

**Supplementary Table 1 -- List of nsLTPs with known or putative biological functions used for phylogenetic analysis**

Gene	Accession #	Function
AtLTP1(At2g38540)	NP_181388.1	calmodulin-binding protein and cell differentiation
AtLTP2(At2g38530)	NP_181387.1	cuticle –cell wall interface integrity and etiolated hypocotyl permeability
AtLTP3(At5g59310)	NP_568905.1	freezing and drought stress
AtLTP4(At5g59310)	NP_568904.1	pathogen defense
AtLTP5(At3g51600)	NP_190728.1	pollen tube tip growth and fertilization
DIR1 (AT5G48485)	NP_568699.1	system resistance signaling
AZI1 (AT4G12470.1)	NP_192984.1	systemic acquired resistance and induced systemic resistance, interacts with lipid derived azelaic acid
BraLTP1(Bra011229)	XP_009127438.1	epicuticular wax deposition, cell proliferation and flower development
nsLTP[Ginkgo biloba](DQ836633)	ABI26087.1	Proteinase inhibitor
LTP2(AAA03283)[barley, cv. Bomi]	Q43871.1	antibacterial
LTP4(Q43875.1) [barley, cv. Bomi]	Q43875.1	response to bacterial pathogens
BcMF15(ABQ63061.1 or EF600901)[Brassica rapa subsp. oleifera]	ABQ63061.1	microspore development
BcLTP(ABM69132.1 or EF216852)[Brassica rapa subsp. pekinensis]	XP_009143379.1	secrete and combine extracellular CaM
CaMF2(JF411954 or AEE92794.1)[Capsicum annuum]	AEE92794.1	pollen development
LTP(AF171094 or AAD46683.1)[Lilium longiflorum cv. Nellie White]	Q9SW93.1	pollen tube adhesion
Ace-AMP1 (AF004946.1 or AAB60896.1)[Allium cepa]	Q41258.1	antimicrobial
OsC6(AK064672 or BAG89152.1)[Oryza sativa Japonica Group]	XP_015615738.1	postmeiotic anther development
OsDIL(Os10g0148000) [Oryza sativa Japonica Group]	AAK91879.1	drought tolerance
MtN5(MTR_5g094210 or AET00633.1)[Medicago truncatula]	XP_003617674.1	efficient nodulation
NtLTP1 (AB625593 or BAK19150.1)[Nicotiana tabacum cv Xanthi]	XP_016433981.1	lipid secretion from glandular tissues
NtLTP2(Q03461.1) [Nicotiana tobacum cv Petit Havana SR1]	Q03461.1	Cell wall extension
NtnsLTP2-like	XP_009631888.1	antimicrobial resistance
CALTPI (AF2088232 or AAF23458.1) [Capsicum annuum]	AAF23458.1	Pathogen resistance and long distance signaling
CALTPII (AF208833 or AAF23459.1)[Capsicum annuum]	AAF23459.1	Pathogen resistance and long distance signaling

## Supplementary Table 2 – Sequences of nsLTPs used for tree building

>Bra000068

MAGLMKLACFLVACMIVAGPITANAALTCASVVSNMARCISYLGGETISGACCSGIRSINGLSR  
TPSDRQIACGCLKRVATLPNINADRAAGLPNACGVSLPYNISKSANCTLYVDFNLSRYLSLSL

>Bra001345

MRSFLLLALFLVLAFFHHGEAAVTCNNVVDLYPCLSYVMQGGNSPSTNCCSGVRTLNSQAQT  
TADRQSVCRICKNAIGGASYSSSNLKNALSPLAKCGVNLFPFSISPSTNCNR

>Bra005098

MAGLVKLACLVLACMIVAGPITSKAALSCGTVNTNVAACIGYLTQGGPLPRACCTGVSKLNSIAR  
TTPDRKQACRCLKTAASALGSGLNAGRAAGLPKACGVNVPFPISTINCNGHREISSVRMKLE  
WIIPML

>Bra005099

MAGLMKLACLVLACMIVAGPITSNAALSCGTVSGYVAPCIGYLAQGAPALPRACCSGVTSLNLL  
ARTTPDRQQACRCLVGAANAFPTLNAARAAGLPKACGVNIPYKISKTTNCNSVK

