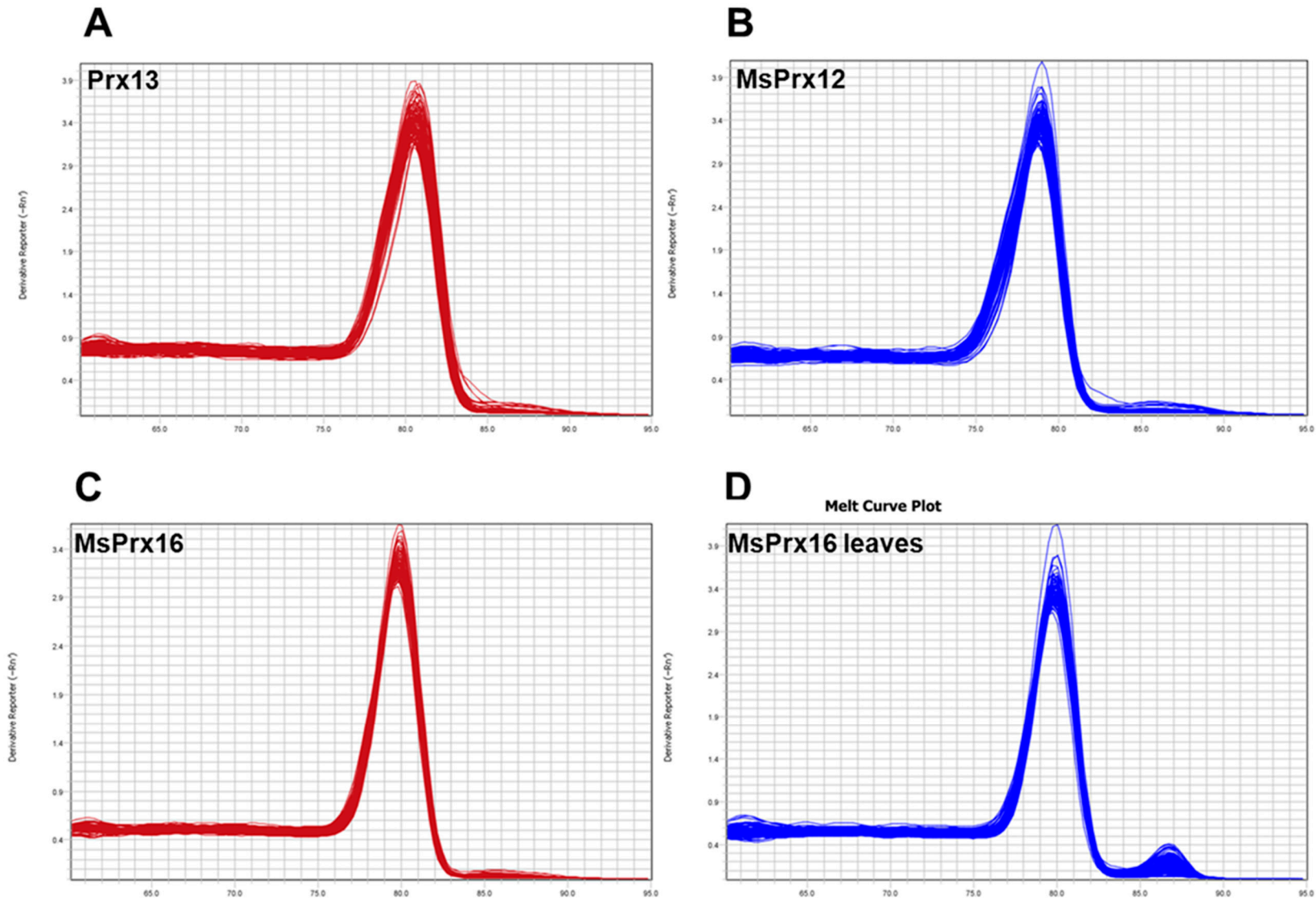


Figure S5. Melt curve analysis of the three class III peroxidases Prx 13 (A); MsPrx12 (B); MsPrx16 (C) in roots and stems of alfalfa; In (D) the melt curve analysis of MsPrx16 in alfalfa leaves shows two peaks, therefore the gene was not retained for study in these organs.

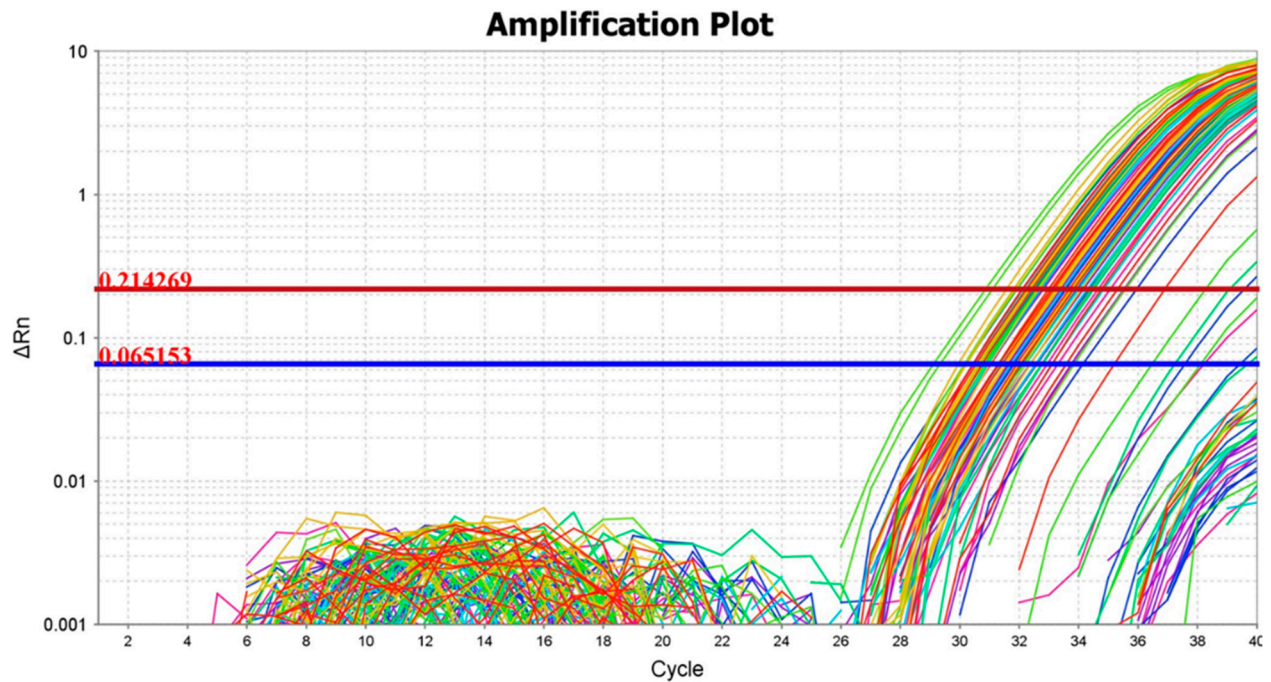


Figure S6. Amplification curves for Medtr4g078885.1 in alfalfa roots.

Table S1. Characteristics of putative dirigent/dirigent-like proteins from *M. truncatula*. Details concerning the gene accession, the protein length, the subfamily, the localization, the signal peptide (SP) length and the *N*-glycosylation sites are provided. The positions corresponding to putative *N*-glycosylation sites followed by a proline, which are very unlikely to be modified, are indicated in *italics*. “S” is secreted, “other” indicates a localization that is neither chloroplastic, nor mitochondrial, nor apoplastic (as computed by TargetP).