>Bra006721

MALALRFFTCLVLTVCIVASVDAAVSCGTVTSSLAPCANYLSKGGDVPPPCCAGVTKLNGMAQ  
TTPDRQQACKCLQSAAKTVSGLDPSLAAGLPKCGVSIPIYPIISMSTNCDNVK

>Bra006736

MASTLRFLTCLVTVSIVASVGAIPISCGTVVQSMSPCITYLSGRMDLTAACCGGVRDLNIAAQT  
PDRQQTCKCLQAVAKKIPGFNQTRASDLPGKCRVSFPFPISTNCDNVHHEDEEYMVYVQ

>Bra012848

MMFPSKITTTCLLVAVYMASPSESTITCGTVTSTLARCIGYLTNSGSLPSDCCVGVKSLNQMAQ  
TTPDRRQVCECLKSAAKDITGLNTDLVATLPTTCGVSVPIYPIRSTNCDTISTAV

>Bra017112

MAGVMKLVCLVLACMIVAGPITANAALTCGTVNSNVAPCIGYITQGGPLPGACCTGVSKLNSMA  
RTTPDRQQACRCLKTAASALGPSLNAGRAAGIPKACGVSVFPPISTNTNCNSVK

>Bra017113

MAGLMKLACLVLACMIVAGPITNAALSCGTVSGNLAACIGYLTQNGPLPRGCCTGVTNLNNM  
ARTTPDRQQACRCLVGAANSFPTLNAARAAGLPKACGVNIPYKISKSTNCNSVR

>Bra020322

MAIALRFFTCLVLTVCIVASVDAAITCGTVTSSLAPCATYLSGGGEVPPPCCAGVKKLNGMAQTT  
ADRQQACKCLKAAAQGINPSLASSLPKCSVSIPIYPIISMSTNCDNVK

>Bra020323

MTMGLKFFTCLVLTVCIAASVDAALTCGTVTSSLAPCATYLSKGGAVVPGPCCAGVKKLNDMA  
QTPDRQQACKCLKAAAKSINPSLASGLPGKCSVSIPIYPIISMSTNCDK

>Bra024983

MAYSKIALLLLILNVIFFTLVSSNPVPIYRKPCTCKNALFKKVCANVLDLVKVSPLPTRSKCCGLIKGLV  
DLEAAVCLAAVCLCTALKADLLGLKLNVPISLSVILNHCGKKVPSGFKCA

>Bra029172

MASALSFFTCLVLTVCIVASVDAAISCGTVTSNLVPCAGYLMKGGPVPASCCAGVSKLNSMAKT  
TPDRQQACKCLKTAAKSVNPSLASSLPGKCGVSIYPISMSTNCNT

>Bra029719

MRSLLLALFLVLAHRGEEAAVSCNAVVGDLYPCLSYVVQGGNVPANCCNGIRTLNSQAQTPVD  
RQGVCRCIKNAIGGVSFSSNNVNNAQSLPAKCGVNLPYSISPSTNCDR

>Bra036788

MEGLLKLSTLVIVCMLVSAPMASEAAISCGAVASNLGQCINYLTRGGFVPRGCCSGVRRLLNSM  
ARTTRDRQQACRCIQGAARALGSRLNPGRAARLPGACRVRIAYPISARTNCNK

>Bra036789

MAFASKIITCLLVLVKHYMAAPAESHITCGIVTSTLAQCMGYLTNFFPVPSDYCCAIEVKGLNQMAQ  
TTPDRRQVCKCLKAVAKENKGFISIELVGLTPTICGVSVPYPFNFSTNCDTISTAV

>Bra037222

MSILKSLVTIFVLGIFLTPRYSESAISCSVWLSDLQPCVSYLTSGSGQPPECCDGVRS LDAATTT  
SADKKAACQCISVANSVTVKPELAKALASNCNASLPVDASSTVDCNTVG

>Bra038907

MTFASKIITCLLVLTIIYAAPTESHITCGTVTSTMTQCISYLTNGGPLPSSCCVAVKSLNQMAQTT  
PDRRQVCECLKSAGKEIKGLNIDLVAALPTTCGVLSYPIGFNTNCDISISIAV

>Bra038908

MEGFIKSTLLIVCMLVSAPMAEAAISCGAVASNLGQCINYLTRGGFVPRGCCSGVQRLHSMAR  
TTRDRQQACRCIQGAARALGSRLNPGRAARLPGACRVRIAYPISARTNCNK

>Bra008112

MKFSCSKPVLFTCAILLLLIVAQENRVVAGQSCDPMQLIPCEEAILKGSKPSDTCCTRLNQQQH  
CVCQYMKNPNFKSFLDSPNAKKIATDCHCPKPKC

>Bra008375

MKFTGVVCI AFVIVLV SASAPTKEVLEEKVACNSTEHITCIPALQSGSQPSAECCGKLKEEESCL  
CGYIQNPLFSQYVTSANVHMLVTCGIPYPSC

>Bra014154

MVKVMWGSSSLALAAALLLVTVANIPVAEGVTCSPTELTSCSSAFMSASPPSATCCA KLREQKP  
CLCGYLRNPALSQYVNSPNAKKVASSCNVATPKC

>Bra015966

MKASCTKPV LITCTILLLLIVAQENRVAAAEQCNPMLPCEDAIMKGSTPSNECCTRLKQQQH  
CICQYMKNPNFKSFLNSPNAKMVASHCQCKPKC

>Bra018687

MNFTGAICIAFVIVLVSSLALTNAAVEDEKVLACNPKELNPCSPAVKTGSKPSTECCAMLKKEEP  
CLCGYINDPVYGGYIKSKNAHKAFSSCGIPPLSC

>Bra021299

MEMIKAKWVSIVALAAIFLVVILVPAAEAVTCSMQLSPCASAITSSSQTSALCCA KLKEQKPCLC

GYMRNRSRRFVSSPNARKVSNRCKLPIPRC

>Bra022308

MVMIKATWVSIFAIAAVLLVILAPAAEAVTCSPMQLSPCAQAITSSSPPSALCCA KLKEQKPCLC  
GYMRNPSLRRFVSSPNARKVSNRCKLPIPRC

>Bra025378

MKLT AIGLVAMVTIVVQLSPTMACDVKDLSPCLLP IAVFPESPTAACCCQTLRDQGPCLCVFINNS  
WIWIGPTLTSPNGHKLFAACQVFPFSCGN

>Bra027111

MKFTGAICIALVIVLVSSDLTSAAVEEEEIKVACVVTELIPCLESSIIGVHPYPECCVTLKAQQSCL  
CGYIQNPVYGGFFKNAHSVFTGCGVPYPTC

>Bra027114

MKFTGAICIALVIVLVSSDLTSAAVEEEEIKVACVQTELIPCFVAAFISQPSAECCEKLKEQQSCL  
CGYISNPVFGQFYKNAQNVFKACGVPYPTC

>Bra028162

MKFTTLMVITLVIIAMSSPVPIRATSVESFGEVAQSCVVTELAPCLPAMTTAGDPTTECCDKLVE  
QKPCLCGYIRNPAYSMYVTSPNGRKLDFCKVFPFSC

>Bra030699

MRFTGVVCI AFVIVLV SALAPTKADLEEKVACI TELMTCIPALQTGSQPSAECCKLKEQESCL  
CGYIQNPLFSQYVTSENAHKILATCGIPYPTC

>Bra032265

MVKVMWV FVLALVAALLLVTEKIPVAEGVTC SVTELS PCLAAFMSSSQPSASCCA KLREQKP  
CLCGYMRNPGLRQYVTSPNAKKVSNCKVASPNC

>Bra033084

MKFTTLASIAFVVVLFSSSTAAPINSQLIQSNSPCTTIDITGCVPAIYGAPLSPECCRNLNQQP  
CYCDFIKNAGLKP YITSPQGHAAALASCGIPYPTC

>Bra040627

MVLTLMVFVILLTFPAPNEAADTNVEAACDPKQLQPCLAAITGGGQPSGDCCA KLKEQQPCLC  
GFSKNPAFAQYISSPNSRKVLTACGIPYPSC

>Bra009282

MEFLKSFTTILFVMFLAMSALETVPMVRAQQCLDNLSNMQVCAPLVLP GAVNPAPNSNCCIALQ  
ATNKDCICNALRAATTFTTTCNLPSLDCGITI

>Bra028294

MVSISSSSKSSTIMKVVMVAVVLVATVVDGQSCNTHLSGLNVCGEFVVP GADTTNPSAEC CN  
ALEAVPSDCICNTFRIASRLPTRCNIPTLSCN