Gene Accession	Length	Subfamily	Location	SP (length)	<i>N</i> -Glycosylation
Medtr4g122130.1	180	f	S	28	6-33-174
Medtr4g122110.1	180	f	S	26	6-33-174
Medtr1g056370.1	186	e	S	20	88-169
Medtr7g093850.1	194	b/d	S	28	16
Medtr7g093820.1	194	b/d	S	28	16
Medtr3g034030.1	186	e	S	24	56-179
Medtr7g093830.1	193	b/d	S	27	15-132
Medtr7g093870.1	218	b/d	S	24	23-133
Medtr7g093790.1	191	b/d	S	25	130
Medtr4g049550.1	179	f	S	28	31-103
Medtr5g096120.1	189	b/d	S	22	54-64-129-172-183
Medtr3g105630.1	189	b/d	S	23	91-112
Medtr3g105640.1	188	b/d	S	23	65-90-111-182
Medtr7g070390.1	192	b/d	S	22	62-132
Medtr4g013770.1	192	b/d	S	23	2-59-94-131
Medtr7g021300.1	389	e	other	-	-
Medtr8g073770.1	190	-	S	26	52-90
Medtr8g073850.1	190	-	S	26	52-90

Table S1. *Cont.*

Gene Accession	Length	Subfamily	Location	SP (length)	N-Glycosylation
Medtr8g106405.1	170	a	other	-	39-68
Medtr8g099135.1	185	a	S	21	51-64-121
Medtr8g099115.1	189	a	S	21	68-143
Medtr8g106450.1	180	a	S	29	49-78
Medtr0433s0040.1	191	b/d	other	24	7-35-77
Medtr1g046500.1	250	e	S	26	51
Medtr1g054525.1	192	b/d	S	26	63-134-137
Medtr1g115510.1	353	e	S	32	8-58-97
Medtr1g115515.1	236	e	M	28	52
Medtr1g046800.1	250	e	S	26	51
Medtr4g013345.1	196	b/d	S	22	65-79-136
Medtr4g062520.1	303	e	S	32	94
Medtr4g062460.1	257	e	S	31	68-82-139
Medtr4g013310.1	197	b/d	S	23	68-82-139
Medtr4g013330.1	199	b/d	S	25	66-139
Medtr4g013350.1	197	b/d	S	23	66-80-137
Medtr4g073950.1	192	b/d	S	25	60-132-186
Medtr4g013355.1	180	b/d	S	22	24-42-72
Medtr4g013325.1	199	b/d	S	23	68-82-139
Medtr4g013335.1	196	b/d	S	22	67-136
Medtr4g062470.1	304	e	S	31	96
Medtr4g078885.1	186	e	S	24	179
Medtr4g074020.1	99	b/d	S	23	-
Medtr4g049570.1	178	f	S	26	30-47
Medtr1g046490.1	236	e	other	-	7-35-77
Medtr4g013320.1	199	b/d	S	22	68-82-139
Medtr4g013385.1	191	b/d	S	24	44-60-74-130

Table S2. Expression values \pm standard deviations relative to the heat map in Figure 2 and retrieved from the *Medicago* eFP browser.

Tissue	Medtr4g 122130.1	Medtr1g 056370.1	Medtr7g 093850.1	Medtr7g 093820.1	Medtr4g 078885.1	Medtr7g 093830.1	Medtr7g 093790.1	Medtr4g 049550.1	Medtr7g 070390.1	Medtr8g 073770.1	Medtr1g 046500.1	Medtr1g 054525.1	Medtr4g 062520.1	Medtr4g 013320.1	Medtr4g 013385.1	Medtr4g 073950.1
Root	457.1 \pm	841.34 \pm	2503.74 \pm	614.16 \pm	280.76 \pm	614.16 \pm	1068.5 \pm	8.39 \pm	243.23 \pm	157.59 \pm	968.42 \pm	791.6 \pm	3237.18 \pm	85.07 \pm	12734.9 \pm	3484.67
	52.16	142.83	469.78	192.12	41.02	192.12	63.19	9.64	43.96	12.9	51.19	31.06	249.53	1.53	633.43	\pm 195.25
Stem	6.37 \pm	8.51 \pm	2264.75 \pm	94.12 \pm	6439.02 \pm	94.12 \pm	645.49 \pm	16.65 \pm	1004.8 \pm	420.88 \pm	31.59 \pm	3712.7 \pm	18.24 \pm	605.5 \pm	78.1 \pm	1131.03
	1.33	8.08	543.39	15.05	414.88	15.05	44.05	0.86	95.31	47.27	11.04	196.55	11.12	36.19	45.67	\pm 91.34
Leaf with	33.1 \pm	32.87 \pm	227.26 \pm	41.52 \pm	1382.79 \pm	41.52 \pm	1537.27 \pm	12.8 \pm	109.73 \pm	1065.89 \pm	43.67 \pm	7096.96 \pm	19.19 \pm	45.5 \pm	241.64 \pm	393.18 \pm
Petiolules	21.38	2.22	59.28	29.85	87.38	29.85	12.81	7.22	14.28	95.95	10.87	574.28	20.77	22.39	28.35	60.55
Vegetative	34.6 \pm	7.92 \pm	1733.22 \pm	31.01 \pm	8153.66 \pm	31.01 \pm	346.94 \pm	6.37 \pm	452.48 \pm	358.24 \pm	7.5 \pm	3165.97 \pm	24.77 \pm	503.5 \pm	32.38 \pm	540.19 \pm
Bud	9.11	4.84	564.59	19.39	409.89	19.39	35.58	6.16	76.4	6.13	1.48	176.84	9.56	45.36	11.49	14.34
Flower	78.2 \pm	14.06 \pm	263.08 \pm	53.55 \pm	575.5 \pm	53.55 \pm	465.62 \pm	45.09 \pm	967.92 \pm	213.1 \pm	22.23 \pm	2567.76 \pm	173.03 \pm	113.97 \pm	23.35 \pm	467.92 \pm
	8.04	15.31	16.3	11.79	50.95	11.79	12.89	12.49	72.69	32.99	21.12	283.83	22.02	26.42	10.54	25.02
Pod	29.0 \pm	23.48 \pm	245.41 \pm	35.58 \pm	660.9 \pm	35.58 \pm	322.14 \pm	1071.18 \pm	5645.75 \pm	374.17 \pm	13.46 \pm	2270.72 \pm	56.15 \pm	465.53 \pm	16.28 \pm	936.18 \pm
	8.5	16.33	48.69	23.24	16.2	23.24	76.69	137.22	1142.7	49.66	10.92	324.81	12.72	48.51	10.23	89.01
Nodule	2141.12 \pm	82.13 \pm	3451.47 \pm	338.52 \pm	680.17 \pm	338.52 \pm	502.83 \pm	27.23 \pm	51.76 \pm	149.31 \pm	238.94 \pm	986.46 \pm	1166.64 \pm	50.43 \pm	1425.33 \pm	5843.43 \pm
Mature (4w)	75.73	10.25	1054.2	180.98	201.03	180.98	31.29	16.34	13.23	27.88	17.7	184.97	246.66	8.71	278.31	348.56

Table S3. Details of *M. truncatula* peroxidases showing the accession numbers, length, occurrence of XYLAT elements and best hits in *A. thaliana*. Accession numbers and length were retrieved from Phytozome v10.2. MtPrx116 (partial amino acid sequence retrieved from PeroxiBase, no prediction from Phytozome, no EST found) was omitted from the Table. The (+) and (-) signs indicate XYLAT elements on the (+)- and (-)-strand respectively.

Name	Gene Accession	Length (amino acids)	XYLAT	<i>A. thaliana</i> Best Hit (e value)
MtPrx01	Medtr5g074860.1	325	-	AtPrx52 (8e – 121)
MtPrx02	Medtr5g074740.1	323	-	AtPrx52 (4e – 114)
MtPrx03	Medtr3g467600.1	324	-	AtPrx52 (7e – 111)
MtPrx04	Medtr7g107520.1	320	-	AtPrx03 (4e – 120)
MtPrx05	Medtr2g088770.1	326	1873 (-)	AtPrx39 (1e – 160)
MtPrx06	Medtr2g008710.1	325	-	AtPrx25 (3e – 144)
MtPrx07	Medtr3g092990.1	327	-	AtPrx03 (5e – 97)
MtPrx08	Medtr5g022870.1	316	1061 (-)	AtPrx64 (3e – 122)
MtPrx09	Medtr4g125940.1	330	-	AtPrx59 (3e – 145)
MtPrx10	Medtr2g029800.1	353	1770 (+)	AtPrx22 (8e – 129)
MtPrx11	Medtr2g029820.1	355	-	AtPrx54 (5e – 132)
MtPrx12	Medtr2g029815.1	352	111 (+); 1733 (-)	AtPrx54 (2e – 130)
MtPrx13	Medtr1g101830.1	322	-	AtPrx66 (1e – 164)
MtPrx14	Medtr4g127670.1	323	1518 (-)	AtPrx16 (1e – 173)
MtPrx15	Medtr2g029850.1	352	-	AtPrx54 (1e – 125)
MtPrx16	Medtr2g029750.1	354	-	AtPrx22 (1e – 127)
MtPrx17	Medtr2g029740.1	355	-	AtPrx22 (2e – 130)
MtPrx18	Medtr4g133800.1	335	-	AtPrx07 (6e – 105)
MtPrx19	Medtr1g077000.1	326	-	AtPrx47 (4e – 169)
MtPrx20	Medtr2g029830.1	355	-	AtPrx54 (2e – 130)
MtPrx21	Medtr2g008160.1	323	-	AtPrx43 (2e – 147)
MtPrx22	Medtr5g083860.1	325	-	AtPrx52 (3e – 161)
MtPrx23	Medtr7g093370.1	373	-	AtPrx53 (4e – 166)
MtPrx24	Medtr4g029200.1	338	-	AtPrx52 (1e – 122)
MtPrx25	Medtr8g076820.1	332	-	AtPrx72 (0.0)
MtPrx26	Medtr2g029860.1	353	-	AtPrx54 (3e – 129)
MtPrx27	Medtr2g040000.1	332	-	AtPrx59 (2e – 132)
MtPrx28	Medtr2g084020.1	318	-	AtPrx52 (6e – 133)
MtPrx29	Medtr5g074970.1	326	-	AtPrx67 (1e – 140)
MtPrx30	Medtr2g029730.1	345	1436 (+)	AtPrx53 (1e – 127)
MtPrx32	Medtr4g029190.1	341	-	AtPrx52 (6e – 118)
MtPrx33	Medtr7g072480.1	316	-	AtPrx52 (5e – 95)
MtPrx34	Medtr3g072190.1	318	-	AtPrx52 (2e – 126)
MtPrx35	Medtr2g029910.1	353	-	AtPrx54 (5e – 129)
MtPrx36	Medtr7g072510.1	312	-	AtPrx52 (2e – 131)
MtPrx37	Medtr3g072210.1	238	-	AtPrx52 (3e – 91)
MtPrx38	Medtr4g095450.1	323	-	AtPrx38 (9e – 162)
MtPrx39	Medtr1g115900.1	330	1460 (+)	AtPrx52 (1e – 112)
MtPrx40	Medtr5g049280.1	338	-	AtPrx11 (1e – 169)

Table S3. Cont.

Name	Gene Accession	Length (amino acids)	XYLAT	<i>A. thaliana</i> Best Hit (e value)
MtPrx41	Medtr7g029030.1	320	-	AtPrx55 (2e – 137)
MtPrx42	Medtr5g016010.1	328	-	AtPrx35 (3e – 153)
MtPrx43	Medtr2g084010.1	318	-	AtPrx52 (1e – 129)
MtPrx44	Medtr2g084000.1	319	1691 (-)	AtPrx52 (2e – 126)
MtPrx45	Medtr1g022970.1	347	-	AtPrx9 (1e – 172)
MtPrx46	Medtr5g021060.1	331	-	AtPrx72 (0.0)
MtPrx47	Medtr4g132110.1	335	-	AtPrx42 (0.0)
MtPrx48	Medtr6g043240.1	352	1982 (+)	AtPrx12(1e – 117)
MtPrx49	Medtr4g029180.1	321	-	AtPrx52 (1e – 95)
MtPrx50	Medtr1g038680.1	332	-	AtPrx39 (2e – 89)
MtPrx52	Medtr5g017850.1	326	-	AtPrx10 (4e – 132)
MtPrx53	Medtr4g046713.1	326	1928 (+)	AtPrx03 (5e – 144)
MtPrx54	Medtr3g094650.1	322	1941 (+)	AtPrx52 (2e – 159)
MtPrx55	Medtr1g025980.1	318	318 (+)	AtPrx64 (3e – 169)
MtPrx56	Medtr1g066380.1	325	-	AtPrx21 (3e – 177)
MtPrx57	Medtr2g084080.1	317	-	AtPrx52 (3e – 137)
MtPrx58	Medtr5g017860.1	326	892 (-)	AtPrx10 (1e – 130)
MtPrx60	Medtr2g099175.1	336	-	AtPrx26 (4e – 134)
MtPrx61	Medtr7g026990.1	323	460 (+)	AtPrx52 (3e – 112)
MtPrx63	Medtr2g084090.1	318	-	AtPrx52 (2e – 132)
MtPrx64	Medtr0147s0010.1	393	-	AtPrx48 (5e – 111)
MtPrx65	Medtr1g086320.1	333	590 (+)	AtPrx66 (6e – 82)
MtPrx66	Medtr4g114210.1	320	-	AtPrx25 (1e – 172)
MtPrx67	Medtr4g083710.1	321	23 (-); 222 (-)	AtPrx05 (9e – 163)
MtPrx70	Medtr5g074760.1	323	-	AtPrx52 (3e – 114)
MtPrx71	Medtr2g028980.1	355	-	AtPrx53 (4e – 125)
MtPrx74	Medtr4g087965.1	346	-	AtPrx19 (3e – 156)
MtPrx75	Medtr6g043460.1	348	-	AtPrx12 (1e – 100)
MtPrx76	Medtr4g074990.1	320	-	AtPrx5 (6e – 156)
MtPrx78	Medtr6g027440.1	319	-	AtPrx57 (2e – 105)
MtPrx79	Medtr6g008075.1	334	-	AtPrx63 (3e – 152)
MtPrx81	Medtr4g029170.1	321	-	AtPrx52 (8e – 128)
MtPrx82	Medtr2g067440.1	389	-	AtPrx48 (1e – 96)
MtPrx83	Medtr5g033470.1	377	-	AtPrx28 (3e – 64)
MtPrx84	Medtr3g094630.1	322	346 (+)	AtPrx52 (5e – 173)
MtPrx85	Medtr4g122640.1	336	-	AtPrx40 (4e – 136)
MtPrx86	Medtr5g074710.1	323	-	AtPrx52 (2e – 114)
MtPrx87	Medtr1g086490.1	342	-	AtPrx28 (5e – 82)
MtPrx88	Medtr7g086870.1	312	1026 (-)	AtPrx44 (1e – 120)
MtPrx89	Medtr7g086820.1	315	-	AtPrx44 (4e – 129)
MtPrx90	Medtr5g014100.1	332	-	AtPrx20 (2e – 121)
MtPrx91	Medtr8g062780.1	329	711 (+); 757 (-)	AtPrx65 (7e – 134)
MtPrx92	Medtr8g075100.1	319	-	AtPrx64 (6e – 123)
MtPrx93	Medtr4g132490.1	327	-	AtPrx29 (6e – 108)