>Bra029135

MIMKVAALVALVLVATEVDGQSCNRHLSGLNVCGEFVVP GADKTNPSAEC CSALEAVPSECLC  
NTMRIASRLPTRCSIPTLSCS

>Bra002906

MDENNTRTIVAALVIVFVSLVLMEEPTSIPLCNINANTLEKCRPAVTGNNPPLPGDACCIVLQAAD  
LECVCKFKSHIPILATKSHKVHDLLRKCGIKTIPPACQDKTKVS

>Bra002907

MGKNNTKILITALVMIVTASMMIEEAKSVRICNVSTKDLKKCRPAVTGNNPPPPTPQCCQLAKAA  
NLECLCPFLSRSGIDPSKIKALGANCGITKNPSCLPW

>Bra002914

MGKNNTKILVTALVMVVTAAMMIEEATSIPICGVNTNDLKKCSPAVTGNNPPPPTPQCCQVAKA  
ANLECLCPYFTRSGLDTAKIKALGTNCGITKKPSCLPW

>Bra020696

MASKKVGVMVMMMMIVVMAIFAERSVAIDLCGMTQSELNECKPAVSKENPTNPSTLCCDYLK  
HADISCLCGYKNSPLLGSFGIDPALAAGLPTKCDMPNAPTC

>Bra020839

MAYVNKVSAAVAILFFAVAVAPLLAEPQTPMFPKMDPVCASLMPNLEKCFSTVRETPTDDCCS  
DLKSATTTQVTCLCDNYIANPAVVNFTGPYSAGITTKCGVFDKYSCNGSSNGT

>Bra022364

MEPNTKLVVITLVLALTLTAATGEFCGMSVSDLYSCKPYVQSKNPVTS AIDPKGPCCTALSKAD  
FQCLCKQKTKTNPFLSSIDL DLASKLPEKCGLSGATC

>Bra028980 (BraNeLTP)

MGKNNTTILIAMVLTTAMIMIEEAKSYPICNTDTNDLQKCSPAVTGNNPPAPGPDCCAVAKSADL  
ECLCPYLSLSGIDPSKIKSVLASCVGGNPSCLSW

>Bra035573

MGKNNTNILTQSTVLAMVLTAAIMVKEVSSLTICKIDINDMQKCRPAVIGINPPPPVNECCVVVRS  
ANLECFCGFKFYLPILGIDPSKVAALVAKCDVTTIPPSCQVSKVLASRSLKNGA

>Bra005153

MKWCKFISVALMSLLITLASVEAAGECGRMPIGQAAASLSPCLAATKNPRGKVPPVCCA KVGAL  
IRTNPRCLCAVMLSPLAKKAGINPGVAIAIPKRCNIRNRPSGKRCGRYIVP

>Bra014853

MASFMKFLCVLGLFLLVGTVDGAGECGRSTPDNEAMKLAPCVGAAQDANA AVPGGCCAQIK  
RFSQNP KCLCAVLLSDTAKASGVQPEVAL TIPKRCNFANRPVGYKCGVLRVQIHGLYDEALEFT  
TTS

>Bra011229 (BraLTP1) (XP\_009127438.1)

MATGSRVLIGLAMILII SGELLVPGQGT CQGDIEGLMRECAVYVQRPGPKVNPSAACCKVVKRS  
DIPCACGRITPSVQKMIDMNKVVLVTSFCGRPLAHGTKCGSKSVIN

>Bra034567

MGSGMITVMVVAIAFFMIGSDNVNMATAQLCGANLSGLVNECQRYVSNAGPNSPPPSRSCCA  
LIRPIDIPCGCRYVTRDVMNTFDMDKLIYVARSCGKKIPSGYKCGSYTIPAA

>Bra034568

MASGRIIIMVVAIAFFMIGSDNVNVATAQFCGANVSGLMNECQRYVSNAGPNSPPPSRSCCALI  
RPIDVPCACRYVSRDVTNYIDMDKVYVARSCGKKIPSGYKCGSYTIPAA

>Bra034570

MASGRIIIIMVVAIAFFMIGSDNVNVATAQFCGANVSGLMNECQRYVSNAGPNSPPPSRSCCALI  
RPIDVPCACRYVSRDVTNYIDMDKVYVARSCGKKIPSGYKCGSYTIPAA

>Bra015984

MEICKFLTVIFVAIVVLYSVQAAEQGGDHHSMACMQKLMPCQNYIHAVNPAPPASCCGPMKEIV  
EKDSKCLCTVFNNPELLKSLNLTKENALDLPKACGVNPDVSICTKTACKFFIIFSTKIPHIYFI