Table S3. *Cont.*

Name	Gene Accession	Length (amino acids)	XYLAT	<i>A. thaliana</i> Best Hit (e value)
MtPrx94	Medtr4g030890.1	415	-	AtPrx17 (0.0)
MtPrx95	Medtr4g031140.1	343	-	AtPrx17 (5e – 175)
MtPrx97	Medtr2g084110.1	317	-	AtPrx52 (2e – 133)
MtPrx98	Medtr3g094670.1	322	-	AtPrx52 (2e – 134)
MtPrx100	Medtr2g437770.1	343	-	AtPrx07 (6e – 131)
MtPrx107	Medtr3g105790.1	324	-	AtPrx46 (1e – 144)
MtPrx110	Medtr4g074980.1	294	1040 (+)	AtPrx5 (3e – 128)
MtPrx111	Medtr2g029560.1	344	-	AtPrx54 (3e – 131)
MtPrx114	Medtr3g105790.1	324	-	AtPrx46 (1e – 144)

Table S4. Expression values \pm standard deviations relative to the heat map in Figure 4 and retrieved from the *Medicago* eFP browser.

Tissue	MtPrx01	MtPrx03	MtPrx04	MtPrx06	MtPrx07	MtPrx08	MtPrx10	MtPrx13	MtPrx14	MtPrx15
Root	1594.56 \pm 194.77	36.09 \pm 9.1	8838.53 \pm 1522.58	2148.74 \pm 101.46	2591.25 \pm 94.57	633.48 \pm 51.82	15,320.5 \pm 1278.95	5164.14 \pm 436.11	6269.31 \pm 545.36	21,339.63 \pm 1506.78
Stem	10.63 \pm 13.43	23.55 \pm 21.13	74.02 \pm 11.68	417.75 \pm 24.32	20.09 \pm 19.02	17,797.36 \pm 858.95	661.28 \pm 36.66	6996.69 \pm 1232.39	30.47 \pm 5.48	6690.71 \pm 794.09
Leaf with Petiolules	7.94 \pm 5.82	24 \pm 16.48	24.66 \pm 26.79	1062.55 \pm 105.58	48.35 \pm 14.63	4504.04 \pm 277.34	1467.57 \pm 160.8	2271.08 \pm 198.85	47.51 \pm 15.45	4962.9 \pm 307.51
Vegetative Bud	17.56 \pm 11.62	19.42 \pm 9.01	43.96 \pm 4.46	95.68 \pm 43.47	32.34 \pm 10.15	5183.08 \pm 184.67	1846.61 \pm 97.33	2084.12 \pm 232.6	58.57 \pm 8.46	10,255.53 \pm 894.87
Flower	4.65 \pm 2.7	31.54 \pm 16.89	17.18 \pm 10.51	788.98 \pm 26.77	41.36 \pm 22.05	3097.78 \pm 365.62	90.06 \pm 23.35	2383.17 \pm 120.43	27.52 \pm 14.16	1528.73 \pm 109.39
Pod	86.96 \pm 35.93	4.25 \pm 1.91	86.25 \pm 27.64	33.29 \pm 9.95	33.08 \pm 21.42	22,513.1 \pm 1346.44	301.69 \pm 75.01	6703.42 \pm 1258.03	52.16 \pm 18.58	9044.48 \pm 447.21
Nodule Mature (4w)	1556.12 \pm 334.65	13,258.56 \pm 956.71	205.58 \pm 69.52	293.35 \pm 219.11	1998.81 \pm 93.56	98.29 \pm 28.85	9445.96 \pm 679.62	399.55 \pm 104.79	4180.66 \pm 738.72	18,453.83 \pm 727.15
Tissue	MtPrx16	MtPrx18	MtPrx19	MtPrx20	MtPrx22	MtPrx23	MtPrx25	MtPrx27	MtPrx29	MtPrx30
Root	15,663.03 \pm 787.73	436.61 \pm 21.3	12,407.7 \pm 972.52	118.97 \pm 21.53	2488.86 \pm 127.76	1149.55 \pm 104.15	3204.13 \pm 236.1	4413.84 \pm 262.51	6049.6 \pm 490.06	20.81 \pm 12.4
Stem	102.04 \pm 17.6	7.64 \pm 3.52	1071.46 \pm 26.6	2457.01 \pm 259.21	59.91 \pm 13.41	490.2 \pm 53.18	842.07 \pm 68.86	52.5 \pm 34.38	2591.73 \pm 133.62	13.97 \pm 14.73
Leaf with Petiolules	56.4 \pm 25.67	11.3 \pm 9.89	659.27 \pm 64.09	6532.35 \pm 540.54	66.06 \pm 20.95	39.46 \pm 20.81	187.16 \pm 19.38	32.94 \pm 27.16	297.57 \pm 45.04	25.97 \pm 1.11
Vegetative Bud	108.52 \pm 24.16	18.08 \pm 10.26	416.96 \pm 6.66	4743.75 \pm 119.62	58.28 \pm 8.49	83.18 \pm 15.43	185.39 \pm 37.25	24.9 \pm 10.97	539.91 \pm 20.19	4.01 \pm 1.46
Flower	24.27 \pm 14.78	97.49 \pm 16.47	7002.84 \pm 163.01	827.91 \pm 16.2	51.03 \pm 16.83	248.74 \pm 29.13	240.59 \pm 49.82	8.63 \pm 8.48	1610.46 \pm 281.5	20.31 \pm 26.04
Pod	46.7 \pm 4.19	23.72 \pm 14.55	462.52 \pm 10.3	2802 \pm 192.84	97.26 \pm 22.91	10,166.21 \pm 3760.63	264.29 \pm 11.39	159.68 \pm 63.58	354.71 \pm 98.77	116.08 \pm 25.15
Nodule Mature (4w)	7693.85 \pm 482	37.78 \pm 19.76	1214.38 \pm 383.15	1305.82 \pm 40.34	1728.34 \pm 158.91	215.51 \pm 39.84	557.9 \pm 91.8	1903.93 \pm 505.47	1432.26 \pm 129	16.4 \pm 9.55

Table S4. *Cont.*

Tissue	MtPrx36	MtPrx37	MtPrx38	MtPrx39	MtPrx41	MtPrx42	MtPrx43	MtPrx44	MtPrx47	MtPrx52
Root	6503.73 ± 294.23	76 ± 19.23	19,933.83 ± 1144.04	4591.92 ± 273.31	4988.4 ± 499.32	2626.66 ± 191.6	391.07 ± 37.65	3838.35 ± 79.5	10,583.07 ± 691.13	9628.54 ± 1011.28
Stem	14.92 ± 9.13	1769.5 ± 102.46	7259.35 ± 446.77	16.9 ± 4.67	183.57 ± 3.81	11,770.56 ± 753.09	56.45 ± 13.28	30.33 ± 27.81	2739.68 ± 112.86	19.51 ± 8.71
Leaf with Petiolules	16.38 ± 10.39	4982.21 ± 216.17	684.68 ± 47.49	6.23 ± 5.8	3648.11 ± 229.22	2764.65 ± 182.8	31.08 ± 11.95	39.41 ± 9.09	76.47 ± 24.68	13.63 ± 13.5
Vegetative Bud	9.46 ± 10.58	1668.85 ± 188.02	4429.07 ± 290.77	1.42 ± 0.39	279.3 ± 3.39	8579.15 ± 230.39	145.11 ± 24.69	40.08 ± 10.47	226.57 ± 35.97	19.84 ± 14.14
Flower	4.8 ± 2.6	582.12 ± 97.95	2772.81 ± 382.81	9.27 ± 10.24	58.87 ± 11.58	4376.59 ± 152.68	1053.52 ± 52.82	30.63 ± 26.39	737.37 ± 87.64	12.64 ± 7.58
Pod	4.16 ± 2.87	3752.27 ± 223.42	12,410.9 ± 1444.4	4.48 ± 3.68	68.64 ± 2.47	16,312.2 ± 1202.62	63.18 ± 11.55	34.37 ± 14.58	21,587.23 ± 1484.06	29.33 ± 11.78
Nodule Mature (4w)	2980.48 ± 311.15	351.93 ± 85.25	5289.36 ± 1198.59	152.58 ± 12.74	4559.98 ± 130.46	8266.33 ± 475.92	91.99 ± 36.57	2543.42 ± 517.57	7585.6 ± 503.42	362.31 ± 109.9
Tissue	MtPrx54	MtPrx55	MtPrx56	MtPrx57	MtPrx61	MtPrx63	MtPrx64	MtPrx66	MtPrx67	MtPrx71
Root	37.39 ± 14.36	837.09 ± 83.35	777.52 ± 141.69	85.56 ± 24.38	2862.53 ± 350.41	8.25 ± 6.38	14.46 ± 4.48	3538.31 ± 165.35	29.45 ± 15.3	214.84 ± 64.44
Stem	9057.28 ± 582.76	19.44 ± 11.44	148.12 ± 26.56	31.43 ± 8.56	13.83 ± 8.04	1.87 ± 0.7	16.09 ± 19.33	72.94 ± 4.57	38.43 ± 25.61	38.52 ± 2.6
Leaf with Petiolules	784.98 ± 61.34	11.44 ± 11.36	143.59 ± 16.52	35.43 ± 19.84	6.24 ± 3.12	19.63 ± 10.12	5.09 ± 2.41	20.35 ± 14.83	36.86 ± 22.5	26.53 ± 14.14
Vegetative Bud	2604.66 ± 83.88	8.71 ± 4.83	50.75 ± 3.21	28.4 ± 18.19	29.22 ± 20.16	16.2 ± 5.06	7.98 ± 4.59	16.19 ± 16.19	41.69 ± 24	37.8 ± 34.56
Flower	5620.42 ± 761.83	9.37 ± 9.97	171.02 ± 15.21	39.88 ± 15.82	15.35 ± 9.06	28.7 ± 21.94	11.19 ± 9.27	12.87 ± 11.36	9.44 ± 2.03	17.23 ± 5.32
Pod	1106.2 ± 272.13	23.45 ± 6.87	336.51 ± 84.03	33.69 ± 22.49	59.94 ± 21.76	920.87 ± 226.65	9.34 ± 7.18	11.08 ± 10.93	23.01 ± 16.18	11.01 ± 5.51
Nodule Mature (4w)	23.03 ± 23.74	56.52 ± 15.67	147.02 ± 50.74	45.95 ± 6.24	73.46 ± 22.25	26.86 ± 16.06	8.58 ± 3.89	881.46 ± 92.43	34.49 ± 16.46	36.06 ± 11.83

Table S4. Cont.

Tissue	MtPrx75	MtPrx78	MtPrx81	MtPrx83	MtPrx85	MtPrx86	MtPrx90	MtPrx91	MtPrx94	MtPrx110
Root	61.81 ± 31.8	23.88 ± 9.87	5885.43 ± 449.21	25.58 ± 11.67	10.56 ± 6.68	2198.78 ± 317.12	439.32 ± 27.16	31.87 ± 13.04	1017.54 ± 24.87	6.41 ± 6.72
Stem	7.06 ± 4.05	7.79 ± 3.56	8.85 ± 4.69	27.13 ± 13	56.23 ± 7.1	18.38 ± 12.44	12.19 ± 6.22	20.13 ± 21.75	631.45 ± 50.6	1.94 ± 0.27
Leaf with Petiolules	6.57 ± 3.3	20.35 ± 14.95	10.33 ± 10.95	18.93 ± 6.52	289.45 ± 53.47	12.31 ± 11.63	19.91 ± 8.48	31.16 ± 34.99	437.06 ± 97.53	23.14 ± 12.89
Vegetative Bud	9.41 ± 7.3	4.34 ± 4.18	8.83 ± 7.1	14.26 ± 13.19	26.14 ± 19.31	9.39 ± 5.27	14.02 ± 12.25	15.9 ± 11.71	661.99 ± 35.01	10.24 ± 12.02
Flower	4.59 ± 0.82	103.72 ± 26.82	11.29 ± 6.56	4980.06 ± 662.31	6.39 ± 1.56	5.98 ± 2.61	26.76 ± 17.83	276.67 ± 63.12	2079.65 ± 171.48	13.31 ± 15.1
Pod	13.96 ± 5.59	967.16 ± 223.73	2.46 ± 0.42	284.94 ± 71.42	6.94 ± 3.47	17.61 ± 13.42	23.21 ± 16.45	33.27 ± 2.55	1003.83 ± 34.45	13.88 ± 14.3
Nodule Mature (4w)	10.5 ± 3.58	11.96 ± 10.48	253.24 ± 31.77	31.64 ± 12.97	30.69 ± 24.45	127.2 ± 74.25	310.74 ± 65.14	8.91 ± 9.16	2324.17 ± 176.36	2.52 ± 0.58

Table S5. Normalized Relative Expression for *CesA* genes in alfalfa roots. Normalized Relative Expression values ± standard error of the mean and significance (Sign.). Data were normalized using PAB4/TFIIA. Means sharing a letter are not significantly different at $\alpha = 0.05$ (Tukey post hoc test). * The asterisk indicates genes showing non-normal distribution of the variances, but individually ranked using the ANOVA one-way for clarity of presentation. These data have been analysed with the test of Kruskal-Wallis and have shown rejection the null hypothesis (*i.e.*, the mean ranks of the different groups are different).