>Bra001252

MILMVLVESGLLKEATAHPCGRTFLSALIELVPCTLSVVPFSTLSPNEPCCTAIKTLGQPCLCVIA  
NGPSIPGVDHTLALQLPGKCSANFPPCN

>Bra006901

MKAMRVGLAMALLMTITVLTIVTAQLEDQQPPPPMLPEEEVGGCSRTFFSALVQLIPCRAAVAP  
FSPPIPTQSCSAVVTLGRPCLCLLANGPPLSGIDRSMALQLPQRCSANFPPCDIIN

>Bra012819

MMMRPMPRVGLAMALLMTITVLTIVIAQQEDQQPPPPMLPVEEVGMCSRTFFSALVQLIPCRAAV  
APFSPIPTESCCSAVVTLGRPCLCLLANGPPLSGIDRSMALQLPQRCFANFPPCDVIN

>Bra000287

MAAKTSTILITIFLVINLLFLNFIPLVVAENTCPRDQLKLSTCANILNLINLNLGAPAMRPCCSVLLG  
LIDLIALCFCSALKLSILGITNTPIHLNLALNACGGTLPDGFRCPT

>Bra018483

MAPRTSLALFLFNLLFFTYTTAAGTTCPRNALQIGACTNVLNALDLTLGNPPPPVPPCCSLIAGLA  
DLEAAVCLCTALDVNVLGNVHLPIDISVLLNACSRFAPPSFQCP

>Bra018544

MAISKAFPLLLVLLLVLNSTFSFCHAVKQCPPPRKQSSMKCPRDTVKFGVCGSWLGLVHEVIGT  
PPSQECCSLVKGLADLEAALCLCTALKTSLLGVAPVKLPVALTLLLNSCGKTLPPQGFVC

>Bra024980

MAYSKIALLLLILNVIFFTLVSSNPVYPYRKPTCKNALKFKVCANVLDLVKVSPLPTRSKCCGLIKGLV  
DLEAAVCLCTALKADLLGLKLNVPISLSVILNHCGKKVPSGFKCA

>Bra024981

MAYSKIALLLLILNVIFFTLVSSNPVYPYRKPTCKNALKFKVCANVLDLVKVSPLPTRSKCCGLIKGLV  
DLEAAVCLCTALKADLLGLKLNVPISLSVILNHCGKKVPSGFKCA

>Bra024982

MAYSKIALLLLILNVIFFTLVSSNPVYPYRKPTCKNALKFKVCANVLDLVKVSPLPTRSKCCGLIKGLV  
DLEAAVCLCTALKADLLGLKLNVPISLSVILNHCGKKVPSGFKCA

>Bra024207

MKIHRAILVTLALIKTAVSQLQSIEQCREVFDSFMPCMGFVEGIFEQPSPQCCRGVSHLNNV  
KFKTPGSRKNEQGTGQLERVCECIEMMGKSDHLPFLASAINNLPPLCSLSLSPISVGMDCSQF  
RNMKELDAEKVN

>Bra040156

MMMMRVAFAMTCMLFAITTADKDRPWPRECLEVANVMVEECKLFFVEQESPTAECCGWF  
SSRREKAKDRRRICRCMEFLTTAFEAIKPSVLALSDQCHFGGGFPISKNHACACKLHSFDQTL

>AtLTP1 (NP\_181388.1)

MAGVMKLACLLACMIVAGPITSNAALSCGSVNSNLAACIGYVLQGGVIPPACCSGVKNLNSIAK  
TTPDRQQACNCIQGAARALGSGLNAGRAAGIPKACGVNIPYKISTSTNCKTVR

>AtLTP2 (NP\_181387.1)