Time Point	CesA1 *	Sign.	CesA3 *	Sign.	CesA6B *	Sign.	CesA6C *	Sign.	CesA6F *	Sign.	CesA4	Sign.	CesA7B *	Sign.	CesA7A *	Sign.	CesA8 *	Sign.
Ctrl 0 h	0.82 ± 0.12	a	1.32 ± 0.09	d	0.9 ± 0.07	abc	1.52 ± 0.23	cd	1.17 ± 0.06	bc	1.11 ± 0.14	bc	1.63 ± 0.13	c	1.69 ± 0.06	d	1.9 ± 0.16	d
Ctrl 24 h	0.85 ± 0.07	a	0.88 ± 0.01	abcd	0.9 ± 0.06	abc	1.86 ± 0.45	d	1.27 ± 0.17	bc	0.97 ± 0.11	bc	1.08 ± 0.12	c	1.12 ± 0.1	cd	1.32 ± 0.16	cd
Ctrl 72 h	1.09 ± 0.11	ab	1.11 ± 0.07	bcd	1.3 ± 0.05	bc	1.77 ± 0.08	d	2.07 ± 0.26	c	2.29 ± 0.12	c	1.92 ± 0.05	c	1.96 ± 0.35	d	2.6 ± 0.41	d
Ctrl 96 h	0.92 ± 0.13	a	0.97 ± 0.12	abcd	1.21 ± 0.21	bc	1.45 ± 0.14	cd	1.67 ± 0.09	bc	1.93 ± 0.31	bc	1.68 ± 0.19	c	2.08 ± 0.26	d	2.22 ± 0.45	d
Cold-24 h	1.7 ± 0.14	b	1.54 ± 0.34	d	1.47 ± 0.34	c	0.99 ± 0.17	cd	0.88 ± 0.13	abc	1.55 ± 0.22	bc	1.36 ± 0.1	c	1.05 ± 0.23	cd	1.83 ± 0.16	d
Cold-72 h	1.32 ± 0.02	ab	1.42 ± 0.03	d	1.26 ± 0.09	bc	0.94 ± 0.09	cd	0.72 ± 0.04	abc	1.63 ± 0.19	bc	1.5 ± 0.19	c	1.89 ± 0.19	d	1.92 ± 0.3	d
Cold-96 h	1.23 ± 0.08	ab	1.41 ± 0.21	d	1.33 ± 0.13	bc	0.7 ± 0.07	bc	1.07 ± 0.09	abc	1.07 ± 0.16	bc	1.5 ± 0.31	c	1.26 ± 0.1	cd	2.28 ± 0.57	d
Heat-24 h	0.93 ± 0.04	a	0.69 ± 0.05	abc	0.71 ± 0.06	ab	0.8 ± 0.19	bc	1.07 ± 0.15	abc	0.84 ± 0.2	b	0.8 ± 0.25	bc	0.62 ± 0.29	bc	0.39 ± 0.14	bc
Heat-72 h	0.79 ± 0.01	a	0.62 ± 0.04	ab	0.55 ± 0.01	a	0.38 ± 0.03	ab	0.6 ± 0.1	ab	0.26 ± 0.02	a	0.27 ± 0.06	ab	0.32 ± 0.01	ab	0.06 ± 0.01	a
Heat-96 h	0.8 ± 0.02	a	0.54 ± 0.01	a	0.77 ± 0.11	abc	0.3 ± 0.05	a	0.56 ± 0.38	a	0.21 ± 0.05	a	0.26 ± 0.14	a	0.18 ± 0.01	a	0.13 ± 0.06	ab
Salt-24 h	0.9 ± 0.08	a	1.2 ± 0.21	cd	1.06 ± 0.14	bc	1.34 ± 0.3	cd	1.03 ± 0.2	abc	1.12 ± 0.15	bc	1.31 ± 0.12	c	1.5 ± 0.13	d	1.74 ± 0.24	d
Salt-72 h	0.98 ± 0.06	a	0.97 ± 0.09	abcd	1.07 ± 0.05	bc	1.54 ± 0.05	cd	1.35 ± 0.09	bc	1.32 ± 0.16	bc	1.13 ± 0.07	c	1.01 ± 0.23	cd	1.67 ± 0.39	d
Salt-96 h	1.06 ± 0.19	ab	1.07 ± 0.07	bcd	1.07 ± 0.09	bc	1.45 ± 0.04	cd	1.08 ± 0.2	abc	1.5 ± 0.31	bc	1.37 ± 0.36	c	1.46 ± 0.32	d	2.14 ± 0.55	d

Table S6. Normalized Relative Expression for CAD, PAL, genes encoding dirigent-like proteins and class III peroxidases in alfalfa roots. Normalized Relative Expression values \pm standard error of the mean and significance (Sign.). Data were normalized using PAB4/TFIIA. Means sharing a letter are not significantly different at $\alpha = 0.05$ (Tukey post hoc test). * The asterisk indicates genes showing non-normal distribution of the variances, but individually ranked using the ANOVA one-way for clarity of presentation. These data have been analysed with the test of Kruskal-Wallis and have shown rejection the null hypothesis (*i.e.*, the mean ranks of the different groups are different).

Time Point	CAD	Sign.	PAL	Sign.	Prx13	Sign.	MsPrx12 *	Sign.	MsPrx16 *	Sign.	Medtr7g093850.1	Sign.	Medtr1g054525.1	Sign.
Ctrl 0 h	1.09 \pm 0.13	ab	1.17 \pm 0.28	a	1.13 \pm 0.07	ab	1.17 \pm 0.17	abc	1.55 \pm 0.06	cde	0.56 \pm 0.08	a	1.34 \pm 0.17	cd
Ctrl 24 h	0.83 \pm 0.07	a	0.87 \pm 0.13	a	0.84 \pm 0.1	a	1.19 \pm 0.15	abc	1.12 \pm 0.06	cd	0.87 \pm 0.17	ab	1.23 \pm 0.21	abc
Ctrl 72 h	1.47 \pm 0.14	b	1.17 \pm 0.24	a	2.52 \pm 0.45	c	1.99 \pm 0.23	c	2.47 \pm 0.43	e	0.38 \pm 0.18	a	2.33 \pm 0.6	d
Ctrl 96 h	1.24 \pm 0.14	ab	1.28 \pm 0.45	a	1.83 \pm 0.19	bc	1.31 \pm 0.19	abc	2.06 \pm 0.4	de	0.56 \pm 0.08	a	1.34 \pm 0.17	cd
Cold-24 h	0.9 \pm 0.04	ab	0.82 \pm 0.09	a	0.89 \pm 0.1	ab	0.62 \pm 0.17	a	1.12 \pm 0.07	cd	1.17 \pm 0.51	ab	0.87 \pm 0.07	abc
Cold-72 h	0.97 \pm 0.12	ab	0.98 \pm 0.11	a	0.91 \pm 0.15	ab	0.6 \pm 0.03	a	1.51 \pm 0.04	cde	1.01 \pm 0.17	ab	1.16 \pm 0.22	abc
Cold-96 h	0.81 \pm 0.1	a	1.5 \pm 0.12	a	0.76 \pm 0.06	a	0.6 \pm 0.07	a	0.79 \pm 0.08	c	0.87 \pm 0.17	ab	1.23 \pm 0.21	abc
Heat-24 h	1.16 \pm 0.02	ab	1.04 \pm 0.22	a	1.26 \pm 0.32	abc	1.42 \pm 0.03	bc	0.35 \pm 0.06	ab	1.3 \pm 0.28	ab	1.12 \pm 0.12	abc
Heat-72 h	1.13 \pm 0.08	ab	0.98 \pm 0.11	a	0.68 \pm 0.07	a	0.66 \pm 0.13	ab	0.17 \pm 0.01	a	3.04 \pm 0.5	b	0.55 \pm 0.08	ab
Heat-96 h	0.74 \pm 0.02	a	0.97 \pm 0.24	a	0.62 \pm 0.11	a	1.1 \pm 0.08	abc	0.39 \pm 0.08	b	1.17 \pm 0.51	ab	0.87 \pm 0.07	abc
Salt-24 h	0.92 \pm 0.13	ab	1.14 \pm 0.09	a	1.02 \pm 0.18	ab	1.17 \pm 0.29	abc	1.61 \pm 0.2	cde	1.19 \pm 0.25	ab	1 \pm 0.12	abc
Salt-72 h	0.96 \pm 0.12	ab	1.04 \pm 0.1	a	0.88 \pm 0.12	ab	1.47 \pm 0.12	c	1.65 \pm 0.13	de	0.36 \pm 0.03	a	1.16 \pm 0.17	abc
Salt-96 h	1.07 \pm 0.08	ab	0.69 \pm 0.07	a	0.98 \pm 0.1	ab	0.89 \pm 0.12	abc	1.64 \pm 0.33	cde	1.3 \pm 0.28	ab	1.12 \pm 0.12	abc

Table S7. Normalized Relative Expression for *CesA* genes in alfalfa leaves. Normalized Relative Expression values \pm standard error of the mean and significance (Sign.). Data were normalized using eif4A/TFIIA. Means sharing a letter are not significantly different at $\alpha = 0.05$ (Tukey post hoc test). * The asterisk indicates genes showing non-normal distribution of the variances, but individually ranked using the ANOVA one-way for clarity of presentation. These data have been analysed with the test of Kruskal-Wallis and have shown rejection the null hypothesis (*i.e.*, the mean ranks of the different groups are different).