MAGVMKLACMVLACMIVAGPITANALMSCGTVNGNLAGCIAYLTRGAPLTQGCCNGVTNLKNM  
ASTTPDRQQACRCLQSAAKAVGPGLNTARAAGLPSACKVNIPYKISASTNCNTVR

>AtLTP3 (NP\_568905.1)

MAFALRFFTCVLTVCVIVASVDAAISCGTVAGSLAPCATYLSKGGVPPSCCAGVKTLSMAKT  
TPDRQQACRCIQSTAKSISGLNPSLASGLPGKCGVSIPYPIISMSTNCNNIK

>AtLTP4 (NP\_568904.1)

MAFALRFFTCFVLTVFIVASVDAAITCGTVASSLSPCLGYLSKGGVPPPCAGVKKLNGMAQT  
TPDRQQACRCLQSAAKGVNPSLASGLPGKCGVSIPYPISTSTNCATIK

>AtLTP5 (NP\_190728.1)

MEGLLKLSTLVIVCMLVTAPMASEAAISCGAVTGSLGQCYNYLTRGGFIPRGCCSGVQRLNSLA  
RTTRDRQQACRCIQGAARALGSRLNAGRAARLPGACRVRISYPISARTNCNTVR

>AtDIR1 (NP\_568699.1)

MASKKAAMVMMAMIVIMAMLVDTSVAILDCGMSQDELNECKPAVSKENPTSPSQPCCTALQH  
ADFACLCGYKNPWLGSFGVDPELASALPKQCGLANAPTC

>AtAZI1 (NP\_192984.1)

MASKNSASLALFFALNILFFTLTVATNCNCKPSPKPKVPSPKPKVQCPPPPRPSVPSNPRP  
VTPPRTPGSSGNSCIDALKLGVCANVLSLLNIQLGQPSSQQCCSLIQGLVDVDAIICLCTALR  
ANVLGINLNVPISSLVLLNVCNRKLPSGFQCA

>AtAZI7 (NP\_192990.1)

MSMAPKTSTTLALFLVTNILFLNLITLSCADNTCPRDVLKLTCSNVLNINLKLKLGAPAMRPCCSIL  
FGLIDLDAVCLCTALKLSLLGITIDTPIHLNLALNACGGTLPDGFRCPT

>GbTP (ABI26087.1)

MMKISWQLWLLVAFVAVMVCVWTPLSTAAPGCDTVDLAPCISYLQTGTGNPTVQCCSGVKT  
LAGTAQTTEDRKAICECIKTAAIRVKPVANAVKSLPGLCSVTLPPFISIAATDCNKIV

>HvLTP2 (Q43871.1)

MARTAATKLALVALVAAMLLVAADAAITCGQVSSALGPCAAYAKGSGTSPSAGCCSGVKRLAG  
LARSTADKQATCRCLKSVAGAYNAGRAAGIPSRGVSVPYTIASVDCSKIH

>HvLTP4 (Q43875.1)

MARAAATQLVLVAMVAAMLIVATDAAISCGQVSSALSPCISYARGNGAKPPVACCSGVKRLAG  
AAQSTADKQAACKCIKSAAGGLNAGKAAGIPSMCGVSVPYAISASVDCSKIR

>BcMF15 (ABQ63061.1)

MKLISLMCIAFVILLTSFPATAITFNPACIKNHDTGGLVAVKGRWRPECCKIWSGNVLPETRQ  
CACYVLKHSFLGNGVLPLILAKCKLGGIEQFKCEVET

>BcLTP (XP\_009143379.1)

MAGLMKLA<sup>~</sup>CLVLACMIVAGPITSNAALSCGTVSGYVAPCIGYLAQGAPALPRACCSGVTSLNNL  
ARTTPDRQQACRCLVGAANAFPTLNAARAAGLPKACGVNIPYKISKTTNCNSVK

>CaMF2 (AEE92794.1)

MADVKSSVSLFLLGLLVVVLQSGVIECQPQICNPSLTSLNVCAPFVVPGAPSASAECCCTALQSI  
NHGCMCDTMRIAAQIPAQC�LPPLSCAAN

>LILTP (Q9SW93.1)