Time Point	CesA1 *	Sign.	CesA3 *	Sign.	CesA6B *	Sign.	CesA6C	Sign.	CesA6F *	Sign.	CesA4	Sign.	CesA7B	Sign.	CesA7A	Sign.	CesA8 *	Sign.
Ctrl 0 h	0.82 \pm 0.09	a	1.05 \pm 0.03	abc	0.81 \pm 0.05	ab	0.97 \pm 0.04	b	0.82 \pm 0.04	a	0.97 \pm 0.07	abc	1.21 \pm 0.14	cd	0.97 \pm 0.06	abc	1.97 \pm 0.23	c
Ctrl 24 h	0.94 \pm 0.08	ab	0.94 \pm 0.12	ab	0.78 \pm 0.04	ab	1.19 \pm 0.16	b	1.11 \pm 0.06	a	0.93 \pm 0.04	abc	1.34 \pm 0.13	cd	1 \pm 0.04	abc	1.43 \pm 0.2	c
Ctrl 72 h	0.95 \pm 0.06	abc	0.83 \pm 0.07	a	0.98 \pm 0.05	abcd	1.16 \pm 0.22	b	1.24 \pm 0.26	a	1.1 \pm 0.07	bcd	1.09 \pm 0.19	cd	1.18 \pm 0.06	abc	1.31 \pm 0.12	c
Ctrl 96 h	1.34 \pm 0.04	cd	1.12 \pm 0.06	abc	1.1 \pm 0.01	bcde	1.02 \pm 0.11	b	0.89 \pm 0.11	a	1.63 \pm 0.2	cd	1.4 \pm 0.22	cd	1.36 \pm 0.27	bc	1.15 \pm 0.3	c
Cold-24 h	1.05 \pm 0	abc	1.13 \pm 0.01	abc	1.45 \pm 0.13	de	0.49 \pm 0.03	a	0.92 \pm 0.1	a	0.98 \pm 0.08	abc	1.16 \pm 0.15	cd	0.99 \pm 0.16	abc	1.38 \pm 0.2	c
Cold-72 h	1.53 \pm 0.06	d	1.57 \pm 0.16	c	1.67 \pm 0.06	e	0.98 \pm 0.07	b	1.08 \pm 0.34	a	1.27 \pm 0.27	bcd	1.45 \pm 0.28	cd	1.19 \pm 0.16	abc	1.39 \pm 0.12	c
Cold-96 h	0.94 \pm 0.07	ab	1.31 \pm 0.06	bc	1.12 \pm 0.04	bcde	0.45 \pm 0.02	a	0.64 \pm 0.06	a	0.93 \pm 0.09	abc	1.06 \pm 0.09	cd	0.62 \pm 0.09	a	1.06 \pm 0.23	bc
Heat-24 h	0.85 \pm 0.07	a	0.79 \pm 0.1	a	0.65 \pm 0.05	a	1.09 \pm 0.19	b	1.01 \pm 0.08	a	0.72 \pm 0.08	ab	0.77 \pm 0.1	bc	1.09 \pm 0.13	abc	0.59 \pm 0.15	abc
Heat-72 h	0.91 \pm 0.09	a	0.8 \pm 0.1	a	0.82 \pm 0.07	ab	1.31 \pm 0.14	b	1.36 \pm 0.15	a	0.66 \pm 0.09	ab	0.31 \pm 0.05	ab	0.82 \pm 0.14	abc	0.29 \pm 0.12	ab
Heat-96 h	0.89 \pm 0.02	a	0.79 \pm 0	a	0.89 \pm 0.05	abc	1.2 \pm 0.12	b	1.26 \pm 0.02	a	0.52 \pm 0.05	a	0.27 \pm 0.11	a	0.63 \pm 0.05	ab	0.19 \pm 0.07	a
Salt-24 h	1 \pm 0.02	abc	0.94 \pm 0.01	ab	0.85 \pm 0.04	ab	1.48 \pm 0.23	b	0.88 \pm 0.13	a	1.04 \pm 0.06	bcd	1.35 \pm 0.17	cd	1.06 \pm 0.16	abc	1.3 \pm 0.13	c
Salt-72 h	0.77 \pm 0.03	a	0.96 \pm 0.08	ab	0.98 \pm 0.03	abcd	1.25 \pm 0.29	b	1.28 \pm 0.33	a	1.21 \pm 0.21	bcd	1.62 \pm 0.5	cd	1.2 \pm 0.16	abc	3.04 \pm 1.72	c
Salt-96 h	1.28 \pm 0.03	bcd	1.07 \pm 0.14	abc	1.41 \pm 0.35	cde	1.26 \pm 0.01	b	1.1 \pm 0.34	a	1.94 \pm 0.39	d	2.47 \pm 0.73	d	1.53 \pm 0.42	c	2.46 \pm 0.92	c

Table S8. Normalized Relative Expression for CAD, PAL, genes encoding dirigent-like proteins and class III peroxidases in alfalfa leaves. Normalized Relative Expression values \pm standard error of the mean and significance (Sign.). Data were normalized using eif4A/TFIIA. Means sharing a letter are not significantly different at $\alpha = 0.05$ (Tukey post hoc test). * The asterisk indicates genes showing non-normal distribution of the variances, but individually ranked using the ANOVA one-way for clarity of presentation. These data have been analysed with the test of Kruskal-Wallis and have shown rejection the null hypothesis (*i.e.*, the mean ranks of the different groups are different).

Time Point	CAD	Sign.	PAL *	Sign.	Prx13	Sign.	MsPrx12	Sign.	Medtr7g093850.1 *	Sign.	Medtr1g054525.1	Sign.	Medtr4g078885.1	Sign.
Ctrl 0 h	1.14 \pm 0.12	a	0.83 \pm 0.11	ab	1.41 \pm 0.04	ab	2.02 \pm 0.29	ef	1.1 \pm 0.3	ab	1.16 \pm 0.09	bcd	0.9 \pm 0.14	bcd
Ctrl 24 h	0.98 \pm 0.13	a	0.58 \pm 0.05	a	1.14 \pm 0.01	ab	2.09 \pm 0.22	ef	2.78 \pm 1.04	b	1.12 \pm 0.08	bcd	0.8 \pm 0.21	abc
Ctrl 72 h	0.93 \pm 0.18	a	0.75 \pm 0.03	ab	1.04 \pm 0.1	ab	1.07 \pm 0.05	bcde	0.7 \pm 0.58	a	1.91 \pm 0.27	d	1.95 \pm 0.49	cde
Ctrl 96 h	1.1 \pm 0.19	a	1.92 \pm 0.41	b	1.67 \pm 0.34	b	0.42 \pm 0.03	a	1.29 \pm 0.42	ab	1.16 \pm 0.25	bcd	2.46 \pm 0.53	cde
Cold-24 h	0.66 \pm 0.12	a	1.6 \pm 0.25	ab	1.05 \pm 0.15	ab	0.85 \pm 0.09	abcd	0.46 \pm 0.04	ab	1.09 \pm 0.17	abcd	0.19 \pm 0.05	a
Cold-72 h	1.34 \pm 0.17	a	1.18 \pm 0.08	ab	0.74 \pm 0.23	a	0.57 \pm 0.09	ab	0.63 \pm 0.13	ab	0.91 \pm 0.1	abc	0.27 \pm 0.14	ab
Cold-96 h	0.91 \pm 0.12	a	0.9 \pm 0.07	ab	0.73 \pm 0.09	ab	0.65 \pm 0.09	abc	0.86 \pm 0.3	ab	1.2 \pm 0.05	bcd	0.25 \pm 0.05	ab
Heat-24 h	1.21 \pm 0.18	a	0.89 \pm 0.2	ab	0.97 \pm 0.12	ab	1.18 \pm 0.13	cdef	0.91 \pm 0.27	ab	0.56 \pm 0.06	a	2.1 \pm 0.35	cde
Heat-72 h	1.15 \pm 0.09	a	1.2 \pm 0.07	ab	0.72 \pm 0.2	a	0.85 \pm 0.14	abcd	1.94 \pm 0.17	ab	0.55 \pm 0.09	a	4.31 \pm 1.06	de
Heat-96 h	1.08 \pm 0.19	a	2.36 \pm 1.2	b	0.72 \pm 0.04	ab	0.62 \pm 0.06	abc	1.77 \pm 0.21	ab	0.64 \pm 0.01	ab	5.52 \pm 2.53	e
Salt-24 h	1.02 \pm 0.19	a	0.59 \pm 0.08	a	1.22 \pm 0.09	ab	2.25 \pm 0.23	f	0.71 \pm 0.21	ab	1.08 \pm 0.2	abcd	0.87 \pm 0.25	abc
Salt-72 h	0.83 \pm 0.09	a	0.7 \pm 0.01	ab	1.08 \pm 0.14	ab	1.67 \pm 0.24	def	1.54 \pm 0.36	ab	1.04 \pm 0.16	abcd	0.8 \pm 0.18	abc
Salt-96 h	1.07 \pm 0.15	a	1.39 \pm 0.47	ab	1.28 \pm 0.34	ab	0.82 \pm 0.18	abc	2.65 \pm 0.67	b	1.53 \pm 0.16	bc	2.01 \pm 0.76	cde

Table S9. Normalized Relative Expression for genes encoding dirigent-like proteins and class III peroxidases in alfalfa stems. Normalized Relative Expression values \pm standard error of the mean and significance (Sign.). Data were normalized using eif4A/PAB4. Means sharing a letter are not significantly different at $\alpha = 0.05$ (Tukey post hoc test). * The asterisk indicates genes showing non-normal distribution of the variances, but individually ranked using the ANOVA one-way for clarity of presentation. These data have been analysed with the test of Kruskal-Wallis and have shown rejection the null hypothesis (*i.e.*, the mean ranks of the different groups are different).

Time Point	Medtr7g093850.1 *	Sign.	Medtr1g054525.1	Sign.	Medtr4g078885.1	Sign.	Prx13	Sign.	MsPrx12 *	Sign.	MsPrx16	Sign.
Ctrl 0 h	1.97 \pm 0.87	ab	1.62 \pm 0.25	e	1.94 \pm 0.63	b	1.53 \pm 0.3	bc	1.7 \pm 0.33	f	1.04 \pm 0.2	abc
Ctrl 24 h	1.68 \pm 0.43	ab	1.35 \pm 0.17	de	1.12 \pm 0.11	b	0.98 \pm 0.03	abc	1.54 \pm 0.12	ef	0.85 \pm 0.08	abc
Ctrl 72 h	0.51 \pm 0.4	a	1.49 \pm 0.1	e	0.61 \pm 0.13	ab	1.79 \pm 0.01	c	0.95 \pm 0.06	bcde	1 \pm 0.13	abc
Ctrl 96 h	1.77 \pm 0.59	ab	1.45 \pm 0.17	de	2.2 \pm 0.77	b	1.89 \pm 0.39	c	1.01 \pm 0.14	bcdef	1.38 \pm 0.09	bc
Cold-24 h	0.62 \pm 0.03	ab	0.68 \pm 0.1	abc	0.19 \pm 0.05	a	1.1 \pm 0.16	abc	0.4 \pm 0.01	a	0.46 \pm 0.07	a
Cold-72 h	0.39 \pm 0.04	ab	0.81 \pm 0.01	abcd	0.58 \pm 0.11	ab	0.63 \pm 0.05	a	0.61 \pm 0.07	ab	0.86 \pm 0.15	abc
Cold-96 h	1.09 \pm 0.1	ab	1.11 \pm 0.11	bcde	0.61 \pm 0.17	ab	0.68 \pm 0.01	a	0.86 \pm 0.06	bcd	1.11 \pm 0.15	bc
Heat-24 h	1.05 \pm 0.21	ab	0.59 \pm 0.02	a	0.93 \pm 0.18	b	0.72 \pm 0.13	a	1.08 \pm 0.12	cdef	1.73 \pm 0.38	c
Heat-72 h	1.27 \pm 0.11	ab	0.46 \pm 0.04	a	1.36 \pm 0.3	b	0.8 \pm 0.11	ab	0.86 \pm 0.03	bcd	1.02 \pm 0.27	abc
Heat-96 h	3.02 \pm 0.66	b	0.64 \pm 0.09	ab	2.03 \pm 0.56	b	0.6 \pm 0.03	a	0.77 \pm 0.04	bc	1.17 \pm 0.1	bc
Salt-24 h	0.56 \pm 0.26	ab	1.23 \pm 0.13	cde	1.86 \pm 0.36	b	1.04 \pm 0.02	abc	1.59 \pm 0.02	ef	0.69 \pm 0.09	ab
Salt-72 h	1.36 \pm 0.26	ab	1.22 \pm 0.08	cde	1.13 \pm 0.5	b	1.24 \pm 0.21	abc	1.36 \pm 0.07	def	1.42 \pm 0.22	bc
Salt-96 h	2.52 \pm 0.19	b	1.48 \pm 0.26	de	2.29 \pm 0.31	b	1.14 \pm 0.25	abc	1.3 \pm 0.16	cdef	1.26 \pm 0.11	bc

Table S10. List of primers used for the RT-qPCR in this study. The names of the primers are in bold. Details concerning the primer sequences, amplicon length and T_m, PCR efficiencies and regression coefficients are included.

Name	Sequence (5'→3')	Amplicon Length (bp)	Amplicon T_m (°C)	PCR Efficiency (%)	Regression Coefficient (R²)
qPCR Medtr7g093850.1 Fwd	ATCACCATCGCCACAATCAC	118	77.7	98.3	0.997
qPCR Medtr7g093850.1 Rev	TGTGTGACTCCAGCATTTC				
qPCR Medtr1g054525.1 Fwd	TTCCGAAGTTGTGGGAAGAG	98	80.7	101.9	0.998
qPCR Medtr1g054525.1 Rev	TCCCTCGTGTGAAAGCAAAG				
qPCR Medtr4g078885.1 Fwd	ACTTGTAATCGTTGGTGTAGCAG	108	76.1	110.7	0.985
qPCR Medtr4g078885.1 Rev	GCACATCCTCTTTTCGTGTG				
qPCR Prx13 Fwd	CAGCCCGTATTTTGAGGATG	92	80.2	97.3	0.998
qPCR Prx13 Rev	TGCTTGGTTAGTGGCAGTTG				
qPCR Prx38 Fwd	GCTTCAGTTTTGGTGGCATC	137	78.5	93.0	0.995
qPCR Prx38 Rev	TTTCTGCACTGTGGAACAGC				
qPCR Prx42 Fwd	TCTTGCTATGGCAACTCGTG	132	79.6	96.1	0.989
qPCR Prx42 Rev	TTGAATCCAGGCTCAGGAAG				