MARSSAVCFLLLLAFLIGTASAITCGQVDSDLTSCLYARKGGVIPPGCCAGVRTLNNLAKTTPD  
RQTACNCLKSLVNPSLGLNAAIVAGIPGKCGVNIPYPIRMQTD<sup>~</sup>CNKVR

>AceAMP1 (Q41258.1)

MVRVVSLLAASTFILLIMIISPPYANSQNICPRVNRIVTPCVAYGLGRAPIAPCCRALNDLRFVNTR  
NLRRAACRCLVGVNRRNPGLRRNPRFQNI<sup>~</sup>PRDCRNTFVRPFWWRPRIQCGRINLTDKLIYLDA  
EE

>OsC6 (XP\_015615738.1)

MAPSKSTAAAGVLLVLLVAAAGGGAAEAATTCVASLLELSPCLPFFKDKAATAAPEGCCAGLSS  
IVKGEAVCLCHIVNHTLERAIGVDIPVDRAFALLRDVCRLSPADIISTCANEKGGVPPLYSCPAP  
SA

>OsDIL (AAK91879.1)

MSQLKSSSLAALLIFLLAVFTTAAAAAGTECQNDVEVLKTTTCYKFVEKDGPKLQSPDCCTSMK  
GVNVPCVCTYLGSPGVRDNINMDKVFYVTKQCGIAIPGNCGGEQASLDWPH

>MtN5 (XP\_003617674.1)

MAHSQGKALAQWMIGALLFAMLAGSLAVQICNIDPNDLKQSCSKFVTGRNPPRADEACCGVLR  
RANLPCLCGYKSALTYYGINAKKALALPGQCGLQTPSNC

>NtLTP1 (XP\_016433981.1)

MEMVSKIACFVVL<sup>~</sup>CMVVVAPHA<sup>~</sup>EALTCGQVQSSLAPCVPYLLGRGPLGGCCGGVKRLLGAAR  
TPADRKTACNCLKSAANTFKGIDMGNAARLPGTCGVNIPYKISPSTDCSKVQ

>NtLTP2 (Q03461.1)

MEMVGKIACFVVL<sup>~</sup>CMVVVAPHA<sup>~</sup>EALSCGQVQSGLAPCLPYLQGRGPLGSCCGGVKGLLGAAK  
SLSDRKTACTCLKSAANA<sup>~</sup>IKGIDMGKAAGLPGACGVNIPYKISPSTDCSKVQ

>NtnsLTP2-like (XP\_009631888.1)

MEIAGKIACFVVL<sup>~</sup>CMVVAAPCAEAITCGQVTSNLAPCLAYLRNTGPLGRCCGGVKALVNSARTT  
EDRQIACTCLKSAAG<sup>~</sup>AISGINLGKAAGLPSTCGVNIPYKISPSTDCSKVQ

>CaLTPI (AAF23458.1)

MLTDFVRGVD<sup>~</sup>CPHAEAVTCGQIQVGVVNCLPYLQNRGPLGRCCGVIKDLLKCKTPHERRKSC  
KCVKTAANTIKGIDFGKAAGLSGVC<sup>~</sup>GVKIPFEISPSVDCSKVK

>CaLTPII (AAF23459.1)

MDMFGKIACFVLL<sup>~</sup>CMVVVAPSAEALSCS<sup>~</sup>QVTSGLAPCLPYLQGRGPLGGCCSGVKDLLAAAKT  
PADRKTACTCMKSTANSIKGIDAGKAASIPATCGVNIPYKISPSTDC<sup>~</sup>TKVE



**Supplementary Table 3 – Oligonucleotides used in this study**

<b>Primer name</b>	<b>Primer Sequence (5'→3')</b>	<b>Used For</b>
pMDC85 LTP XbaI F	AAA AAA TCT AGA ATG GGT AAG AAC AAT ACC ACA	Cloning into pMDC85
pMDC85 LTP AscI R	AAA AAA GGC GCG CC T CAG GAG GGA TTG CCC ACG CC	Cloning into pMDC85
neLTP pET21a-F BamHI	AAA GGA TCC TAT CCT ATA TGC AAC AC	Cloning into pET21a(+)
neLTP pET21a-R XhoI	AAA CTC GAG TGA CAA ACA GGA GGG AT	Cloning into pET21a(+)